



Gerome Breen

Kontakt

Gerome Breen

Publikationen (8)

Adey B, Cooper-Knock J, Al Khleifat A, Fogh I, Van Damme P, Corcia P, Couratier P, Hardiman O, McLaughlin R, Gotkine M, Drory V, Silani V, Ticozzi N, Veldink J, van den Berg L, de Carvalho M, Pinto S, Mora J, Povedano Panades M, Andersen P, Weber M, Bařak N, Shaw C, Openshaw P, Morrison K, Landers J, Glass J, Vourc'h P, Dobson R, Breen G, Al-Chalabi A, Jones A, Iacoangeli A. Large-scale analyses of CAV1 and CAV2 suggest their expression is higher in post-mortem ALS brain tissue and affects survival. *Front Cell Neurosci* 2023; 17:1112405.

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, Bařak 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.

van Rheenen W, van der Spek R, Bakker M, Farei-Campagna 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, Openshaw P, Hardy J, Orrell R, Sendtner M, Meyer T, Bařak 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 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, Klein-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. Common and rare variant association analyses in amyotrophic lateral sclerosis identify 15 risk loci with distinct genetic architectures and neuron-specific biology. *Nat Genet* 2021; 53:1636-1648.

Ruigrok Y, Sargurupremraj M, Dichgans M, Malik R, Klijn C, Zaroff J, Breen G, Coleman J, Kim H, Ko N, Bown M, Jones G, Martin O, Dauvillier J, Schilling S, Hirsch S, Tatlisumak T, Amouyel P, Debette S, Veldink J, Kamatani Y, Bijlenga P, Redon R, Woo D, Werring D, Broderick J, Lindgren A, von Und Zu Fraunberg M, Jaaskelainen J, Niemelä M, Gaal-Paavola E, Slowik A, Pera J, Worrall B, Rinkel G, Friedrich C, Verschuren W, Zwart J, Chen Z, Millwood I, Liang L, Lin K, Walters R, Matsuda K, Terao C, Akiyama M, Koido M, van Eijk K, Alg V, Hostettler I, Bourcier R, Morel S, van Rheenen W, van der Spek R, Rouleau G, Zhou S, Rannikmäe K, Hveem K, Willer C, Sandvei M, Brumpton B, Johnsen M, Børte S, Winsvold B, Desal H, Eugène F, Shotar E, Gentric J, Naggara O, Dina C, van den Berg L, Houlden H, Sudlow C, Bakker M. Author Correction: Genome-wide association study of intracranial aneurysms identifies 17 risk loci and genetic overlap with clinical risk factors. *Nat Genet* 2021; 53:254.

Ruigrok Y, Sargurupremraj M, Dichgans M, Malik R, Klijn C, Zaroff J, Breen G, Coleman J, Kim H, Ko N, Bown M, Jones G, Martin O, Dauvillier J, Schilling S, Hirsch S, Tatlisumak T, Amouyel P, Debette S, Veldink J, Kamatani Y, Bijlenga P, Redon R, Woo D, Werring D, Broderick J, Lindgren A, von Und Zu Fraunberg M, Jaaskelainen J, Niemelä M, Gaal-Paavola E, Slowik A, Pera J, Worrall B, Rinkel G, Friedrich C, Verschuren W, Zwart J, Chen Z, Millwood I, Liang L, Lin K, Walters R, Matsuda K, Terao C, Akiyama M, Koido M, van Eijk K, Alg V, Hostettler I, Bourcier R, Morel S, van Rheenen W, van der Spek R, Rouleau G, Zhou S, Rannikmäe K, Hveem K, Willer C, Sandvei M, Brumpton B, Johnsen M, Børte S, Winsvold B, Desal H, Eugène F, Shotar E, Gentric J, Naggara O, Dina C, van den Berg L, Houlden H, Sudlow C, Bakker M. Genome-wide association study of intracranial aneurysms identifies 17 risk loci and genetic overlap with clinical risk factors. *Nat Genet* 2020; 52:1303–1313.

