

36th GfH Annual Conference

March 4-6, 2026 | Science Congress Center Munich



*programme subject to change

As of March 2026

Legend: # = Speaker is applying for the poster prize

Wednesday, 4 March 2026

Time	Session	Room
11:00 AM – 02:00 PM	Registration opens	Foyer
12:00 PM – 01:00 PM	Lunch Symposium	
01:15 PM – 02:45 PM	EDU 1 AI in the genetic dx	Audimax, First Floor
	Organised by: <i>Stephan Ossowski, Tuebingen (Germany)</i>	
	AI-assisted genome diagnostics <i>Stephan Ossowski, Tuebingen (Germany)</i>	
	Genomic language models <i>Pedro Tomaz da Silva, Munich (Germany)</i>	
	AI-assisted disease diagnostics using facial phenotypes <i>Peter Krawitz, Bonn (Germany)</i>	
	Broadening variant interpretation from coding to non-coding variant effects <i>Martin Kircher, Luebeck (Germany)</i>	
	Single-cell tissue-specific gene prioritization using machine learning <i>Malte Spielmann, Berlin (Germany)</i>	
01:15 PM – 02:45 PM	Symposium 1 Towards a variant effect catalogue Chair: <i>Malte Spielmann, Berlin (Germany)</i> & <i>Kerstin Ludwig, Bonn (Germany)</i>	Hörsaal, Ground Floor
01:15 PM – 01:45 PM	Towards a Systematic Framework for Functional Annotation of Missense Variants in Parkinson's Disease <i>Esther Sammler, Dundee (UK)</i>	
01:45 PM – 02:15 PM	Mapping variant effects with Saturation Genome Editing <i>Gregory Findlay, London (UK)</i>	
02:15 PM – 02:45 PM	Towards at Atlas of Variant Effect <i>Lea Starita, Seattle (USA)</i>	

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01:15 PM – 02:45 PM	Symposium 2 Monogenic movement disorders Chair: Juliane Winkelmann, Munich (Germany) & Katja Lohmann, Luebeck (Germany)	Venus 1+2, Third Floor
01:15 PM – 01:45 PM	Genetics of hypokinetic movement disorders Enza Maria Valente, Padua (Italy)	
01:45 PM – 02:15 PM	Genetics of hyperkinetic movement disorders <i>Michael Zech, Munich (Germany)</i>	
02:15 PM – 02:45 PM	Comprehensive Pheno-Genotyping of Disorders caused by PSMF1 and WARS2 Variants Francesca Magrinelli, London (UK)	
03:00 PM – 04:30 PM	Poster Slam 1 - Clinical Genetics Adults and Tools Chair: Rainer Siebert, Ulm & Christiane Zweier, Bern (Switzerland)	Audimax, First Floor
	P-56: Novel TECTA Variants Reveal Domain-Specific Pathways in Genetic Hearing Loss (A-302) <i>Daniel Bengl, Wuerzburg (Germany)</i>	
	P-113: Episodic nystagmus as predominant phenotypic presentation: Supporting a genotype-phenotype correlation for FRMD5-related disorders) (A-257) <i>Suzette Block, Hamburg (Germany)</i>	
	# P-179: Understanding Nicolaidis-Baraitser Syndrome Beyond Childhood: Key Differences and Challenges in Adults (A-288) <i>Svenja Daschkey, Duesseldorf (Germany)</i>	
	P-44: Genes4All the Video Game – a Serious Game as preparation for genetic counselling for neurodegenerative conditions (A-344) <i>Camila Gabriel, Heidelberg (Germany)</i>	
	P-43: FindMe2care after two years: A platform empowering patients with genetic diagnoses (A-210) <i>Christian Gebhard, Munich (Germany)</i>	
	P-62: Psoriasis – A monogenic disease after all? IFIH1 and its diverse phenotypes within a family (A-242) <i>Vanessa Geiger, Munich (Germany)</i>	
	P-66: Likely pathogenic hemizygous PLS3-variant as a rare cause of X-linked congenital diaphragmatic hernia in two deceased siblings and further relatives (A-297) <i>Corinna Hendrich, Hannover (Germany)</i>	
	P-103: Full of Spleen: Atypical Presentation of a Patient With a Heterozygous RPSA Variant (A-201) <i>Johanna Herwig, Hamburg (Germany)</i>	

	P-50: Clinical and Molecular Characterization of Adults with Cardio-Facio-Cutaneous Syndrome (A-324) <i>Mert Karakaya, Duesseldorf (Germany)</i>	
	# P-189: CFTR Complex Alleles in Individuals with Cystic Fibrosis Showing Limited Response to Elexacaftor/Tezacaftor/Ivacaftor (ETI) Triple Modulator Therapy (A-124) <i>Maike Karnstedt, Leipzig (Germany)</i>	
	P-94: A novel intron variant in the COL4A5 gene potentially causing Alport syndrome identified by genome sequencing (A-254) <i>Isabel Kellner, Munich (Germany)</i>	
	P-58: Clinical and molecular findings in patients with primary lymphedema (A-152) <i>Charlotte Kemper, Berlin (Germany)</i>	
	P-98: Adult hypophosphatasia with ectodermal dysplasia (A-380) <i>Katalin Komlosi, Freiburg (Germany)</i>	
	P-119: Expanding the genotypic and phenotypic spectrum of ROM1-associated macular dystrophy: evidence for a new pathogenic variant (A-268) <i>Patrick Krätschmer, Hamburg (Germany)</i>	
	P-100: The high phenotypic variability of Marfan syndrome: Consequences for diagnosis and personalized management (A-318) <i>Johanna Nowitzky, Martinsried (Germany)</i>	
	# P-178: Symptom Annotation Made Simple for Patients: Developing a Web-App for Symptom Documentation with the HPO in Collaboration with Rare Disease Patients (A-248) <i>Janina Schönberger, Berlin (Germany)</i>	
	P-97: Wiedemann-Steiner syndrome: Delineation of the clinical phenotype in adults (A-370) <i>Friedrich Stock, Essen (Germany)</i>	
	P-87: Evaluation of Stakeholder Perspectives in the German Model Project on Genomics-Based Healthcare (A-183) <i>Gunda Schwaninger, Innsbruck (Austria)</i>	
	P-88: Evaluation of Patient Perspectives in the German Model Project on Genomics-Based Healthcare (A-185) <i>Kathrin Taxer, Innsbruck (Austria)</i>	

