



Severine Vermeire

Kontakt

Severine Vermeire

Publikationen (7)

Momozawa Y, Hoentjen F, Löwenberg M, Oldenburg B, Pierik M, Vander Meulen-de Jong A, Janneke van der Woude C, Visschedijk M, International IBD Genetics Consortium, Lathrop M, Hugot J, Weersma R, De Vos M, Franchimont D, Vermeire S, Kubo M, Louis E, Bouma G, Amininejad L, Dmitrieva J, Theatre E, Deffontaine V, Rahmouni S, Charlotheaux B, Crins F, Docampo E, Elansary M, Gori A, Lecut C, Mariman R, Mni M, Oury C, Altukhov I, Alexeev D, Aulchenko Y, Georges M. IBD risk loci are enriched in multigenic regulatory modules encompassing putative causative genes. *Nat Commun* 2018; 9:2427.

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.

Franke A, Büning C, Duerr R, Nöthen M, Wang J, Vatn M, Mathew C, Sanderson J, Rutgeerts P, Vermeire S, McArdle W, Strachan D, Wijmenga C, Sans M, Brand S, Glas J, Parkes M, Schreiber S, Rosenstiel P, Subramani S, Karlsen T, Nothnagel M, Daly M, D'Amato M, Halfvarson J, Annese V, Latiano A, Illig T, Winkelmann J, Ponsioen C, Weersma R, Nikolaus S, Liu X, Doncheva N, Skieceviciene J, Rivas M, Keller A, Ellinghaus E, Bromberg Y, Stade B, Jiang T, Till A, Lipinski S, Zeissig S, Zhang H, Liu Q, Jiang F, Krawczak M, Kayser M, Kupcinkas L, Vogel U, Andersen V, Lee J, Berzuini C, Goodall J, Boehm B, Häslér R, Albrecht M, Mayr G, Forster M, Ellinghaus D. Association between variants of PRDM1 and NDP52 and Crohn's disease, based on exome sequencing and functional studies. *Gastroenterology* 2013; 145:339-47.

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, Følseraas 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, Ananthakrishnan 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.

Kantonsspital St.Gallen

Rorschacher Strasse 95

CH-9007 St.Gallen

T: +41 71 494 11 11

support.forschung@kssg.ch