Packard C, Pers T, Person T, Peters A, Petersen E, Peyser P, Pirie A, Polasek O, Polderman T, Puolijoki H, Raitakari O, Perry J, Perry J, Perola M, Padmanabhan S, Palmer C, Palmer N, Pasterkamp G, Patel A, Pattie A, Pedersen O, Peissig P, Peloso G, Pennell C, Rasheed A, Rauramaa R, Reilly D, Samani N, Sapkota Y, Sattar N, Schoen R, Schreiner P, Schulze M, Scott R, Segura-Lepe M, Shah S, Sheu W, Salomaa V, Saleheen D, Ruth K, Renström F, Rheinberger M, Ridker P, Rioux J, Rivas M, Roberts D, Robertson N, Robino A, Rolandsson O, Rudan I, Sim X, Lin K, Lubitz S, Lyytikäinen L, Männistö S, Marenne G, Mazul A, McCarthy M, McKean-Cowdin R, Medland S, Meidtner K, Milani L, Luan J, Loukola A, Lotery A, Lin L, Lin X, Lind L, Lindström J, Linneberg A, Liu C, Liu D, Liu Y, Lo K, Lophatananon A, Mistry V, Mitchell P, Mohlke K, Neville M, Nielsen S, Nikus K, Njølstad P, Nordestgaard B, Nyholt D, O'Connell J, O'Donoghue M, Olde Loohuis L, Ophoff R, Nelson C, Narisu N, Nalls M, Moilanen L, Moitry M, Montgomery G, Mook-Kanamori D, Moore C, Mori T, Morris A, Müller-Nurasyid M, Munroe P, Owen K, Slater A, Walker M, Witte D, Wood A, Wu Y, Yaghoobkar H, Yao J, Yao P, Yerges-Armstrong L, Young R, Zeggini E, Zhan X, Wilson J, Willer C, White H, Wallentin L, Wang F, Wang C, Wang S, Wang Y, Ware E, Wareham N, Warren H, Waterworth D, Wessel J, Zhang W, Zhao J, Zhao W, CHD Exome+ Consortium, EPIC-CVD Consortium, ExomeBP Consortium, Global Lipids Genetic Consortium, GoT2D Genes Consortium, EPIC InterAct Consortium, INTERVAL Study, ReproGen Consortium, T2D-Genes Consortium, MAGIC Investigators, Loos R, Hirschhorn J, Lindgren C, Zhou W, Zondervan K, Rotter J, Pospisilik J, Rivadeneira F, Borecki I, Deloukas P, Frayling T, Lettre G, North K, Understanding Society Scientific Group, Small K, Swift A, Tada H, Tansey K, Tardif J, Taylor K, Teumer A, Thompson D, Thorleifsson G, Thorsteinsdottir U, Thuesen B, Surendran P, Sun L, Stumvoll M, Smith A, Southam L, Spector T, Speliotes E, Starr J, Stefansson K, Steinthorsdottir V, Stirrups K, Strauch K, Stringham H, Tönjes A, Tromp G, Trompet S, Varga T, Varma R, Velez Edwards D, Vermeulen S, Veronesi G, Vestergaard H, Vitart V, Vogt T, Völker U, Vuckovic D, Varbo A, Vanhala M, van Setten J, Tsaftakias E, Tuomilehto J, Tybjaerg-Hansen A, Tyrer J, Uher R, Uitterlinden A, Uusitupa M, Laan S, Duijn