03:00 PM – 04:30 PM	Poster Slam 2 - Complex Diseases / Bioinformatics Chair: Nataliya Di Donato, Hannover (<i>Germany</i>) & Frank Tüttelmann, Muenster (<i>Germany</i>)	Hörsaal, Ground Floor
	# P-173: umi-pipeline-nf: A modular and scalable workflow for high-accuracy UMI-tagged nanopore sequencing analysis in human genetics (A-159) <i>Stephan Amstler, Innsbruck (Austria)</i>	
	P-129: Genome sequencing in patients with Long COVID - the „genomLC” study (A-231) <i>Meike Bröckelmann, Bonn (Germany)</i>	
	P-16: Finding genetic factors for eQTLs: Genetic variability of lymphangiogenesis in Collaborative Cross mice (A-233) <i>Emily Melissa Brockmann, Erlangen (Germany)</i>	
	P-14: From Genome Analysis to Patient Counseling: The Use of Large Language Models in Genetics - Their Potential, Performance, and Limitations (A-283) <i>Annemarie Faber, Hannover (Germany)</i>	
	P-124: Genetic analyses of a susceptibility locus for psoriatic arthritis unravel a common RUNX3 missense variant affecting differentiation of CD8+ T cells (A-275) <i>Ulrike Hüffmeier, Erlangen (Germany)</i>	
	P-15: Large Language Models for Phenotype Extraction and Variant Prioritization Using Reasoning (A-163) <i>Tanhim Islam, Aachen (Germany)</i>	
	# P-171: Genolator: A multimodal language model integrating genomic and structural data for functional protein queries utilizing natural language (A-179) <i>Jeremias Krause, Aachen (Germany)</i>	
	P-17: PrimerDesigner: Automating Primer Design and Validation for Efficient Variant Confirmation (A-319) <i>Oliver Kuechler, Berlin (Germany)</i>	
	P-20: Analysis of clinically relevant large tandem repeats using nanopore sequencing (A-338) <i>Silvia Madritsch, Vienna (Austria)</i>	
	# P-172: Evaluation Strategies in Trio Analyses within the Genomic Sequencing Pilot Project (“Modellvorhaben Genomsequenzierung”) (A-120) <i>Sophie Pernickel, Hannover (Germany)</i>	
	P-128: Genetic variation in HLA, IGKV and HHEX loci influence mRNA vaccine-induced long-lasting humoral protection against COVID-19 (A-374) <i>Barbara Puzek, Neuherberg (Germany)</i>	

	P-123: Host control of persistent Epstein-Barr virus infection (A-265) <i>Axel Schmidt, Bonn (Germany)</i>	
	P-19: Evaluation of AT/GC temperature-sensitive enrichment bias in relevant diagnostics genes (A-304) <i>Veronika Scholz, Munich (Germany)</i>	
	P-18: HPO-ira: Inter-rater agreement of HPO-based phenotyping (A-299) <i>Dominik Seelow, Berlin (Germany)</i>	
	P-127: n-silico modeling of interactions between susceptibility genes for bipolar disorder and their effect in regulation of neurodevelopmental processes (A-309) <i>Priyadarshini Thirunvaukkarasu, Basel (Switzerland)</i>	
03:00 PM – 04:30 PM	Poster Slam 3 - Cancer / Basic Mechanisms Chair: Miriam Elbracht, Aachen (Germany) & Chrisitan Schaaf, Heidelberg (Germany)	Venus 1+2, Third Floor
	P-7: Expansions in length of the polypurine-polypyrimidine minisatellite in RPGR exon ORF15 occur at low frequency in human sperm (A-300) <i>Ingrid Bader, Tuebingen (Germany)</i>	
	P-25: Rare TCOF1 variants impact glioma risk via changes in rDNA copy number and rRNA levels (A-121) <i>Frank Brand, Hannover (Germany)</i>	
	P-38: Questioning the Parent-of-Origin Effect in TRIM28-Associated Wilms Tumor Predisposition (A-178) <i>Sofia D Augello, Aachen (Germany)</i>	
	P-39: De novo occurrence of pathogenic variants in breast cancer core genes in Germany (A-341) <i>Carlotta Dencker, Leipzig (Germany)</i>	
	P-32: Expanding Risk Assessment: The Value of the PRS in Women with Breast Cancer Meeting German HBOC Criteria Without Detectable Monogenic Cause (A-347) <i>Paulina Diepers, Leipzig (Germany)</i>	
	# P-176: The spectrum of immunoglobulin heavy chain enhancer hijacking in chronic lymphocytic leukemia (A-214) <i>Cosima Drewes, Ulm (Germany)</i>	
	# P-170: Towards establishment of photochemical approaches for genome-wide and targeted measurement of charge transfer through DNA (A-261) <i>Sven Fauth, Ulm (Germany)</i>	

