

2026

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/>

Mutational Landscape of Colorectal Tumors From Individuals With Unexplained Adenomatous or Serrated Colorectal Polyposis.

Sommer AK, Te Paske IBAW, Jansen EAM, Gschwind A, Demidov G, Steinke-Lange V, Spier I, Steyaert W, Yaldiz B, Steehouwer M, Hommerding O, Dietrich D, Peters S, Garcia-Pelaez J, Laner A, Oliveira C, Capellá G, Nagtegaal ID, Bläker H, Ellwanger K, Hoischen A, Gilissen C, van der Post RS, Kristiansen G, Hoogerbrugge N, Ossowski S, Valle L, Holinski-Feder E, Ligtenberg MJL, Aretz S, de Voer RM.

<https://pubmed.ncbi.nlm.nih.gov/41524686/>

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/>

Next-Generation Sequencing in Congenital Eye Malformations: Identification of Genetic Causes and Comparison of Different Panel-Based Diagnostic Strategies.

Neuhann L, Laner A, Holinski-Feder E, Neuhann T.

<https://pubmed.ncbi.nlm.nih.gov/41155148/>

From Expert Judgment to Structured Guidelines: A Brief History and Bright Future of DNA Variant Interpretation.

Laner A, Zilfaiil BA, Hamed SA, Do H, Lopes-Cendes I, Shrestha T, Tobias E, Solano A, Hamosh A, Kumar D.

<https://pubmed.ncbi.nlm.nih.gov/40660810/>

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/>

Blood biomarker fingerprints in a cohort of patients with CHRNE-related congenital myasthenic syndrome.

Della Marina A, Koutsoulidou A, Natera-de Benito D, Tykocinski LO, Tomazou M, Georgiou K, Laner A, Kölbl H, Nascimento A, Ortez C, Abicht A, Thakur BK, Lochmüller H, Phylactou LA, Ruck T, Schara-Schmidt U, Kale D, Hentschel A, Roos A.

<https://pubmed.ncbi.nlm.nih.gov/39948634/>

Reclassification of VUS in *BRCA1* and *BRCA2* using the new *BRCA1/BRCA2* ENIGMA track set demonstrates the superiority of ClinGen ENIGMA Expert Panel specifications over the standard ACMG/AMP classification system.

Benet-Pagès A, Laner A, Nassar LR, Wohlfrom T, Steinke-Lange V, Haeussler M, Holinski-Feder E.

<https://pubmed.ncbi.nlm.nih.gov/40027238/>

2024

Large-scale application of ClinGen-InSiGHT APC-specific ACMG/AMP variant classification criteria leads to substantial reduction in VUS.

Yin X, Richardson M, Laner A, Shi X, Ognedal E, Vasta V, Hansen TVO, Pineda M, Ritter D, de Dunnen J, Hassanin E, Lin WL, Borrás E, Krahn K, Nordling M, Martins A, Mahmood K, Nadeau E, Beshay V, Tops C, Genuardi M, Pesaran T, Frayling IM, Capellá G, Latchford A, Tavtigian SV, Maj C, Plon SE, Greenblatt MS, Macrae FA, Spier I, Aretz S.

<https://pubmed.ncbi.nlm.nih.gov/39357517/>

Comprehensive reanalysis for CNVs in ES data from unsolved rare disease cases results in new diagnoses.

Demidov G, Yaldiz B, Garcia-Pelaez J, de Boer E, Schuermans N, Van de Vondel L, Paramonov I, Johansson LF, Musacchia F, Benetti E, Bullich G, Sablauskas K, Beltran S, Gilissen C, Hoischen A, Ossowski S, de Voer R, Lohmann K, Oliveira C, Topf A, Vissers LELM, Solve-RD Consortium (Laner A et al.), Laurie S.

<https://pubmed.ncbi.nlm.nih.gov/39461972/>

Comparison of the ABC and ACMG systems for variant classification.

