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Original Articles

Recovery and functional validation of hidden soil enzymes in metagenomic libraries
Dayana Calderon, Luis Peña, Angélica Suarez, Carolina Villamil, Adan Ramirez-Rojas, Juan M. Anzola, Juan C. García-Betancur, Martha L. Cepeda, Daniel Uribe, Patricia Del Portillo, Alvaro Mongui

The stress hormone norepinephrine increases the growth and virulence of Aeromonas hydrophila
Jinwei Gao, Bingwen Xi, Kai Chen, Rui Song, Ting Qin, Jun Xie, Liangkun Pan

Staphylococcus argenteus from rabbits in Thailand
Nitaya Indrawattana, Natapol Pumipuntu, Nawarat Suriyakhun, Arunee Jangsangthong, Suphang Kulpeanprasit, Narisara Chanratita, Nitat Sookrung, Wanpen Chaicumpa, Shutipen Buranasinsup

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Bacteroides fragilis requires the ferrous-iron transporter FeoAB and the CobN-like proteins BtuS1 and BtuS2 for assimilation of iron released from heme
Edson R. Rocha, Hector A. Bergonia, Svetlana Gerdes, Charles Jeffrey Smith

Gut microbial diversity in two insectivorous bats: Insights into the effect of different sampling sources
Haonan Wu, Yutong Xing, Haijian Sun, Xiuguang Mao

Genome-wide screening of potential RNase Y-processed mRNAs in the M49 serotype Streptococcus pyogenes NZ131
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Succession of embryonic and the intestinal bacterial communities of Atlantic salmon (Salmo salar) reveals stage-specific microbial signatures
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High-production dairy cattle exhibit different rumen and fecal bacterial community and rumen metabolite profile than low-production cattle
Yingyu Mu, Xueyan Lin, Zhonghua Wang, Qiuling Hou, Yun Wang, Zhiyong Hu

Wolbachia pipientis grows in Saccharomyces cerevisiae evoking early death of the host and deregulation of mitochondrial metabolism
Cristina Uribe-Alvarez, Natalia Chiquete-Félix, Lilia Morales-Garcia, Arlette Bohórquez-Hernández, Norma Laura Delgado-Buenrostro, Luis Vaca, Antonio Peña, Salvador Uribe-Carvajal

Tillage intensity and pasture in rotation effectively shape soil microbial communities at a landscape scale
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Altered gut microbiota and microbial biomarkers associated with chronic kidney disease
Hengzhong Lun, Weihua Yang, Shuping Zhao, Meijie Jiang, Mingjie Xu, Fenfen Liu, Yunshan Wang

The spectrum of intraoral bacteria seen in patients with cleft palates in an African setting
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Elongation factor P controls translation of the mgtA gene encoding a Mg^{2+} transporter during Salmonella infection
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Do composition and diversity of bacterial communities and abiotic conditions of spring water reflect characteristics of groundwater ecosystems exposed to different agricultural activities?
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Mcr colistin resistance gene: a systematic review of current diagnostics and detection methods
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Antimicrobial efficacy of alternative compounds for use in oral care toward biofilms from caries-associated bacteria in vitro
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Comparative analysis of early immune responses induced by two strains of Newcastle disease virus in chickens

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Community composition of arbuscular mycorrhizal fungi associated with native plants growing in a petroleum-polluted soil of the Amazon region of Ecuador

Mónica Garcés-Ruiz, Carolina Senés-Guerrero, Stéphane Declerck, Sylvie Cranenbrouck

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