	<p>P-1: Compound library screening to modulate the tumor-like proliferation of CCM3 knockout endothelial cells (A-186) <i>Janne Lea Feldmann, Greifswald (Germany)</i></p>	
	<p># P-174: Simultaneous angiosarcoma development in three family members with a POT1 variant: Unregulated telomerase activity and cancer predisposition (A-118) <i>Nergis Güzel, Aachen (Germany)</i></p>	
	<p>P-4: QuantumDNA: an open-source computational framework for quantum physical simulations of energy and charge transfer in DNA (A-164) <i>Dennis Herb, Ulm (Germany)</i></p>	
	<p>P-30: The intermediate penetrant variant BRCA1 R1699Q in the cohort of the Cologne Center of the German Consortium of Hereditary Breast and Ovarian Cancer (A-223) <i>Natalie Herold, Cologne (Germany)</i></p>	
	<p>P-9: Crossing the line: GJB2 a small gene with big impact for hearing loss shows epigenetic signature (A-320) <i>Michaela Angelika Hedwig Hofrichter, Wuerzburg (Germany)</i></p>	
	<p>P-3: CNVs and Epimutations: Dual Alterations in Imprinting Disorders (A-306) <i>Florian Kraft, Aachen (Germany)</i></p>	
	<p>P-27: Standardized Digital Risk Assessment Incorporating PRS for Hereditary Breast and Ovarian Cancer (A-197) <i>Rosanna Krakowsky, Leipzig (Germany)</i></p>	
	<p>P-33: Advancing rare disease diagnostics with whole transcriptome sequencing (A-194) <i>Evgenia Vibe, Munich (Germany)</i></p>	
	<p>P-5: PRPF31-related retinal dystrophy due to a novel deep intronic variant (A-122) <i>Larissa Mattern, Aachen (Germany)</i></p>	
	<p>P-36: Paired WES analysis of 781 FFPE tumour samples and matched normal tissue (FFPE or blood) reveals a high proportion of relevant germline variants (A-219) <i>Verena Rickert-Zacharias, Heidelberg (Germany)</i></p>	
	<p>P-6: Impact of cytosine methylation on the diffusion of charges along DNA: a quantum perspective (A-175) <i>Mirko Rossini, Ulm (Germany)</i></p>	

	P-24: Genomic Homologous Repair Deficiency (HRD) as evidence type for classification of BRCA1/2 variants (A-230) <i>Simon Schnaiter, Innsbruck (Austria)</i>	
	P-10: Recurrent pregnancy loss due to SYCP3 variants (A-234) <i>Marina Evi Spörrer, Munich (Germany)</i>	
	# P-175: A novel polygenic score for multiple myeloma predicts incident disease risk and progression from MGUS independent of clinical factors (A-388) <i>Julian S. Wanner, Potsdam (Germany)</i>	
03:00 PM – 04:30 PM	Poster Slam 4 - Clinical Genetics Paediatrics and ND Chair: Johannes Lemke, Leipzig (Germany) & Dagmar Wieczorek, Duesseldorf (Germany)	Taurus 1+2, Ground Floor
	P-79: Using genome-sequencing to improve diagnostic yield in ACADSD (A-258) <i>Angela Abad Perez, Berlin (Germany)</i>	
	P-95: Genetic diagnostics in adults with neurodevelopmental disorders – coming of age (A-291) <i>Ann-Kathrin Bauer, Oldenburg (Germany)</i>	
	P-92: All signs pointed in that direction – how a presumed Krabbe disease turned out to be an EIF2AK2-related LEUDEN syndrome (A-148) <i>Cord-Christian Becker, Munich (Germany)</i>	
	P-72: Expanding the phenotype of a FAT1-associated syndrome (A-386) <i>Juliane Maria Beuschlein, Berlin (Germany)</i>	
	# P-177: Allelic Missense Variants in FGF13A: Same Site, Different Syndrome, and a Caffeine Fix (A-216) <i>Elisabeth Bosch, Erlangen (Germany)</i>	
	P-90: Inherited Truncating Variant in MBD5-Associated Neurodevelopmental Disorder (MAND): Possible Evidence for Variable Expressivity or Reduced Penetrance (A-317) <i>Bianca Greiten, Luebeck (Germany)</i>	
	P-77: A NFIA-associated neurodevelopmental disorder with macrocephaly in two siblings born to a clinically unaffected mother (A-225) <i>Maximilian Haas, Duesseldorf (Germany)</i>	

	P-136: Second report of a de novo deletion of the non-coding exon 1 in NEXMIF in an adult female with intellectual disability and epilepsy (A-212) <i>Radina Karaivanova, Aachen (Germany)</i>	
	P-91: High Familial Penetrance of a 1.425 Mb 17q12 Microduplication: Clinical and Genetic Characterization of a Multigenerational Family (A-377) <i>Anna-Sophie Liegmann, Luebeck (Germany)</i>	
	P-65: NAA15-Associated Disorder Beyond Childhood: Clinical Insights from Adult Patients (A-295) <i>Manuel Michels, Duesseldorf (Germany)</i>	
	P-54: MAPK8IP3-related neurodevelopmental disorder: insights into a variant-specific phenotypic spectrum via a large follow-up study (A-126) <i>Amica Müller-Nedebock, Leipzig (Germany)</i>	
	P-110: First Adult Patient with SLC6A9-associated Glycine Encephalopathy: A Case Report (A-147) <i>Elia Schlaich, Aachen (Germany)</i>	
	P-73: Maternally Inherited CDKN1C Splice-Site Variant Causing Recurrent Fetal IMAGE Syndrome (A-196) <i>Alexander Schulz, Jena (Germany)</i>	
	P-83: Identification of an intronic likely pathogenic HUWE1 variant in a patient with congenital heart defect, dysmorphic features and developmental delay (A-364) <i>Lisa Siegmund, Munich (Germany)</i>	
	P-140: Girl with non-syndromic prenatal short stature and unbalanced X;15 translocation - A case highlighting fundamental genetic principles (A-246) <i>Houda Soudi, Hannover (Germany)</i>	
	P-122: Novel BCL11A variant in a patient with Dias-Logan syndrome (A-368) <i>Andreas Tzschach, Freiburg (Germany)</i>	
	P-108: Partial CCT3 Deletion in a Patient with Global Developmental Delay, Hypotonia, Microcephaly and signs of connective tissue disorder - A Case Report (A-361) <i>Philipp Weber, Neu-Ulm (Germany)</i>	
	P-107: Familial Presentation of Nystagmus and Optic Nerve Hypoplasia in Noonan Syndrome with Loose Anagen Hair due to a PPP1CB Mutation (A-202) <i>Maren Wenzel, Munich (Germany)</i>	