Houge G, Bratland E, Aukrust I, Tveten K, Žukauskaitė G, Sansovic I, Brea-Fernández AJ, Mayer K, Paakkola T, McKenna C, Wright W, Markovic MK, Lildballe DL, Konecny M, Smol T, Alhopuro P, Gouttenoire EA, Obeid K, Todorova A, Jankovic M, Lubieniecka JM, Stojiljkovic M, Buisine MP, Haukanes BI, Lorans M, Roomere H, Petit FM, Haanpää MK, Beneteau C, Pérez B, Plaseska-Karanfilska D, Rath M, Fuhrmann N, Ferreira BI, Stephanou C, Sjursen W, Maver A, Rouzier C, Chirita-Emandi A, Gonçalves J, Kuek WCD, Broly M, Haer-Wigman L, Thong MK, Tae SK, Hyblova M, den Dunnen JT, Laner A.

<https://pubmed.ncbi.nlm.nih.gov/38778080/>

Clinical and Molecular Spectrum of Autosomal Recessive CA8-Related Cerebellar Ataxia.

Kaiyrzhanov R, Ortigoza-Escobar JD, Stringer BW, Ganieva M, Gowda VK, Srinivasan VM, Macaya A, Laner A, Onbool E, Al-Shammari R, Al-Owain M, Deconinck N, Vilain C, Dontaine P, Self E, Akram R, Hussain G, Baig SM, Iqbal J, Salpietro V, Neshatdoust M, Kasiri M, Yesil G, Uygur T, Pysden K, Berry IR, Alves CA, Giacomotto J, Houlden H, Maroofian R.

<https://pubmed.ncbi.nlm.nih.gov/38581205/>

Mismatch repair gene specifications to the ACMG/AMP classification criteria: Consensus recommendations from the InSiGHT ClinGen Hereditary Colorectal Cancer / Polyposis Variant Curation Expert Panel.

Plazzer JP, Macrae F, Yin X, Thompson BA, Farrington SM, Currie L, Lagerstedt-Robinson K, Frederiksen JH, van Overeem Hansen T, Gravens L, Frayling IM, Akagi K, Yamamoto G, Al-Mulla F, Ferber MJ, Martins A, Genuardi M, Kohonen-Corish M, Baert-Desurmont S, Spurdle AB, Capellá G, Pineda M, Woods MO, Rasmussen LJ, Heinen CD, Scott RJ, Tops CM, Greenblatt MS, Dominguez-Valentin M, Ognedal E, Borrás E, Leung SY, Mahmood K, Holinski-Feder E, Laner A.

<https://doi.org/10.1101/2024.05.13.24307108>

Systematic large-scale application of ClinGen InSiGHT APC-specific ACMG/AMP variant classification criteria substantially alleviates the burden of variants of uncertain significance in ClinVar and LOVD databases.

Yin X, Richardson M, Laner A, Shi X, Ognedal E, Vasta V, Hansen TVO, Pineda M, Ritter D, den Dunnen JT, Hassanin E, Lyman Lin W, Borrás E, Krahn K, Nordling M, Martins A, Mahmood K, Nadeau EAW, Beshay V, Tops C, Genuardi M, Pesaran T, Frayling IM, Capellá G, Latchford A, Tavtigian SV, Maj C, Plon SE, Greenblatt MS, Macrae FA, Spier I, Aretz S.

<https://pubmed.ncbi.nlm.nih.gov/38746299/>

Novel Genetic and Biochemical Insights into the Spectrum of NEFL-Associated Phenotypes.

Della Marina A, Hentschel A, Czech A, Schara-Schmidt U, Preusse C, Laner A, Abicht A, Ruck T, Weis J, Choueiri C, Lochmüller H, Kölbel H, Roos A.

<https://pubmed.ncbi.nlm.nih.gov/38578900/>

Gene-specific ACMG/AMP classification criteria for germline APC variants: recommendations from the ClinGen InSiGHT Hereditary Colorectal Cancer / Polyposis Variant Curation Expert Panel.

Spier I, Yin X, Richardson M, Pineda M, Laner A, Ritter D, Boyle J, Mur P, Hansen TVO, Shi X, Mahmood K, Plazzer JP, Ognedal E, Nordling M, Farrington SM, Yamamoto G, Baert-Desurmont S, Martins A, Borrás E, Tops C, Webb E, Beshay V, Genuardi M, Pesaran T, Capellá G, Tavtigian SV, Latchford A, Frayling IM, Plon SE, Greenblatt M, Macrae FA, Aretz S; InSiGHT - ClinGen Hereditary Colon Cancer / Polyposis Variant Curation Expert Panel.

<https://pubmed.ncbi.nlm.nih.gov/37800450/>

An interconnected data infrastructure to support large-scale rare disease research.

