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Publications (2)

Akhlaghpour M, Haritunians T, More S, Thomas L, Stamps D, Dube S, Li D, Yang S, Landers C, Mengesha E, Hamade H, Murali R, Potdar A, Wolf A, Botwin G, Khrom M, International IBD Genetics Consortium, Ananthakrishnan A, Faubion W, Jabri B, Lira S, Newberry R, Sandler R, Sartor R, Xavier R, Brant S, Cho J, Duerr R, Lazarev M, Rioux J, Schumm L, Silverberg M, Zoghiyan K, Fleshner P, Melmed G, Vasiliauskas E, Ha C, Rabizadeh S, Syal G, Bonthala N, Ziring D, Targan S, Long M, McGovern D, Michelsen K, Brand S. Genetic coding variant in complement factor B (CFB) is associated with increased risk for perianal Crohn's disease and leads to impaired CFB cleavage and phagocytosis. *Gut* 2023; 72:2068-2080.

Li D, Devlin B, Sharma Y, Torkvist L, Targan S, Stempak J, Simms L, Regueiro M, Proctor D, Borneman J, Hakonarson H, McGovern D, Braun J, Cho J, Silverberg M, Rioux J, Brant S, Daly M, Xavier R, Milgrom R, Glas J, Halfvarson J, Radford-Smith G, Brand S, D'Amato M, Hui K, Jacobs J, Haritunians T, Achkar J, Niess J, Kugathasan S, Fiocchi C, Dubinsky M, Baidoo L, Aumais G, Ananthakrishnan A, Klei L, Schumm L, Büning C, Duerr R. A Pleiotropic Missense Variant in SLC39A8 Is Associated With Crohn's Disease and Human Gut Microbiome Composition. *Gastroenterology* 2016; 151:724-32.

Projects (0)

No results found.

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