



Publications **X-omics** consortium

2024

Publications of the X-omics consortium

February

Genome sequencing as a generic diagnostic strategy for rare disease.

Schobers G, Derks R, den Ouden A, Swinkels H, van Reeuwijk J, Bosgoed E, Lugtenberg D, Sun SM, Corominas Galbany J, Weiss M, Blok MJ, Olde Keizer RACM, Hofste T, Hellebrekers D, de Leeuw N, Stegmann A, Kamsteeg EJ, Paulussen ADC, Ligtenberg MJL, Bradley XZ, Peden J, Gutierrez A, Pullen A, Payne T, **Gilissen C**, van den Wijngaard A, Brunner HG, **Nelen M**, Yntema HG, **Vissers LELM**.

Genome Med. 2024 Feb 14;16(1):32. doi: 10.1186/s13073-024-01301-y. PMID: 38355605

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Development of an Untargeted LC-MS Metabolomics Method with Postcolumn Infusion for Matrix Effect Monitoring in Plasma and Feces.

Zhu P, Dubbelman AC, Hunter C, Genangeli M, Karu N, Harms A, **Hankemeier T**.

J Am Soc Mass Spectrom. 2024 Mar 6;35(3):590-602. doi: 10.1021/jasms.3c00418. Epub 2024 Feb 21. PMID: 38379502

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A comprehensive UHPLC-MS/MS method for metabolomics profiling of signaling lipids: Markers of oxidative stress, immunity and inflammation.

Yang W, Schoeman JC, Di X, Lamont L, Harms AC, **Hankemeier T**.

Anal Chim Acta. 2024 Apr 8;1297:342348. doi: 10.1016/j.aca.2024.342348. Epub 2024 Feb 10. PMID: 38438234

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Adipocyte p53 coordinates the response to intermittent fasting by regulating adipose tissue immune cell landscape.

Reinisch I, Michenthaler H, Sulaj A, Moyschewitz E, Krstic J, Galhuber M, Xu R, Riahi Z, Wang T, Vujic N, Amor M, Zenezini Chiozzi R, Wabitsch M, Kolb D, Georgiadi A, Glawitsch L, Heitzer E, Schulz TJ, Schupp M, Sun W, Dong H, Ghosh A, Hoffmann A, Kratky D, Hinte LC, von Meyenn F, **Heck AJR**, Blüher M, Herzig S, Wolfrum C, Prokesch A.

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Rai D, Song Y, Hua S, **Stecker K**, Monster JL, Yin V, Stucchi R, Xu Y, Zhang Y, Chen F, Katrukha EA, Altelaar M, **Heck AJR**, Wieczorek M, Jiang K, Akhmanova A.

Nat Cell Biol. 2024 Feb 29. doi: 10.1038/s41556-024-01366-2. Online ahead of print.
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Validation of biomarkers of aging.

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PMID: 38355974

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N-linked glycosylation of the M-protein variable region: glycoproteogenomics reveals a new layer of personalized complexity in multiple myeloma.

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Using Instrumental Variables to Measure Causation over Time in Cross-Lagged Panel Models.

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Krefman AE, Stephen J, Carolan P, Sedaghat S, Mansolf M, Soumare A, Gross AL, Aiello AE, Singh-Manoux A, **Ikram MA**, Helmer C, Tzourio C, Satizabal C, Levine DA, Lloyd-Jones D, Briceño EM, Sorond FA, Wolters FJ, Himali J, Launer LJ, Zhao L, Haan M, Lopez OL, Debette S, Seshadri S, Judd SE, Hughes TM, Gudnason V, Scholtens D, Allen NB.

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Association of blood cell-based inflammatory markers with gut microbiota and cancer incidence in the Rotterdam study.

Najjary S, Kros JM, Stricker BH, Ruiter R, Shuai Y, Kraaij R, Van Steen K, van der Spek P, Van Eijck CHJ, **Ikram MA**, Ahmad S.