Johansson LF, Laurie S, Spalding D, Gibson S, Ruvolo D, Thomas C, Piscia D, de Andrade F, Been G, Bijlsma M, Brunner H, Cimerman S, Dizjikan FY, Ellwanger K, Fernandez M, Freeberg M, van de Geijn GJ, Kanninga R, Maddi V, Mehtarizadeh M, Neerincx P, Ossowski S, Rath A, Roelofs-Prins D, Stok-Benjamins M, van der Velde KJ, Veal C, van der Vries G, Wadsley M, Warren G, Zurek B, Keane T, Graessner H, Beltran S, Swertz MA, Brookes AJ, Solve-RD consortium (u. a. Holinski-Feder E, Laner A, Steinke-Lange V et al.).

<https://pubmed.ncbi.nlm.nih.gov/39302238/>

2023

Novel Homozygous FA2H Variant Causing the Full Spectrum of Fatty Acid Hydroxylase-Associated Neurodegeneration (SPG35).

German A, Jukic J, Laner A, Arnold P, Socher E, Mennecke A, Schmidt MA, Winkler J, Abicht A, Regensburger M.

<https://pubmed.ncbi.nlm.nih.gov/38275596/>

Diagnostic yield and clinical relevance of expanded germline genetic testing for nearly 7000 suspected HBOC patients

Jan Henkel, Andreas Laner, Melanie Locher, Tobias Wohlfrom, Birgit Neitzel, Kerstin Becker, Teresa Neuhann, Angela Abicht, Verena Steinke-Lange, Elke Holinski-Feder

<https://pubmed.ncbi.nlm.nih.gov/37188824/>

Highly sensitive liquid biopsy Duplex sequencing complements tissue biopsy to enhance detection of clinically relevant genetic variants.

Hallermayr A, Neuhann TM, Steinke-Lange V, Scharf F, Laner A, Ewald R, Liesfeld B, Holinski-Feder E, Pickl JMA.

<https://pubmed.ncbi.nlm.nih.gov/36636551/>

Transcript capture and ultradeep long-read RNA sequencing (CAPLRseq) to diagnose HNPCC/Lynch syndrome.

Schwenk V, Leal Silva RM, Scharf F, Knaust K, Wendlandt M, Häusser T, Pickl JMA, Steinke-Lange V, Laner A, Morak M, Holinski-Feder E, Wolf DA.

J Med Genet. 2023 Jan 2:jmg-2022-108931. doi: 10.1136/jmg-2022-108931. Online ahead of print. PMID: 36593122

<https://pubmed.ncbi.nlm.nih.gov/36593122/>

2022

Biallelic PRMT7 pathogenic variants are associated with a recognizable syndromic neurodevelopmental disorder with short stature, obesity, and craniofacial and digital abnormalities.

Cali E, Suri M, Scala M, Ferla MP, Alavi S, Faqeih EA, Bijlsma EK, Wigby KM, Baralle D, Mehrjardi MYV, Schwab J, Platzer K, Steindl K, Hashem M, Jones M, Niyazov DM, Jacober J, Littlejohn RO, Weis D, Zadeh N, Rodan L, Goldenberg A, Lecoquierre F, Dutra-Clarke M, Horvath G, Young D, Orenstein N, Bawazeer S, Vulto-van Silfhout AT, Herenger Y, Dehghani M, Seyedhassani SM, Bahreini A, Nasab ME, Ercan-Sencicek AG, Firoozfar Z, Movahedinia M, Efthymiou S, Striano P, Karimiani EG, Salpietro V, Taylor JC, Redman M, Stegmann APA, Laner A, Abdel-Salam G, Li M, Bengala M, Müller AJ, Digilio MC, Rauch A, Gunel M, Titheradge H, Schweitzer DN, Kraus A, Valenzuela I, McLean SD, Phornphutkul C, Salih M, Begtrup A, Schnur RE, Torti E, Haack TB, Prada CE, Alkuraya FS, Houlden H, Maroofian R.