	P-99: Pathogenic germline variant in ABL1 – just a rare connective tissue disease or much more? (A-190) <i>Sarah Westeppe, Frankfurt (Germany)</i>	
	P-42: SMN1 variants causing false-positive SMA newborn screening: Diagnostic pitfalls, functional insights, and clinical and therapeutic implications (A-132) <i>Brunhilde Wirth, Cologne (Germany)</i>	
03:00 PM – 04:30 PM	Poster Slam 5 - Technology, Methods, Omics Chair: Diana Le Duc, Dresden (Germany) & Alexander Hoischen, Nijmegen (The Netherlands)	Mars 1+2 Third Floor
	P-166: Integrative Long-Read and Bioinformatic Analysis of STRC and OTOA in Hearing Loss Diagnostics (A-339) <i>Joshua Bopp, Wuerzburg (Germany)</i>	
	P-89: Discrepant Results of Invasive and Non-Invasive Prenatal Testing in a Case of Confirmed Ring Chromosome 13 (A-264) <i>Tabea Dittrich, Ulm (Germany)</i>	
	P-51: Use of cell-free DNA from amniotic fluid supernatant in routine prenatal diagnostics (A-331) <i>Paul Dremsek, Vienna (Austria)</i>	
	# P-185: When single-modality testing falls short: GLS-related neurodevelopmental movement disorder as a unique example of multi-omics-driven diagnosis (A-145) <i>Ivana Dzinovic, Munich (Germany)</i>	
	P-70: Clinical Relevance of Synonymous Single Nucleotide Variants (A-228) <i>Johannes Ferl, Dresden (Germany)</i>	
	P-190: Adeno-Associated Virus (AAV)-Based Gene Therapy Approach for the Treatment of L-2-Hydroxyglutaric Aciduria (A-207) <i>Hans Zempel, Cologne (Germany)</i>	
	P-133: Chromosome 8 gains in mosaic form: postnatal resolution of prenatal brain–renal anomalies (A-280) <i>Mykyta Kachanov, Hamburg (Germany)</i>	
	P-101: Phasing of complex CYP21A2 alleles in patients with Congenital Adrenal Hyperplasia (CAH) (A-128) <i>Stephanie Kleinle, Munich (Germany)</i>	
	P-57: From Face to Function: SEC24C Deficiency Mimics GPI-Anchor Biosynthesis Disorders (A-321) <i>Alexej Knaus, Bonn (Germany)</i>	

	<p>P-69: Trio re-analysis of HPO-negative genomes with the MorbidGenes Panel identifies new diagnoses in children with (severe) developmental delay (A-277) <i>Marlene Kullik, Oldenburg (Germany)</i></p>	
	<p>P132: DUCKS4: A comprehensive workflow for Nanopore sequencing analysis of Facioscapulohumeral Muscular Dystrophy (FSHD) (A-350) <i>Tamara Löwenstern, Vienna (Austria)</i></p>	
	<p>P-167: Regulatory Pathways for the Validation of Omics-Based Diagnostics: European and National Implementation Frameworks (A-244) <i>Annalisa Musola, Wuerzburg (Germany)</i></p>	
	<p>P-41: Long-read sequencing reveals pathogenic short tandem repeat expansions in patients with movement disorders (A-247) <i>Denny Popp, Leipzig (Germany)</i></p>	
	<p>P-165: Analysis of short tandem repeat loci using long-read Oxford Nanopore (ONT) and Pacific Biosciences (PacBio) HiFi sequencing (A-181) <i>Vitus Prokosch, Munich (Germany)</i></p>	
	<p>P-168: Exploring the limits of ultra-sensitive cfDNA duplex sequencing: relationships between input material, sequencing depth, and detection sensitivity (A-213) <i>Andreas Risch, Munich (Germany)</i></p>	
	<p># P-187: CITE-seq enables high-resolution profiling of rare neonatal immune cell populations (A-375) <i>Paula Rothämel, Munich (Germany)</i></p>	
	<p>P-55: Diagnosing and exploring ALDH1A2-related disorder through integrated clinical, genomic, in silico and functional analyses (A-239) <i>Anna Schaffeldt, Oldenburg (Germany)</i></p>	
	<p>P-164: Streamlining diagnostics in over 400 men with azoospermia – reliable detection of Y-chromosomal AZF deletions using genome sequencing (A-243) <i>Isabell Schumann, Muenster (Germany)</i></p>	
	<p>P-134: Characterization of a complex CHD2 structural variant using nanopore-based long-read sequencing (A-276) <i>Ugo Sorrentino, Munich (Germany)</i></p>	
	<p># P-186: Long-Read RNA sequencing reveals tissue-specific isoform landscapes for rare disease research (A-256) <i>Maren Spaeter, Bad Homburg (Germany)</i></p>	

