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Publications (3)

Rahmioglu N, Mortlock S, Ghiasi M, Møller P, Stefansdottir L, Galarneau G, Turman C, Danning R, Law M, Sapkota Y, Christofidou P, Sarp S, Giri A, Banasik K, Krassowski M, Lepamets M, Marciniak B, Nõukas M, Perro D, Sliz E, Sobalska-Kwapis M, Thorleifsson G, Topbas-Selcuki N, Vitonis A, Westergaard D, Arnadottir R, Burgdorf K, Campbell A, Cheuk C, Clementi C, Cook J, De Vivo I, DiVasta A, Dorien O, Donoghue J, Edwards T, Fontanillas P, Fung J, Geirsson R, Girling J, Harkki P, Harris H, Healey M, Heikinheimo O, Holdsworth-Carson S, Hostettler I, Houlden H, Houshdaran S, Irwin J, Jarvelin M, Kamatani Y, Kennedy S, Kepka E, Kettunen J, Kubo M, Kulig B, Kurra V, Laivuori H, Laufer M, Lindgren C, MacGregor S, Mangino M, Martin N, Matalliotaki C, Matalliotakis M, Murray A, Ndungu A, Nezhat C, Olsen C, Opoku-Anane J, Padmanabhan S, Paranjpe M, Peters M, Polak G, Porteous D, Rabban J, Rexrode K, Romanowicz H, Saare M, Saavalainen L, Schork A, Sen S, Shafrir A, Siewierska-Górska A, Słomka M, Smith B, Smolarz B, Szaflik T, Szyłł K, Takahashi A, Terry K, Tomassetti C, Treloar S, Vanhie A, Vincent K, Vo K, Werring D, Zeggini E, Zervou M, DBDS Genomic Consortium, FinnGen Study, FinnGen Endometriosis Taskforce, Celmatix Research Team, 23andMe Research Team, Adachi S, Buring J, Ridker P, D'Hooghe T, Goulielmos G, Hapangama D, Hayward C, Horne A, Low S, Martikainen H, Chasman D, Rogers P, Saunders P, Sirotta M, Spector T, Strapagiel D, Tung J, Whiteman D, Giudice L, Velez Edwards D, Uimari O, Kraft P, Salumets A, Nyholt D, Mägi R, Stefansson K, Becker C, Yurttas-Beim P, Steinhorsdottir V, Nyegaard M, Missmer S, Montgomery G, Morris A, Zondervan K. The genetic basis of endometriosis and comorbidity with other pain and inflammatory conditions. *Nat Genet* 2023; 55:423-436.

van Rheenen W, van der Spek R, Bakker M, Van Vugt J, Hop P, Zwamborn R, de Klein N, Westra H, Bakker O, Deelen P, Shireby G, Hannon E, Moisse M, Baird D, Restuadi R, Dolzhenko E, Dekker A, Gawor K, Westeneng H, Tazelaar G, van Eijk K, Kooyman M, Byrne R, Doherty M, Heverin M, Al Khleifat A, Iacoangeli A, Shatunov A, Ticozzi N, Cooper-Knock J, Smith B, Gromicho M, Chandran S, Pal S, Morrison K, Shaw P, Hardy J, Orrell R, Sendtner M, Meyer T, Başak N, van der Kooi A, Ratti A, Fogh I, Gellera C, Lauria G, Corti S, Cereda C, Sproviero D, D'Alfonso S, Sorarù G, Siciliano G, Filosto M, Padovani A, Chio A, Calvo A, Moglia C, Brunetti M, Canosa A, Grassano M, Beghi E, Pupillo E, Logroscino G, Nefussy B, Osmanovic A, Nordin A, Lerner Y, Zabari M, Gotkine M, Baloh R, Bell S, Vourc'h P, Corcia P, Couratier P, Millecamps S, Meininger V, Salachas F, Mora Pardina J, Assialioui A, Rojas-García R, Dion P, Ross J, Ludolph A, Weishaupt J, Brenner D, Freischmidt A, Bensimon G, Brice A, Dürr A, Payan C, Saker-Delye S, Wood N, Topp S, Rademakers R, Tittmann L, Lieb W, Franke A, Ripke S, Braun A, Kraft J, Whiteman D, Olsen C, Uitterlinden A, Hofman A, Rietschel M, Cichon S, Nöthen M, Amouyel P, SLALOM Consortium, PARALS Consortium, SLAGEN Consortium, SLAP Consortium, Traynor B, Singleton A, Mitne Neto M, Cauchi R, Ophoff R, Wiedau-Pazos M, Lomen-Hoerth C, Van Deerlin V, Grosskreutz J, Roediger A, Gaur N, Jörk A, Barthel T, Theele E, Ilse B, Stubendorff B, Witte O, Steinbach R, Hübner C, Graff C, Brylev L, Fominykh V, Demeshonok V, Ataulina A, Rogelj B, Koritnik B, Zidar J, Ravnik-Glavač M, Glavač D, Stević Z, Drory V, Povedano M, Blair I, Kiernan M, Benyamin B, Henderson R, Furlong S, Mathers S, McCombe P, Needham M, Ngo S, Nicholson G, Pamphlett R, Rowe D, Steyn F, Williams K, Mather K, Sachdev P, Henders A, Wallace L, de Carvalho M, Pinto S, Petri S, Weber M, Rouleau G, Silani V, Curtis C, Breen G, Glass J, Brown R, Landers J, Shaw C, Andersen P, Groen E, van Es M, Pasterkamp R, Fan D, Garton F, McRae A, Davey Smith G, Gaunt T, Eberle M, Mill J, McLaughlin R, Hardiman O, Kenna K, Wray N, Tsai E, Runz H, Franke L, Al-Chalabi A, Van Damme P, van den Berg L, Veldink J. Author Correction: Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. *Nat Genet* 2022; 54:361.

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Projects (0)

No results found.

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