<https://pubmed.ncbi.nlm.nih.gov/36399134/>

Long-term chemoprevention in patients with adenomatous polyposis coli: an observational study

Teresa M Neuhann, Katharina Haub, Verena Steinke-Lange, Monika Morak, Andreas Laner, Melanie Locher, Elke Holinski-Feder

<https://pubmed.ncbi.nlm.nih.gov/35570229/>

Constitutional chromothripsis of the APC locus as a cause of genetic predisposition to colon cancer

Florentine Scharf, Rafaela Magalhaes Leal Silva, Monika Morak, Alex Hastie, Julia M A Pickl, Kai

Sendelbach, Christian Gebhard, Melanie Locher, Andreas Laner, Verena Steinke-Lange, Udo Koehler, Elke Holinski-Feder, Dieter A Wolf
<https://pubmed.ncbi.nlm.nih.gov/34911816/>

Human Mutation special issue on “Variant Effect Prediction”

Andreas Laner, Ales Maver, Johan T den Dunnen
<https://pubmed.ncbi.nlm.nih.gov/35839310/>

Splicing analyses for variants in MMR genes: best practice recommendations from the European Mismatch Repair Working Group

Monika Morak, Marta Pineda, Alexandra Martins, Pascaline Gaildrat, H el ene Tubeuf, Aur elie Drouet, Carolina G omez, Estela D amaso, Kerstin Schaefer, Verena Steinke-Lange, Udo Koehler, Andreas Laner, Julie Hauchard , Karine Chauris, Elke Holinski-Feder, Gabriel Capell a
<https://pubmed.ncbi.nlm.nih.gov/35676339/>

Long-term chemoprevention in patients with adenomatous polyposis coli: an observational study

Teresa M Neuhann, Katharina Haub, Verena Steinke-Lange , Monika Morak , Andreas Laner , Melanie Locher , Elke Holinski-Feder
<https://pubmed.ncbi.nlm.nih.gov/35570229/>

Solving the genetic aetiology of hereditary gastrointestinal tumour syndromes- a collaborative multicentre endeavour within the project Solve-RD

Anna K Sommer, Iris B A W Te Paske, Jos e Garcia-Pelaez, Andreas Laner, Elke Holinski-Feder, Verena Steinke-Lange, Sophia Peters, Laura Valle, Isabel Spier, David Huntsman, Solve-RD-GENTURIS group; Carla Oliveira, Richarda M de Voer, Nicoline Hoogerbrugge, Stefan Aretz
<https://doi.org/10.1016/j.ejmg.2022.104475>

2021

Solve-RD: systematic pan-European data sharing and collaborative analysis to solve rare diseases.

B. Zurek, K. Ellwanger, L. E. L. M. Vissers, R. Sch ule, M. Synofzik, A. T opf, R. M. de Voer, S. Laurie, L. Matalonga, C. Gilissen, S. Ossowski, P. A. C. ’t Hoen, A. Vitobello, J. M. Schulze-Hentrich, O. Riess, H. G. Brunner, A. J. Brookes, A. Rath, G. Bonne, G. Gumus, A. Verloes, N. Hoogerbrugge, T. Evangelista, T. Harmuth, M. Swertz, D. Spalding, A. Hoischen, S. Beltran, H. Graessner, & Solve-RD consortium, European journal of human genetics: EJHG, (2021).
<https://doi.org/10.1038/s41431-021-00859-0>.

A mosaic PIK3CA variant in a young adult with diffuse gastric cancer: case report.

I. B. A. W. Te Paske, J. Garcia-Pelaez, A. K. Sommer, L. Matalonga, T. Starzynska, A. Jakubowska, Solve-RD-GENTURIS group, R. S. van der Post, J. Lubinski, C. Oliveira, N. Hoogerbrugge, & R. M. de Voer, European journal of human genetics: EJHG, (2021).
<https://doi.org/10.1038/s41431-021-00853-6>

Stepwise ABC system for classification of any type of genetic variant.

G. Houge, A. Laner, S. Cirak, N. de Leeuw, H. Scheffer, & J. T. den Dunnen, European journal of human genetics: EJHG, (2021).
<https://doi.org/10.1038/s41431-021-00903-z>.

Actionable secondary findings in arrhythmogenic right ventricle cardiomyopathy genes: impact and challenge of genetic counseling. A. Abicht, U. Sch on, A. Laner, E. Holinski-Feder, & I. Diebold, Cardiovascular Diagnosis and Therapy, 11 (2021) 637–649. <https://doi.org/10.21037/cdt-20-585>.

HPO-driven virtual gene panel: a new efficient approach in molecular autopsy of sudden unexplained death.