	P-40: Resolution of a cryptic intragenic duplication in FLCN through combined nanopore DNA and RNA analyses (A-177) <i>Pauline Wittig, Aachen (Germany)</i>	
03:00 PM – 04:30 PM	Poster Slam 6 - Genes and Mechanisms Chair: Christian Kubisch, Hamburg (Germany) & Kerstin Ludwig, Bonn (Germany)	Orion 1+2 Second Floor
	P-147: Neofunctionalization of CELA2B: From pancreatic elastase to putative metabolic regulator (A-323) <i>Liana Abramian, Hamburg (Germany)</i>	
	P-183: Integrating targeted Nanopore mRNA Sequencing into CFTR Variant Interpretation: Functional Evidence for Clinical Classification (A-149) <i>Simone Ahting, Leipzig (Germany)</i>	
	P-153: Novel adjacent dominant NARS1 variants in families with peripheral neuropathy (A-129) <i>Danique Beijer, Aachen (Germany)</i>	
	P-159: Phenotype of KRT10-nEDD-revertant-mosaic patients correlates with the localisation of the variant (A-292) <i>Bettina Burger, Basel (Switzerland)</i>	
	# P-181: Evidence that disruption of Discoidin Domain Receptor 2 contributes to palatomalformations through effects on the extracellular matrix (A-260) <i>Nina Ishorst, Bonn (Germany)</i>	
	P-161: A de novo ALX4 frameshift variant expands the spectrum of dominant ALX4-related disorders (A-270) <i>Nicole Cesarato, Bonn (Germany)</i>	
	P-162: Whole-exome sequencing of a young adult sibling from a family affected by severe periodontitis revealed a functional premature stop codon in CD300C (A-333) <i>Avneesh Chopra, Berlin (Germany)</i>	
	P-149: Transcriptome-informed Genome Analysis in Neurodevelopmental Disorder (A-116) <i>Andreas Fink, Erlangen (Germany)</i>	
	P-154: Sensory polyneuropathy-causing duplication variant in ATL3 leads to aberrant ER membrane shaping (A-173) <i>Lena Franken, Aachen (Germany)</i>	
	P-160: Biallelic GTF3C5 Variants Cause a Multisystem Developmental Disorder: Further Evidence for Gene-Disease Association (A-206) <i>Anne Frederiksen, Kiel (Germany)</i>	

	P-157: A recurrent c.-11C>T change located upstream of the normal ATG initiation codon of ANKH causes self-limited familial infantile epilepsy (A-369) <i>Josua Kegele, Tuebingen (Germany)</i>	
	# P-184: Histological and molecular characterisation of meiotic arrest due to M1AP and SHOC1 variants (A-204) <i>Nadia Korthals, Muenster (Germany)</i>	
	P-145: Sphingolipid and Phospholipid Homeostasis Disruption as a Pathogenic Mechanism in Neuroacanthocytosis Syndromes: Evidence from VPS13A and XK Disease (A-174) <i>Gabriel Miltenberger-Miltenyi, Munich (Germany)</i>	
	# P-182: The Impact of variants in LDHA on low density lipoprotein metabolism (A-127) <i>Melina Musfeldt, Hamburg (Germany)</i>	
	P-150: Genetic testing in paroxysmal dyskinesia (A-157) <i>Lena Antonietta Nothacker, Luebeck (Germany)</i>	
	P-148: Functional investigation of de novo variants in CNOT9 causing neurodevelopmental delay <i>Henry Oppermann, Leipzig (Germany)</i>	
	P-155: Expansion of molecular and clinical aspects of EPS8L2 (DFNB106)-associated hearing loss emphasizes a potential therapeutic window (A-119) <i>Daniel Owrang, Goettingen (Germany)</i>	
	P-158: Biallelic pathogenic variants in SDHC are associated to a Leigh syndrome-like phenotype (A-123) <i>Sharlaine Piel, Hamburg (Germany)</i>	
	P-144: Intellectual disability and skin anomalies - an unexpected high rate of somatic mosaicism (A-113) <i>Fei Song, Duesseldorf (Germany)</i>	
	P-151: Endoplasmic reticulum storage of mutant haptoglobin as a cause of chronic liver damage (A-170) <i>Amelie Stalke, Hannover (Germany)</i>	
04:30 PM – 06:00 PM	Get-Together	Foyer 0 +1 +2
05:00 PM – 06:00 PM	Sitzung der Jungen Humangenetik (Young Human Geneticists)	Hörsaal, Ground Floor

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06:00 PM – 06:15 PM	Opening Session	Audimax, First Floor
06:00 PM – 06:15 PM	Award of the GfH Medal of Honour	Audimax, First Floor
06:15 PM – 07:00 PM	Keynote Lecture	Audimax, First Floor
07:00 PM – 07:45 PM	Non-viral gene therapies powered by DNA, nanotechnology, and AI Hendrik Dietz, Munich (Germany)	Audimax, First Floor

Thursday, 5 March 2026

Time	Session	Room
08:45 AM – 09:30 AM	Plenary Session 1 Chair: Juliane Winkelmann, Munich (<i>Germany</i>) & Rami Abou Jamra, Leipzig (<i>Germany</i>)	Audimax, First Floor
	ReNU'd hope for families: snRNAs in neurodevelopmental disorders <i>Nicola Whiffin, Oxford (UK)</i>	
09:30 AM – 10:30 AM	Selected Presentations Chair: Juliane Winkelmann, Munich (<i>Germany</i>) & Rami Abou Jamra, Leipzig (<i>Germany</i>)	Audimax, First Floor
09:30 AM – 09:45 AM	De novo variants in LDB1 are linked to distinct neurodevelopmental disorders depending on variant location and consequences (A-139) <i>Anne Gregor, Bern (Switzerland)</i>	
09:45 AM – 10:00 AM	Rare functional variants in <i>FBN2</i> represent major genetic determinants of bicuspid aortic valve disease (A-266) <i>Laura Liane Koebbe, Bonn (Germany)</i>	
10:00 AM – 10:15 AM	Pathogenic variants in the cohesin loader subunit MAU2 lead to a new Cornelia de Lange Syndrome subtype (A-138) <i>Ilaria Parenti, Essen (Germany)</i>	
10:15 AM – 10:30 AM	Discovery and Validation of Mitochondrial Disease Biomarkers in the Largest Patient Cohort Study to Date (A-381) <i>Dmitrii Smirnov, Munich (Germany)</i>	
10:30 AM – 11:00 AM	Coffee Time / Poster Viewing	Foyer 0 +1 +2
11:00 AM – 12:30 PM	EDU 2 Long Read Sequencing	Audimax, First Floor
	Organised by: <i>Florian Kraft, Aachen (Germany)</i>	
	Nanopore Adaptive Sampling: A Dynamic Approach to Target Enrichment in Clinical Diagnostics <i>Matthias Linke, Mainz (Germany)</i>	
	Short tandem repeat expansion disorders and long-read sequencing: the good, the bad und the ugly <i>Denny Popp, Leipzig (Germany)</i>	
	Long road towards long-read genome sequencing for comprehensive first line diagnostics? <i>Tobias Haack, Tuebingen (Germany)</i>	