C, Leeuwen N, Wagenknecht L, Lin H, Bots M, Caulfield M, Chambers J, Chasman D, Chen Y, Chowdhury R, Christensen C, Chu A, Cocca M, Collins F, Cook J, Catamo E, Carey D, Cappellani S, Bottinger E, Bowden D, Brandslund I, Breen G, Brilliant M, Broer L, Brumat M, Burt A, Butterworth A, Campbell P, Corley J, Corominas Galbany J, Cox A, Ruijter H, Dennis J, Denny J, Di Angelantonio E, Drenos F, Du M, Dubé M, Dunning A, Easton D, Edwards T, Hollander A, Heijer M, Demerath E, Crosslin D, Cuellar-Partida G, D'Eustacchio A, Danesh J, Davies G, Bakker P, Groot M, Mutsert R, Deary I, Dedoussis G, Ellinghaus D, Turcot V, Locke A, Mahajan A, Marouli E, Sivapalaratnam S, Young K, Alfred T, Feitosa M, Masca N, Manning A, Medina-Gomez C, Lempradl A, Karaderi T, Hendricks A, Lu Y, Highland H, Schurmann C, Justice A, Fine R, Bradfield J, Esko T, Giri A, Graff M, Guo X, Mudgal P, Ng M, Reiner A, Barroso I, Bastarache L, Bønn M, Bergmann S, Bielak L, Blüher M, Boehnke M, Boeing H, Boerwinkle E, Böger C, Bang L, Balkau B, Auer P, Vedantam S, Willems S, Winkler T, Abecasis G, Aben K, Alam D, Alharthi S, Allison M, Amouyel P, Asselbergs F, Bork-Jensen J, Ellinor P, Howson J, Jukema J, Kahali B, Kahn R, Kähönen M, Kamstrup P, Kanoni S, Kaprio J, Karaleftheri M, Kardia S, Karpe F, Jørgensen T, Jørgensen M, Johansson S, Hu Y, Huang P, Huffman J, Ikram M, Ingelsson E, Jackson A, Jansson J, Jarvik G, Jensen G, Jia Y, Kathiresan S, Kee F, Kiemeny L, Lamparter D, Lange E, Lange L, Langenberg C, Larson E, Lee N, Lehtimäki T, Lewis C, Li H, Li J, Lakka T, Laakso M, Kuusisto J, Kim E, Kitajima H, Komulainen P, Kooner J, Kooperberg C, Korhonen T, Kovacs P, Kuivaniemi H, Kutalik Z, Kuulasmaa K, Li-Gao R, Elliott P, Franks P, Friedrich N, Frikke-Schmidt R, Galesloot T, Gan W, Gandin I, Gasparini P, Gibson J, Giedraitis V, Gjesing A, Franke A, Franco O, Fornage M, Evangelou E, Farmaki A, Farooqi I, Faul J, Fauser S, Feng S, Ferrannini E, Ferrieres J, Florez J, Ford I, Gordon-Larsen P, Gorski M, Grabe H, Have C, Hayward C, He L, Heard-Costa N, Heath A, Heid I, Helgeland Ø, Hernessniemi J, Hewitt A, Holmen O, Hattersley A, Harris T, Harris K, Grant S, Grarup N, Griffiths H, Grove M, Gudnason V, Gustafsson S, Haessler J, Hakonarson H, Hammerschlag A, Hansen T, Hovingh G. Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nat Genet* 2017; 50:26–41.