U. Sch on, A. Holzer, A. Laner, S. Kleinle, F. Scharf, A. Benet-Pag es, O. Peschel, E. Holinski-Feder, & I. Diebold, BMC medical genomics, 14 (2021) 94. <https://doi.org/10.1186/s12920-021-00946-7> .

2020

Analysis of 3297 individuals suggests that the pathogenic germline 5'-UTR variant BRCA1 c.-107A>T is not common in south-east Germany.

Laner A, Benet-Pagès A, Neitzel B, Holinski-Feder E. *Fam Cancer*. 2020;19(3):211-213. doi:[10.1007/s10689-020-00175-4](https://doi.org/10.1007/s10689-020-00175-4)

Critical assessment of secondary findings in genes linked to primary arrhythmia syndromes.

Diebold I, Schön U, Scharf F, Benet-Pagès A, Laner A, Holinski-Feder E, Abicht A. *Hum Mutat*. 2020;41(5):1025-1032. doi:[10.1002/humu.23996](https://doi.org/10.1002/humu.23996)

Targeted deep-intronic sequencing in a cohort of unexplained cases of suspected Lynch syndrome.

Arnold AM, Morak M, Benet-Pagès A, Laner A, Frishman D, Holinski-Feder E. *Eur J Hum Genet*. 2020;28(5):597-608. doi:[10.1038/s41431-019-0536-9](https://doi.org/10.1038/s41431-019-0536-9)

Prevalence of CNV-neutral structural genomic rearrangements in MLH1, MSH2, and PMS2 not detectable in routine NGS diagnostics.

Morak M, Steinke-Lange V, Massdorf T, Benet-Pagès A, Locher M, Laner A, Kayser K, Aretz S, Holinski-Feder E. *Fam Cancer*. 2020;19(2):161-167. doi:[10.1007/s10689-020-00159-4](https://doi.org/10.1007/s10689-020-00159-4)

2019

Full-length transcript amplification and sequencing as universal method to test mRNA integrity and biallelic expression in mismatch repair genes.

Morak M, Schaefer K, Steinke-Lange V, Koehler U, Keinath S, Massdorf T, Mauracher B, Rahner N, Bailey J, Kling C, Haeusser T, Laner A, Holinski-Feder E. *Eur J Hum Genet*. 2019;27(12):1808-1820. doi:[10.1038/s41431-019-0472-8](https://doi.org/10.1038/s41431-019-0472-8)

2018

Extending the critical regions for mutations in the non-coding gene RNU4ATAC in another patient with Roifman Syndrome.

Hallermayr A, Graf J, Koehler U, Laner A, Schönfeld B, Benet-Pagès A, Holinski-Feder E. *Clin Case Rep*. 2018;6(11):2224-2228. doi:[10.1002/ccr3.1830](https://doi.org/10.1002/ccr3.1830)

LAMA2 gene mutation update: Toward a more comprehensive picture of the laminin- α 2 variome and its related phenotypes.

Oliveira J, Gruber A, Cardoso M, Taipa R, Fineza I, Gonçalves A, Laner A, Winder TL, Schroeder J, Rath J, Oliveira ME, Vieira E, Sousa AP, Vieira JP, Lourenço T, Almendra L, Negrão L, Santos M, Melo-Pires M, Coelho T, den Dunnen JT, Santos R, Sousa M. *Hum Mutat*. 2018;39(10):1314-1337. doi:[10.1002/humu.23599](https://doi.org/10.1002/humu.23599)

Comprehensive analysis of the MLH1 promoter region in 480 patients with colorectal cancer and 1150 controls reveals new variants including one with a heritable constitutional MLH1 epimutation.

Morak M, Ibisler A, Keller G, Jessen E, Laner A, Gonzales-Fassrainer D, Locher M, Massdorf T, Nissen AM, Benet-Pagès A, Holinski-Feder E. *J Med Genet*. 2018;55(4):240-248. doi:[10.1136/jmedgenet-2017-104744](https://doi.org/10.1136/jmedgenet-2017-104744)

2017

Loss of MSH2 and MSH6 due to heterozygous germline defects in MSH3 and MSH6.