	Longer reads, deeper insights? A second-tier perspective <i>Maureen Jacob, Munich (Germany)</i>	
	Paired Tumor–Normal Long-Read genome sequencing in Blood Cancers <i>Robert Meyer, Aachen (Germany)</i>	
11:00 AM – 12:30 PM	Workshop 1 From Gene Identification to Molecular Mechanism - Genes and Phenotypes Chair: Katja Eggermann, Aachen (Germany) & Nadja Ehmke, Berlin (Germany)	Hörsaal, Ground Floor
11:00 AM – 11:15 AM	<i>ERO1A</i> is a novel disease gene for autosomal recessive ichthyosis and keratoderma with bone fragility (A-354) <i>Tess Holling, Hamburg (Germany)</i>	
11:15 AM – 11:30 AM	Phenotypic and functional insights into the <i>PHF5A</i> -associated spliceosomopathy (A-352) <i>Inken Junod, Hamburg (Germany)</i>	
11:30 AM – 11:45 AM	Uncovering a new enzyme-rescue mechanism as the cause of a rare skeletal dysplasia (A-245) <i>Hristiana Lyubenova, Berlin (Germany)</i>	
11:45 AM – 12:00 PM	The <i>TCTB-C225Y</i> Variant Causing Autosomal Dominant Deafness in a Nicaraguan Family Enhances Sensitivity to Noise-Induced Hearing Loss in Mice (A-187) <i>Barbara Vona, Goettingen (Germany)</i>	
12:00 PM – 12:15 PM	Known Gene, new Phenotype: DGUOK dysfunction as a monogenetic cause of pleuroparenchymal fibroelastosis (A-253) <i>Sandra v. Hardenberg, Hannover (Germany)</i>	
12:15 PM – 12:30 PM	Biallelic <i>WDHD1</i> variants cause microcephalic primordial dwarfism (A-348) <i>Debora Tibbe, Hamburg (Germany)</i>	
11:00 AM – 12:30 PM	Workshop 2 Cancer Chair: Julia Hentschel, Leipzig (Germany) & Anne Quante, Munich (Germany)	Venus 1+2, Third Floor
11:00 AM – 11:15 AM	Cross-species epigenetic profiling of TCL1-associated T- and B-cell leukemias (A-205) <i>Billy Jebaraj, Ulm (Germany)</i>	
11:15 AM – 11:30 AM	Cancer predisposition in the international INFORM (INdividualized Therapy FORe Relapsed Malignancies in	

36th GfH Annual Conference

March 4-6, 2026 | Science Congress Center Munich



	Childhood) Registry (A-273) <i>Steffen Hirsch, Heidelberg (Germany)</i>	
11:30 AM – 11:45 AM	Functional evaluation of <i>SDHB</i> missense variants in vitro (A-326) <i>Arne Jahn, Dresden (Germany)</i>	
11:45 AM – 12:00 PM	Integrative Fragmentomics: Machine Learning–Driven Analysis of cfDNA Whole-Genome Sequencing for Liquid Biopsy in Cancer (A-153) <i>Leonie Pohl, Munich (Germany)</i>	
12:00 PM – 12:15 PM	Functional analyses of <i>RUNX1</i> variants – from optimized transactivation assays towards multiplex assay for variant effects (MAVE) (A-311) <i>Alina Prüne, Hannover (Germany)</i>	
12:15 PM – 12:30 PM	Two years of Multifactorial Breast Cancer Risk Assessment including PGS in routine care in western Austria: Lessons learned and outlook (A-241) <i>Simon Schnaiter, Innsbruck (Austria)</i>	
11:00 AM – 12:30 PM	Workshop 3 Clinical Genetics and Prenatal Diagnostics Chair: Georgia Vasileiou, Hannover (<i>Germany</i>) & Matias Wagner, Munich (<i>Germany</i>)	Taurus 1+2, Ground Floor
11:00 AM – 11:15 AM	Parental diseases and predispositions detected in prenatal trio exome diagnostics (A-235) <i>Uwe Ahting, Martinsried (Germany)</i>	
11:15 AM – 11:30 AM	RNUopathies – expansion of clinical spectra and family-oriented resources (A-135) <i>Nuria Brämswig, Muenster (Germany)</i>	
11:30 AM – 11:45 AM	Deciphering Dup15q syndrome: Integrating the genomic architecture of supernumerary (iso-)dicentric chromosomes with longitudinal deep-phenotyping (A-328) <i>Sebastian Burkart, Heidelberg (Germany)</i>	
11:45 AM – 12:00 PM	Genetic variations in 135 pediatric CAKUT patients requiring kidney replacement therapy and their association with outcome after transplantation (A-200) <i>Helge Martens, Hannover (Germany)</i>	
12:00 PM – 12:15 PM	Clinical Experience with Preimplantation Genetic Testing for Monogenic Disorders at Synlab MVZ Human Genetics Munich: Data and Insights (A-238) <i>Jasmina Ćomić, Munich (Germany)</i>	
12:15 PM – 12:30 PM	<i>NUS1</i> -Related Disease: Uncovering hidden clinical features and novel mutational hotspots (A-195)	

