



Mark S Silverberg

Kontakt

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Publikationen (7)

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, Ananthkrishnan 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, Zaghiyan 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, Ananthkrishnan 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.

Lees C, van der Meulen-de Jong A, Theatre E, Schreiber S, Satsangi J, Lee J, Lawrance I, Kupcinkas L, Kennedy N, Weersma R, Wilson D, Barrett J, McGovern D, Radford-Smith G, Silverberg M, Mansfield J, Rioux J, Vermeire S, Parkes M, Huang H, Hov J, Halfvarson J, Annese V, Andrews J, Andersen V, Ahmad T, Zeissig S, Schumm L, Jostins L, Boucher G, Brand S, Brant S, Cho J, Hakonarson H, Goyette P, Geary R, Franke A, Ferguson L, Duerr R, Dubinsky M, Daly M, Cleyne I. Inherited determinants of Crohn's disease and ulcerative colitis phenotypes: a genetic association study. *Lancet* 2015; 387:156-67.

Thomsen I, Vatn M, Silverberg M, Duerr R, Padyukov L, Brand S, Sans M, Annese V, Achkar J, Melum E, Durie P, Sandford R, Mayr G, König I, Hveem K, Cleyne I, Gutierrez-Achury J, Ricaño-Ponce I, van Heel D, Björnsson E, Boberg K, Marschall H, Schreiber S, Manns M, Färkkilä M, Dale A, Chapman R, Lazaridis K, Franke A, Anderson C, Cho J, Bergquist A, Alexander G, Chazouillères O, Bowlus C, Wijmenga C, Schrupf E, Vermeire S, Albrecht M, Rioux J, Karlsen T, Næss S, Liu J, Gotthardt D, Pares A, Ellinghaus D, Shah T, Juran B, Milkiewicz P, Rust C, Schramm C, Hirschfeld G, Invernizzi P, Eksteen B, Hov J, Folseraas T, Ellinghaus E, Rushbrook S, Doncheva N, Andreassen O, Weersma R, Weismüller T, Müller T, Srivastava B, Saarela J, Leppä V, Dorfman R, Alvaro D, Floreani A, Onengut-Gumuscu S, Rich S, Thompson W, Mason A, Teufel A, Sterneck M, Dalekos G, Nöthen M, Herms S, Winkelmann J, Mitrovic M, Braun F, Ponsioen C, Croucher P, Schork A. Dense genotyping of immune-related disease regions identifies nine new risk loci for primary sclerosing cholangitis. *Nat Genet* 2013; 45:670-5.

Kupcinkas L, Potocnik U, Prescott N, Regueiro M, Rotter J, Russell R, Sanderson J, Sans M, Satsangi J, Schreiber S, Simms L, Sventoraityte J, Ponsioen C, Palmieri O, Kugathasan S, Latiano A, Laukens D, Lawrance I, Lees C, Louis E, Mahy G, Mansfield J, Morgan A, Mowat C, Newman W, Targan S, Taylor K, Tremelling M, Hakonarson H, Brant S, Radford-Smith G, Mathew C, Rioux J, Schadt E, Daly M, Franke A, Parkes M, Vermeire S, Barrett J, Annese V, Silverberg M, Verspaget H, De Vos M, Wijmenga C, Wilson D, Winkelmann J, Xavier R, Zeissig S, Zhang B, Zhang C, Zhao H, Cho J, Karlsen T, Jostins L, Theatre E, Spain S, Raychaudhuri S, Goyette P, Wei Z, Abraham C, Achkar J, Ahmad T, Amininejad L, Ananthkrishnan A, Andersen V, Cleyne I, Ning K, Ripke S, Weersma R, Duerr R, McGovern D, Hui K, Lee J, Schumm L, Sharma Y, Anderson C, Essers J, Mitrovic M, Andrews J, Baidoo L, Balschun T, Ferguson L, Franchimont D, Fransen K, Geary R, Georges M, Gieger C, Glas J, Haritunians T, Hart A, Hawkey C, Hedl M, Ellinghaus D, Edwards C, Bampton P, Bitton A, Boucher G, Brand S, Büning C, Cohain A, Cichon S, D'Amato M, De Jong D, Devaney K, Dubinsky M, Hu X. Host-microbe interactions have shaped the genetic architecture of inflammatory bowel disease. *Nature* 2012; 491:119-24.