Ntalla I, Peissig P, Peloso G, Pennell C, Perola M, Perry J, Perry J, Person T, Pirie A, Polasek O, Pedersen O, Pattie A, Patel A, O'Connel J, Oksa H, Loohuis L, Ophoff R, Owen K, Packard C, Padmanabhan S, Palmer C, Pasterkamp G, Posthuma D, Raitakari O, Saleheen D, Salomaa V, Samani N, Sandow K, Sapkota Y, Sattar N, Schmidt M, Schreiner P, Schulze M, Ruth K, Rudan I, Rolandsson O, Rasheed A, Rauramaa R, Reilly D, Reiner A, Renström F, Ridker P, Rioux J, Robertson N, Robino A, Scott R, Nordestgaard B, Langefeld C, Lindström J, Linneberg A, Liu Y, Liu Y, Lophatananon A, Luan J, Lubitz S, Lyytikäinen L, Mackey D, Lind L, Lin X, Lin L, Langenberg C, Larson E, Lee I, Lehtimäki T, Lewis C, Li H, Li J, Li-Gao R, Lin H, Madden P, Manning A, Morris A, Müller-Nurasyid M, Munroe P, Nalls M, Nauck M, Nelson C, Neville M, Nielsen S, Nikus K, Morris A, Morgan A, Mook-Kanamori D, Männistö S, Marenne G, Marten J, Martin N, Mazul A, Meidtner K, Metspalu A, Mitchell P, Mohlke K, Njølstad P, Walker M, Yaghoobkar H, Yao J, Yao P, Yerges-Armstrong L, Young R, Zeggini E, Zhan X, Zhang W, Zhao J, Wu Y, Woods M, Witte D, Wang F, Wang C, Wang S, Wang Y, Wareham N, Warren H, Wessel J, Willems S, Wilson J, Zhao W, Zheng H, Pers T, Lindgren C, Oxvig C, Kutalik Z, Rivadeneira F, Loos R, Frayling T, Hirschhorn J, Deloukas P, Heard-Costa N, North K, Liu D, Zhou W, Rotter J, Boehnke M, Kathiresan S, McCarthy M, Willer C, Stefansson K, Borecki I, Lettre G, Vozzi D, Segura-Lepe M, Stumvoll M, Surendran P, 't Hart L, Tansey K, Tardif J, Taylor K, Teumer A, Thompson D, Thorsteinsdóttir U, Stringham H, Steinthorsdóttir V, Starr J, Shah S, Sim X, Sivapalaratnam S, Small K, Smith A, Smith J, Southam L, Spector T, Speliotes E, Thuesen B, Tönjes A, van Schoor N, van Setten J, Varbo A, Varga T, Varma R, Edwards D, Vermeulen S, Vestergaard H, Vitart V, van Duijn C, Van Der Leij A, van der Laan S, Tromp G, Trompet S, Tsafantakis E, Tuomilehto J, Tybjaerg-Hansen A, Tyrer J, Uher R, Uitterlinden A, Ulivi S, Vogt T, Boeing H, Butterworth A, Carey D, Caulfield M, Chambers J, Chasman D, Chen Y, Chowdhury R, Christensen C, Chu A, Burt A, Broer L, Brilliant M, Boerwinkle E, Böger C, Bonnycastle L, Bork-Jensen J, Bots M, Bottinger E, Bowden D, Brandslund I, Breen G, Cocca M, Collins F, Deary I, Dedoussis G, Demerath E, den Hollander A, Dennis J, Di Angelantonio E, Drenos F, Du M, Dunning A, de Mutsert R, de Groot M, de Genus S, Cook J, Corley J, Galbani J, Cox A, Cuellar-Partida G, Danesh J, Davies G, de Bakker P, de Borst G, Easton D, Blüher M, Marouli E, Lamparter D, Stirrups K, Turcot V, Young K, Winkler T, Esko T, Karaderi T, Locke A, Masca N, Justice A, Thorleifsson G, Rüeger S, Graff M, Medina-Gomez C, Lo K, Wood A, Kjaer T, Fine R, Lu Y, Schurmann C, Highland H, Ng M, Mudgal P, Appel E, Arveiler D, Asselbergs F, Auer P, Balkau B, Banas B, Bang L, Benn M, Bergmann S, Amouyel P, Allison M, Allin K, Rivas M, Vedantam S, Mahajan A, Guo X, Abecasis G, Aben K, Adair L, Alam D, Albrecht E, Bielak L, Hoynig C, Jørgensen M, Jørgensen T, Jousilahti P, Jukema J, Kahali B, Kahn R, Kähönen M, Kamstrup P, Kanoni S, Johansson S, Jiang X, Jia Y, Huang P, Hveem K, Ikram M, Ingelsson E, Jackson A, Jansson J, Jarvik G, Jensen G, Jhun M, Kaprio J, Karaleftheri M, Kovacs P, Kriebel J, Kuivaniemi H, Küry S, Kuusisto J, La Bianca M, Laakso M, Lakka T, Lange E, Kooperberg C, Kooner J, Kontto J, Kardia S, Karpe F, Kee F, Keeman R, Kiemenev L, Kitajima H, Kluijvers K, Kocher T, Komulainen P, Lange L, Howson J, Ebeling T, Ford I, Fornage M, Franks P, Frikke-Schmidt R, Galesloot T, Gan W, Gandin I, Gasparini P, Giedraitis V, Florez J, Ferrieres J, Ferrario M, Edwards T, Ellinor P, Elliott P, Evangelou E, Farmaki A, Faul J, Feitosa M, Feng S, Ferrannini E, Giri A, Girotto G, He L, Heid I, Heikkilä K, Helgeland Ø, Hernesniemi J, Hewitt A, Hocking L, Hollensted M, Holmen O, Hayward C, Hattersley A, Harris T, Gordon S, Gordon-Larsen P, Gorski M, Grarup N, Grove M, Gudnason V, Gustafsson S, Hansen T, Harris K, Hovingh G. Rare and low-frequency coding variants alter human adult height. *Nature* 2017; 542:186-190.