36th GfH Annual Conference

March 4-6, 2026 | Science Congress Center Munich



	<i>Melissa Pauly, Erlangen (Germany)</i>	
12:30 PM – 02:00 PM	Lunch / Meetingtime / Poster Viewing / Lunch Symposium	Foyer 0 +1 +2
12:45 PM – 01:45 PM	Sitzung der Naturwissenschaftler	Venus 1+2, Third Floor
	Organised by: Christine Neuhaus, Cologne (Germany)	
01:00 PM – 02:00 PM	Scientific Speed Dating	Foyer 3
02:00 PM – 03:30 PM	EDU 3 RNA: how to use RNA to boost diagnostic by identifying variants?	Audimax, First Floor
	Organised by: <i>Holger Prokisch, Munich (Germany)</i>	
	<i>RNAseq "solving the unsolved": clinical implementation of RNAseq in a cohort of 500 mitochondrial disease cases Fatemeh Peimani, Munich (Germany)</i>	
	Technical implementation of RNA-seq for rare disease applications <i>Vicente A. Yépez, Munich (Germany)</i>	
	Diagnostic RNA-seq in unsolved genetic disorders <i>Tjakko van Ham, Rotterdam (The Netherlands)</i>	
	"Viel hilft viel" increasing omics evidence improve confidence in diagnostics <i>Dmitrii Smirnov, Munich (Germany)</i>	
02:00 PM – 03:30 PM	Workshop 4 From Gene Identification to Molecular Mechanism - NDD Chair: <i>Natja Haag, Aachen (Germany) & Gökhan Yigit, Goettingen (Germany)</i>	Hörsaal, Ground Floor
02:00 PM – 02:15 PM	A homozygous synonymous <i>NOP58</i> variant causes a neurodevelopmental disorder by impairing maturation of pre-ribosomal RNAs (A-330) <i>Loisa Dana Bonde, Hamburg (Germany)</i>	
02:15 PM – 02:30 PM	Small RNA-sequencing analysis reveals distinct functional effects of LESKRES-associated AGO2 variants on miRNA binding and processing (A-293) <i>Christina Kiel, Regensburg (Germany)</i>	
02:30 PM – 02:45 PM	Recessive and dominant variants in <i>RNU2-2</i> lead to frequent developmental and epileptic encephalopathies (A-115) <i>Elsa Leitão, Essen (Germany)</i>	

36th GfH Annual Conference

March 4-6, 2026 | Science Congress Center Munich



02:45 PM – 03:00 PM	Pathogenic <i>RBMX</i> variants cause clinically variable syndromic neurodevelopmental disorder with evidence of functional redundancy with retrocopy <i>RBMXL1</i> (A-143) <i>Carolin Mattausch, Essen (Germany)</i>	
03:00 PM – 03:15 PM	Inherited and <i>de novo</i> variants in <i>CACNG3</i> cause a non-syndromic neurodevelopmental disorder (A-193) <i>Kristin Mehner, Leipzig (Germany)</i>	
03:15 PM – 03:30 PM	Elucidating the shared genetic background of dystonia and neurodevelopmental disorders (A-114) <i>Linn Welzel, Luebeck (Germany)</i>	
02:00 PM – 03:30 PM	Workshop 5 Technology and Omics Chair: Felix Boschann, Berlin (Germany) & Christian Schlein, Hamburg (Germany)	Venus 1+2, Third Floor
02:00 PM – 02:15 PM	Feasibility of Whole-Genome Sequencing and Variant Analysis from Dried Blood Spots for Genomic Newborn Screening (A-117) <i>Isabel Rebecca Betzler, Heidelberg (Germany)</i>	
02:15 PM – 02:30 PM	Using long-read sequencing to decipher the <i>SMN2</i> locus in severely affected SMA patients. (A-303) <i>Maureen Jacob, Munich (Germany)</i>	
02:30 PM – 02:45 PM	Transcriptomics analysis achieves new solved cases in rare undiagnosed dystonia (A-158) <i>Alice Saparov, Munich (Germany)</i>	
02:45 PM – 03:00 PM	Saturation mutagenesis of immune genes and gene delivery vectors by oligonucleotide pool synthesis (A-290) <i>Jonathan Schmid-Burgk, Bonn (Germany)</i>	
03:00 PM – 03:15 PM	Benchmarking Mosaic Variant Detection Using NGS Amplicon Spike-In (A-263) <i>Sonja Wegscheider, Leipzig (Germany)</i>	
03:15 PM – 03:30 PM	Harmonized framework for RNA-seq-based rare disease diagnostics allows rapid and robust results interpretation in large cohorts (A-255) <i>Vicente Yépez, Munich (Germany)</i>	