Phillips A, van den Berg L, Vatn M, Verspaget H, Walters T, Wijmenga C, Wilson D, Westra H, Xavier R, Zhao Z, Ponsioen C, Andersen V, Torkvist L, Targan S, Steinhart A, Prescott N, Proctor D, Roberts R, Russell R, Rutgeerts P, Sanderson J, Sans M, Schumm P, Seibold F, Sharma Y, Simms L, Seielstad M, Gazouli M, Anagnou N, Satsangi J, Cho J, Schreiber S, Daly M, Barrett J, Parkes M, Annesse V, Hakonarson H, Radford-Smith G, Duerr R, Vermeire S, Weersma R, Chamaillard M, Brant S, Karlsen T, Kupcinskis L, Sventoraityte J, Mansfield J, Kugathasan S, Silverberg M, Halfvarson J, Rotter J, Mathew C, Griffiths A, Geary R, Ahmad T, Rioux J, Panés J, Anderson C, Baldassano R, Barclay M, Bayless T, Brand S, Büning C, Colombel J, Denson L, De Vos M, Dubinsky M, Edwards C, Ellinghaus D, Fehrmann R, Baidoo L, Bumpstead S, Boucher G, Lees C, Franke A, D'Amato M, Taylor K, Lee J, Goyette P, Imielinski M, Latiano A, Lagacé C, Scott R, Amininejad L, Floyd J, Florin T, Libioulle C, Louis E, McGovern D, Milla M, Montgomery G, Morley K, Mowat C, Ng A, Newman W, Ophoff R, Papi L, Palmieri O, Levine A, Lemann M, Franchimont D, Franke L, Georges M, Glas J, Glazer N, Guthery S, Haritunians T, Hayward N, Hugot J, Jobin G, Laukens D, Lawrance I, Peyrin-Biroulet L. Meta-analysis identifies 29 additional ulcerative colitis risk loci, increasing the number of confirmed associations to 47. *Nat Genet* 2011; 43:246–52.

Glas J, Mowat C, Newman W, Panés J, Phillips A, Proctor D, Regueiro M, Russell R, Rutgeerts P, Sanderson J, Sans M, Louis E, Libioulle C, Van Gossum A, Guthery S, Halfvarson J, Verspaget H, Hugot J, Karban A, Laukens D, Lawrance I, Lemann M, Levine A, Seibold F, Steinhart A, Mansfield J, Vermeire S, Duerr R, Silverberg M, Satsangi J, Schreiber S, Cho J, Annesse V, Hakonarson H, Daly M, Griffiths A, Kugathasan S, Stokkers P, Torkvist L, Kullak-Ublick G, Wilson D, Walters T, Targan S, Brant S, Rioux J, D'Amato M, Weersma R, Parkes M, Franke A, Ellinghaus D, Festen E, Georges M, Green T, Haritunians T, Jostins L, Latiano A, Mathew C, Montgomery G, Prescott N, Bumpstead S, Bis J, McGovern D, Barrett J, Wang K, Radford-Smith G, Ahmad T, Lees C, Balschun T, Lee J, Roberts R, Anderson C, Raychaudhuri S, Rotter J, Colombel J, Cottone M, Stronati L, Denson T, De Vos M, D'Inca R, Dubinsky M, Edwards C, Florin T, Franchimont D, Cohen A, Büning C, Schumm P, Sharma Y, Simms L, Taylor K, Whiteman D, Wijmenga C, Baldassano R, Barclay M, Bayless T, Brand S, Geary R. Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci. *Nat Genet* 2010; 42:1118–25.

Projekte (0)

Keine Resultate gefunden.

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