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Am J Respir Cell Mol Biol. 2024 Feb 5. doi: 10.1165/rcmb.2023-0296OC. Online ahead of print. PMID: 38315810

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EURO-NMD registry: federated FAIR infrastructure, innovative technologies and concepts of a patient-centred registry for rare neuromuscular disorders.

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Rots D, Rooney K, Relator R, Kerkhof J, McConkey H, Pfundt R, Marcelis C, Willemsen MH, van Hagen JM, Zwijnenburg P, Alders M, Öunap K, Reimand T, Fjodorova O, Berland S, Liahjell EB, Bojovic O, Kriek M, Ruivenkamp C, Bonati MT, Brunner HG, **Vissers LELM**, Sadikovic B, Kleefstra T.

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January

A framework for the clinical implementation of optical genome mapping in hematologic malignancies.

Levy B, Kanagal-Shamanna R, Sahajpal NS, Neveling K, Rack K, Dewaele B, Olde Weghuis D, Stevens-Kroef M, Puiggros A, Mallo M, Clifford B, Mantere T, **Hoischen A**, Espinet B, Kolhe R, Solé F, Raca G, Smith AC.

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A case series exploring the human milk polyclonal IgA1 response to repeated SARS-CoV-2 vaccinations by LC-MS based fab profiling.

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A multi-omics data analysis workflow packaged as a FAIR Digital Object.

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Hum Reprod. 2024 Jan 5;39(1):35-42. doi: 10.1093/humrep/dead131. PMID: 38052159

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Trans-ancestral genome-wide association study of longitudinal pubertal height growth and shared heritability with adult health outcomes.

Bradfield JP, Kember RL, Ulrich A, Balkiyarova Z, Alyass A, Aris IM, Bell JA, Broadaway KA, Chen Z, Chai JF, Davies NM, Fernandez-Orth D, Bustamante M, Fore R, Ganguli A, Heiskala A, Hottenga JJ, Íñiguez C, Kobes S, Leinonen J, Lowry E, Lyytikäinen LP, Mahajan A, Pitkänen N, Schnurr TM, Have CT, Strachan DP, Thiering E, Voegelezang S, Wade KH, Wang CA, Wong A, Holm LA, Chesi A, Choong C, Cruz M, Elliott P, Franks S, Frithioff-Bøjsøe C, Gauderman WJ, Glessner JT, Gilsanz V, Griesman K, Hanson RL, Kaakinen M, Kalkwarf H, Kelly A, Kindler J, Kähönen M, Lanca C, Lappe J, Lee NR, McCormack S, Mentch FD, Mitchell JA, Mononen N, Niinikoski H, Oken E, Pahkala K, Sim X, Teo YY, Baier LJ, van Beijsterveldt T, Adair LS, **Boomsma DI**, de Geus E, Guxens M, Eriksson JG, Felix JF, Gilliland FD, Biobank PM, Hansen T, Hardy R, Hivert MF, Holm JC, Jaddoe VVW, Järvelin MR, Lehtimäki T, Mackey DA, Meyre D, Mohlke KL, Mykkänen J, Oberfield S, Pennell CE, Perry JRB, Raitakari O, Rivadeneira F, Saw SM, Sebert S, Shepherd JA, Standl M, Sørensen TIA, Timpson NJ, Torrent M, Willemsen G, Hyppönen E, Power C; Early Growth Genetics Consortium; McCarthy MI, Freathy RM, Widén E, Hakonarson H, Prokopenko I, ... See abstract for full author list →

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Increase in venous thromboembolism in SARS-CoV-2 infected lung tissue: proteome analysis of lung parenchyma, isolated endothelium, and thrombi.

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A genetic association study of circulating coagulation Factor VIII and von Willebrand Factor levels.

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Drug repurposing for rare: progress and opportunities for the rare disease community.

Jonker AH, O'Connor D, Cavaller-Bellaubi M, Fetro C, Gogou M, **'t Hoen PAC**, de Kort M, Stone H, Valentine N, Pasmooij AMG.

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