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Hereditary cancer: Germline testing practices across ERN GENTURIS member countries.

Kiljańczyk M, Daneberga Z, Tooming M, Urbańczyk K, Pöyhönen M, Kahre T, Foretova L, Tham E, Milagre T, Melegh B, Haanpää MK, Blatnik A, Wimmer K, de Putter R, Wadt K, Houdayer C, Holinski-Feder E, Kattamis A, Klink B, Høberg-Vetti H, Blanco Guillermo I, Hoogerbrugge N, Lubiński J.

<https://pubmed.ncbi.nlm.nih.gov/42265275/>

Clinically actionable genomic and transcriptomic landscape of advanced neuroendocrine neoplasms.

Kreutzfeldt S, Apostolidis L, Oleś M, Krieghoff-Henning E, Heilig CE, Heining C, Mock A, Teleanu MV, Hutter B, Gieldon L, Klink B, Beck K, Richter D, Baude-Müller A, Reisinger E, Hammer N, Kamkar L, Pfütze K, Georg C, Lamping M, Rieke DT, Uhrig S, Jann H, Pape UF, Allgäuer M, Stenzinger A, Winkler EC, Wiedenmann B, Jäger D, Brors B, Hübschmann D, Schröck E, Keilholz U, Pavel M, Horak P, Glimm H, Fröhling S.

<https://pubmed.ncbi.nlm.nih.gov/42066764/>

Validation structures for sequence variants of uncertain significance in hereditary cancer.

Lucas MC, Keßler T, Benet-Pagès A, Holinski-Feder E, Laner A, Klink B.

<https://pubmed.ncbi.nlm.nih.gov/41807735/>

Reporting practices for secondary findings among ERN GENTURIS member institutions in 15 European countries.

Taxer K, Wimmer K, Wadt K, Schnaiter S, Rudnik S, Zschocke J, ERN GENTURIS Study Group (Klink B et al.), Schwaninger G.

<https://pubmed.ncbi.nlm.nih.gov/41776345/>

Development of a highly differentiated rat brain organoid model for exploring glioblastoma invasion dynamics and therapy.

Zhou W, Martinez-Garcia E, Sarnow K, Kanli G, Nazarov PV, Li Y, Schwab SG, Meiser J, Jaeger C, Mieczkowski J, Misztak A, Thorsen FA, Grützmann K, Mihaljevic B, Van Loon B, Hossain JA, Zhang Y, Xue Z, Li W, Moreino SS, Golebiewska A, Niclou SP, Bjørås M, Tardito S, Joesph JV, Lunavat TR, Saed HS, Bahador M, Han M, Fabian C, Miletic H, Li X, Dittmar G, Keunen O, Klink B, Wang J, Bjerkvig R.

<https://pubmed.ncbi.nlm.nih.gov/41284925/>

Priority European strategies for sustainable access to high-quality genetic counselling in cancer: A Delphi study.

McCrary JM, Van Valckenborgh E, Horgan D, Aleksandrova E, Bargou R, Behulova RL, Belina I, Bøhme ALE, Brunet J, Burada F, Chirita-Emandi A, Ciuca A, Colas C, Constantinidou A, Curca RO, Cursaru V, Dalmas M, Daneberga Z, de Azambuja E, De Pauw A, De Putter R, Delikurt-Tuncalp T, Donnelly D, Ehrencrona H, Foretova L, Galli F, Genuardi M, Giles R, Grima C, Janavičius R, Kääriäinen H, Klink B, Krajc M, Kufel-Grabowska J, Lace B, Leitsalu L, Le Tourneau C, Lodahl M, Mari F, Matos E, Mазzarella L, Milagre TH, Mistrik M, Moss B, Nolan A, O'Shea R, Paneque M, Patócs A, Pestoff R, Poirel HA, Risch M, Rodrigues M, Roetzer KM, Ros A, Schröck E, Schwaninger G, Slámová L, Stamatopoulos K, Strang-Karlsson S, Szczaluba K, Szymczak V, Theis P, Turner J, Valcina O, Vella C, van Zelst-Stams WAG, Wadt KAW, Zschocke J, Ronez J, Ripperger T, Van Den Bulcke M, Bergmann AK.

<https://pubmed.ncbi.nlm.nih.gov/41688774/>

2025

Improving genetic diagnosis of hereditary tumor syndromes: From expanded gene panels to functional genomics.

Sauer M, Lucas MC, Prokosch V, Keßler T, Risch T, Laner A, Henkel J, Benet-Pagès A, Hallermayr A, Steinke-Lange V, Holinski-Feder E, Klink B.

<https://pubmed.ncbi.nlm.nih.gov/41347847/>

Development of a highly differentiated rat brain organoid model for exploring glioblastoma invasion dynamics and therapy.

Zhou W, Martinez-Garcia E, Sarnow K, Kanli G, Nazarov PV, Li Y, Schwab S, Meiser J, Jaeger C, Mieczkowski J, Misztak A, Thorsen FA, Grützmann K, Mihaljevic B, van Loon B, Hossain JA, Zhang Y, Xue Z, Li W, Moreino SS, Golebiewska A, Niclou SP, Bjørås M, Tardito S, Joesph JV, Lunavat TR, Saed HS, Bahador M, Han M, Fabian C, Miletic H, Li X, Dittmar G, Keunen O, Klink B, Wang J, Bjerkvig R.

<https://pubmed.ncbi.nlm.nih.gov/41284925/>

A series of reviews in familial cancer: genetic cancer risk in context variants of uncertain significance in MMR genes: which procedures should be followed?

Lucas MC, Keßler T, Scharf F, Steinke-Lange V, Klink B, Laner A, Holinski-Feder E.

<https://pubmed.ncbi.nlm.nih.gov/40317406/>

Joint analysis of germline genetic data from over 29,000 cases with suspected hereditary breast and ovarian cancer (HBOC) as part of the NASGE initiative.

Henkel J, Laner A, Locher M, Wohlfrom T, Neitzel B, Becker K, Neuhann T, Abicht A, Steinke-Lange V, Klink B, Eichhorn B, Schmidt W, Berner D, Teubert A, Holtorf A, Heinrich S, Wildhardt G, Schulze M, von der Heyden L, Hörtnagel K, Steinberger D, Kleier S, Lorenz P, Glaubitz R, Biskup S, Holinski-Feder E.

<https://pubmed.ncbi.nlm.nih.gov/39854808/>