



**Mauro D'Amato**

**Contact**

Mauro D'Amato

## Publications (5)

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, Focchi 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.

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, Häsler 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.

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, Bittton 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, Annese V, Hakonarson H, Radford-Smith G, Duerr R, Vermeire S, Weersma R, Chamailard M, Brant S, Karlsen T, Kupcinkas 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, Annese 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.

## Projects (0)

No results found.

---

Kantonsspital St.Gallen

Rorschacher Strasse 95

CH-9007 St.Gallen

T: +41 71 494 11 11

[support.forschung@kssg.ch](mailto:support.forschung@kssg.ch)