Morak M, Käsbaauer S, Kerscher M, Laner A, Nissen AM, Benet-Pagès A, Schackert HK, Keller G, Massdorf T, Holinski-Feder E. *Fam Cancer*. 2017;16(4):491-500. doi:[10.1007/s10689-017-9975-z](https://doi.org/10.1007/s10689-017-9975-z)

2016

Exome Sequencing Identifies Biallelic MSH3 Germline Mutations as a Recessive Subtype of Colorectal Adenomatous Polyposis.

Adam R, Spier I, Zhao B, Kloth M, Marquez J, Hinrichsen I, Kirfel J, Tafazzoli A, Horpaopan S, Uhlhaas S, Stienen D, Friedrichs N, Altmüller J, Laner A, Holzapfel S, Peters S, Kayser K, Thiele H, Holinski-Feder E, Marra G, Kristiansen G, Nöthen MM, Büttner R, Möslin G, Betz RC, Brieger A, Lifton RP, Aretz S. *Am J Hum Genet.* 2016;99(2):337-351. doi:[10.1016/j.ajhg.2016.06.015](https://doi.org/10.1016/j.ajhg.2016.06.015)

Exome sequencing identifies potential novel candidate genes in patients with unexplained colorectal adenomatous polyposis.

Spier I, Kerick M, Drichel D, Horpaopan S, Altmüller J, Laner A, Holzapfel S, Peters S, Adam R, Zhao B, Becker T, Lifton RP, Holinski-Feder E, Perner S, Thiele H, Nöthen MM, Hoffmann P, Timmermann B, Schweiger MR, Aretz S. *Fam Cancer.* 2016;15(2):281-288. doi:[10.1007/s10689-016-9870-z](https://doi.org/10.1007/s10689-016-9870-z)

Low-level APC mutational mosaicism is the underlying cause in a substantial fraction of unexplained colorectal adenomatous polyposis cases.

Spier I, Drichel D, Kerick M, Kirfel J, Horpaopan S, Laner A, Holzapfel S, Peters S, Adam R, Zhao B, Becker T, Lifton RP, Perner S, Hoffmann P, Kristiansen G, Timmermann B, Nöthen MM, Holinski-Feder E, Schweiger MR, Aretz S. *J Med Genet.* 2016;53(3):172-179. doi:[10.1136/jmedgenet-2015-103468](https://doi.org/10.1136/jmedgenet-2015-103468)

2015

Phosphatidylinositol 3-kinase (PI3K) signalling regulates insulin-like-growth factor binding protein-2 (IGFBP-2) production in human adipocytes.

Wilhelm F, Kässner F, Schmid G, Kratzsch J, Laner A, Wabitsch M, Körner A, Kiess W, Garten A. *Growth Horm IGF Res.* 2015;25(3):115-120. doi:[10.1016/j.ghir.2015.03.003](https://doi.org/10.1016/j.ghir.2015.03.003)

Genome-wide CNV analysis in 221 unrelated patients and targeted high-throughput sequencing reveal novel causative candidate genes for colorectal adenomatous polyposis.

Horpaopan S, Spier I, Zink AM, Altmüller J, Holzapfel S, Laner A, Vogt S, Uhlhaas S, Heilmann S, Stienen D, Pasternack SM, Keppler K, Adam R, Kayser K, Moebus S, Draaken M, Degenhardt F, Engels H, Hofmann A, Nöthen MM, Steinke V, Perez-Bouza A, Herms S, Holinski-Feder E, Fröhlich H, Thiele H, Hoffmann P, Aretz S. *Int J Cancer.* 2015;136(6):E578-589. doi:[10.1002/ijc.29215](https://doi.org/10.1002/ijc.29215)

2014

Biallelic MUTYH mutations can mimic Lynch syndrome.

Morak M, Heidenreich B, Keller G, Hampel H, Laner A, de la Chapelle A, Holinski-Feder E. *Eur J Hum Genet.* 2014;22(11):1334-1337. doi:[10.1038/ejhg.2014.15](https://doi.org/10.1038/ejhg.2014.15)

Sirolimus treatment of severe PTEN hamartoma tumor syndrome: case report and in vitro studies.

Schmid GL, Kässner F, Uhlig HH, Körner A, Kratzsch J, Händel N, Zepp F-P, Kowalzik F, Laner A, Starke S, Wilhelm FK, Schuster S, Viehweger A, Hirsch W, Kiess W, Garten A. *Pediatr Res.* 2014;75(4):527-534. doi:[10.1038/pr.2013.246](https://doi.org/10.1038/pr.2013.246)

2010

MUTYH-associated polyposis - variability of the clinical phenotype in patients with biallelic and monoallelic MUTYH mutations and report on novel mutations.