Zhang K, Arcuti S, Brunetti M, Moglia C, Calvo A, Ratti A, Tiloca C, Gellera C, Pensato V, Mazzini L, Capozzo R, Zecca C, Blair I, Stuit R, Muller B, Filosto M, Padovani A, Riva N, Penco S, Lunetta C, Sorarù G, Bertolin C, Blauw H, Curtis C, Hofman A, Estrada K, Rivadeneira F, Uitterlinden A, Dartigues J, Tzourio C, Amouyel P, van der Kooij A, de Visser M, D'Alfonso S, Comi G, Del Bo R, Cereda C, Pansarasa O, Smith B, Shaw C, Weber M, Goris A, Nöthen M, McCann E, Veldink J, Corcia P, Andersen P, Hardiman O, Landers J, Glass J, Brown R, Pers T, Franke L, Van Damme P, Vourc'h P, Silani V, van den Berg L, Al-Chalabi A, Breen G, Lewis C, Pasterkamp R, van Es M, de Bakker P, Visscher P, Wray N, Robberecht W, Weishaupt J, Stubendorff B, Prell T, Ringer T, Witte O, Grosskreutz J, Kiernan M, Pamphlett R, Rowe D, Nicholson G, Kurth I, Hübner C, Ludolph A, Powell J, Logroscino G, Tortelli R, Pupillo E, Beghi E, Chio A, Casale F, Leigh P, Fifita J, Chandran S, Koritnik B, Ravnik-Glavač M, Vrabec K, Rogelj B, Lin K, Ticozzi N, Vajda A, Menelaou A, Medic J, Zidar J, Leonardis L, Polak M, Rojas-García R, Mora J, Pinto S, de Carvalho M, Meininger V, Salachas F, Millecamps S, Grošelj L, Brands W, Schellevis R, Robinson M, de Jong S, Vösa U, van der Spek R, Pulit S, Diekstra F, McLaughlin R, Dekker A, Shatunov A, Yang J, Fogh I, Harschnitz O, van Eijk K, Kenna K, Jones A, Sproviero W, Blokhuis A, Koppers M, Tazelaar G, van Doormaal P, van Rheenen W, Colville S, Cichon S, Maurel C, Andres C, Radivojkov-Blagojevic M, Lichtner P, Meitinger T, Parman Y, Hamzeiy H, Tunca C, Basak A, Bensimon G, Landwehrmeyer B, Rietschel M, Franke A, Lieb W, Tittmann L, Wood N, Dürr A, Saker-Delye S, Payan C, Brice A, McCluskey L, Elman L, Topp S, Malaspina A, Fratta P, Sidle K, Pittman A, Orrell R, Hardy J, Shaw P, Morrison K, Petri S, Abdulla S, Trojanowski J, Van Deerlin V, Lomen-Hoerth C, Wiedau-Pazos M, Staats K, Ophoff R, Meyer T, Sendtner M, Drepper C, Swingle R. Genome-wide association analyses identify new risk variants and the genetic architecture of amyotrophic lateral sclerosis. *Nat Genet* 2016; 48:1043-8.

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