Morak M, Laner A, Bacher U, Keiling C, Holinski-Feder E. *Clin Genet.* 2010;78(4):353-363. doi:[10.1111/j.1399-0004.2010.01478.x](https://doi.org/10.1111/j.1399-0004.2010.01478.x)

Escherichia coli-cloned CFTR loci relevant for human artificial chromosome therapy.

Rocchi L, Braz C, Cattani S, Ramalho A, Christan S, Edlinger M, Ascenzioni F, Laner A, Kraner S, Amaral M, Schindelbauer D. *Hum Gene Ther.* 2010;21(9):1077-1092. doi:[10.1089/hum.2009.225](https://doi.org/10.1089/hum.2009.225)

Clopidogrel and proton pump inhibitor (PPI) interaction: separate intake and a non-omeprazole PPI the solution?

Kenngott S, Olze R, Kollmer M, Bottheim H, Laner A, Holinski-Feder E, Gross M. *Eur J Med Res.* 2010;15(5):220-224. doi:[10.1186/2047-783x-15-5-220](https://doi.org/10.1186/2047-783x-15-5-220)

2008

Report on de-novo mutation in the MSH2 gene as a rare event in hereditary nonpolyposis colorectal cancer.

Morak M, Laner A, Scholz M, Madorf T, Holinski-Feder E. *Eur J Gastroenterol Hepatol.* 2008;20(11):1101-1105. doi:[10.1097/MEG.0b013e328305e185](https://doi.org/10.1097/MEG.0b013e328305e185)

2007

Targeting of the glucocorticoid hormone receptor with plasmid DNA comprising glucocorticoid response elements improves nonviral gene transfer efficiency in the lungs of mice.

Dames P, Laner A, Maucksch C, Aneja MK, Rudolph C. *J Gene Med.* 2007;9(9):820-829. doi:[10.1002/jgm.1082](https://doi.org/10.1002/jgm.1082)

2006

Interaction of polyamine gene vectors with RNA leads to the dissociation of plasmid DNA-carrier complexes.

Huth S, Hoffmann F, von Gersdorff K, Laner A, Reinhardt D, Rosenecker J, Rudolph C. *J Gene Med.* 2006;8(12):1416-1424. doi:[10.1002/jgm.975](https://doi.org/10.1002/jgm.975)

Leigh syndrome caused by mutations in the flavoprotein (Fp) subunit of succinate dehydrogenase (SDHA).

Horváth R, Abicht A, Holinski-Feder E, Laner A, Gempel K, Prokisch H, Lochmüller H, Klopstock T, Jaksch M. *J Neurol Neurosurg Psychiatry.* 2006;77(1):74-76. doi:[10.1136/jnnp.2005.067041](https://doi.org/10.1136/jnnp.2005.067041)

2005

Bacterial transfer of large functional genomic DNA into human cells.

Laner A, Goussard S, Ramalho AS, Schwarz T, Amaral MD, Courvalin P, Schindelbauer D, Grillot-Courvalin C. *Gene Ther.* 2005;12(21):1559-1572. doi:[10.1038/sj.gt.3302576](https://doi.org/10.1038/sj.gt.3302576)

2004

Gene delivery systems--gene therapy vectors for cystic fibrosis.

Klink D, Schindelbauer D, Laner A, Tucker T, Bebok Z, Schwiebert EM, Boyd AC, Scholte BJ. *J Cyst Fibros.* 2004;3 Suppl 2:203-212. doi:[10.1016/j.jcf.2004.05.042](https://doi.org/10.1016/j.jcf.2004.05.042)

Suitability of a CMV/EGFP cassette to monitor stable expression from human artificial chromosomes but not transient transfer in the cells forming viable clones.

Laner A, Schwarz T, Christan S, Schindelbauer D. *Cytogenet Genome Res.* 2004;107(1-2):9-13. doi:[10.1159/000079564](https://doi.org/10.1159/000079564)

2002

Visible transient expression of EGFP requires intranuclear injection of large copy numbers.

Schindelbauer D, Laner A. *Gene Ther.* 2002;9(11):727-730. doi:[10.1038/sj.gt.3301755](https://doi.org/10.1038/sj.gt.3301755)