36th GfH Annual Conference

March 4-6, 2026 | Science Congress Center Munich



02:00 PM – 03:30 PM	Workshop 6 Complex disorders and Population Genetics Chair: Andreas Forstner, Bonn (<i>Germany</i>) & Dario Gajewski, Goettingen (<i>Germany</i>)	Taurus 1+2, Ground Floor
02:00 PM – 02:15 PM	Genetic architecture of COVID-19 in the German National Pandemic Cohort Network (NAPKON): Insights from exome and genome sequencing (A-184) <i>Ayda Abolhassani, Bonn (Germany)</i>	
02:15 PM – 02:30 PM	A combination of biochemical and genetic screening reveals an unexpectedly high prevalence of familial hypercholesterolemia in Bavarian children (A-281) <i>Artem Amosov, Munich (Germany)</i>	
02:30 PM – 02:45 PM	The role of <i>de novo</i> variants in neurodevelopmental disorders with epilepsy (A-249) <i>Andrea Eoli, Potsdam (Germany)</i>	
02:45 PM – 03:00 PM	Massively Parallel Reporter Assays (MPRA) Identify Causal Variants in Complex Inflammatory Disease (A-329) <i>Tim Kühnlenz, Berlin (Germany)</i>	
03:00 PM – 03:15 PM	Impact of Common Genetic Variants in Undiagnosed Rare Early-Onset Epilepsies (A-272) <i>Ala Sahada, Potsdam (Germany)</i>	
03:15 PM – 03:30 PM	Long-read sequencing of >4,000 infertile men – how human genetics can advance the development of novel non-hormonal contraceptives (A-325) <i>Frank Tüttelmann, Muenster (Germany)</i>	
03:30 PM – 04:00 PM	Coffee Time / Poster Viewing	Foyer 0 +1 +2
04:00 PM – 04:45 PM	Plenary Session 2 Chair: Miriam Elbracht, Aachen (<i>Germany</i>) & Uwe Kornak, Goettingen (<i>Germany</i>)	Audimax, First Floor
	Mutational Landscape of the Male Germline and Its Inheritance Consequences <i>Raheleh Rahbari, Cambridge (UK)</i>	
05:00 PM – 06:30 PM	GfH General Assembly	Audimax, First Floor
08:00 PM	Start Networking Evening (Registration required / already sold out)	Bamberger Haus

36th GfH Annual Conference

March 4-6, 2026 | Science Congress Center Munich



Friday, 6 March 2026

Time	Session	Room
08:30 AM – 10:00 AM	Symposium 3 Updates on Polygenic scores Chair: Henrike Heyne, Potsdam (Germany) & Sven Cichon, Basel (Switzerland)	Audimax, First Floor
08:30 AM – 09:15 AM	Translational genomics of complex diseases <i>Eleftheria Zeggini, Munich (Germany)</i>	
09:15 AM – 10:00 AM	Leveraging functional genomic annotations to enhance risk prediction and biological discovery <i>Jian Zeng, St Lucia (Australia)</i>	
08:30 AM – 10:00 AM	Symposium 4 Factors influencing penetrance and expressivity Chair: Johannes Zschocke, Innsbruck (Austria) & Christiane Zweier, Bern (Switzerland)	Hörsaal, Ground Floor
08:30 AM – 09:15 AM	The role of polygenic scores in investigating reduced penetrance <i>Inke König, Luebeck (Germany)</i>	
09:15 AM – 10:00 AM	Reassessing penetrance and expressivity using a genotype first approach in population cohorts <i>Michael Weedon, Exeter (UK)</i>	
08:30 AM – 10:00 AM	Symposium 5: Cardiology meets Genetics – First Joint Symposium of DGIM & GfH Chair: Ulrich Zechner, Cologne (Germany) & Eva Klopocki, Wuerzburg (Germany)	Venus 1+2, Third Floor
	Actionable Cardiac Genes: From Risk Stratification to Gene-specific Treatments <i>Benjamin Meder, Heidelberg (Germany)</i>	
	Inherited cardiac diseases: From genetic mechanisms towards therapy <i>Bernd Wollnik, Goettingen (Germany)</i>	
10:00 AM – 10:30 AM	Coffee Time / Poster Viewing	Foyer 0 +1 +2
10:30 AM – 12:00 PM	EDU 4 Mutations we almost missed Organised by: Bernd Wollnik, Goettingen (Germany)	Audimax, First Floor
	Fallvorstellung <i>Rami Abou Jamra, Leipzig (Germany)</i> <i>Fei Song, Duesseldorf (Germany)</i> <i>Alex Hoischen, Nijmegen (The Netherlands)</i> <i>Henrike Steding, Hannover (Germany)</i>	

36th GfH Annual Conference

March 4-6, 2026 | Science Congress Center Munich



	<i>Gökhan Yigit, Goettingen (Germany)</i>	
10:30 AM – 12:00 PM	Workshop 7 From Gene Identification to Molecular Mechanism - Mechanisms, Models, and Therapies Chair: Anne Gregor, Bern (Switzerland) & Henry Oppermann, Leipzig (Germany)	Hörsaal, Ground Floor
10:30 AM – 10:45 AM	Proof-of-concept for non-viral gene therapy of <i>CLCN7</i> -dependent autosomal recessive osteopetrosis using a transposon (A-342) <i>Dario Gajewski, Goettingen (Germany)</i>	
10:45 AM – 11:00 AM	Development of an Engineered Human Myocardium model to study TOP3A-related cardiomyopathy (A-384) <i>Marianne Gaubert, Goettingen (Germany)</i>	
11:00 AM – 11:15 AM	The Potential of Whole Genome Sequencing in Pharmacogenetics: A Retrospective Health Record Study in Rare Disease Patients (A-182) <i>Jeremias Krause, Aachen (Germany)</i>	
11:15 AM – 11:30 AM	apmer ASO for <i>GRIN1</i> -related Developmental and Epileptic Encephalopathy (A-316) <i>Ilona Krey-Grauert, Leipzig (Germany)</i>	
11:30 AM – 11:45 AM	Sodium channel activity differentially affects abundance of C-LTMR neurons in mice (A-171) <i>Martha Lürkens, Aachen (Germany)</i>	
11:45 AM – 12:00 PM	Using <i>Drosophila melanogaster</i> to determine the pathogenicity of missense variants in piRNA pathway genes identified in infertile men (A-162) <i>Birgit Stallmeyer, Muenster (Germany)</i>	
10:30 AM – 12:00 PM	Workshop 8 Basic Mechanisms and Epigenetics Chair: Tess Holling, Hamburg (Germany) & Denny Popp, Leipzig (Germany)	Venus 1+2, Third Floor
10:30 AM – 10:45 AM	Hyperactivity of the non-canonical inflammasome in SPG11 and SPG48 (A-155) <i>Muhammad Awais Afzal, Jena (Germany)</i>	
10:45 AM – 11:00 AM	Genome-wide Identification and Validation of Human Imprinting Control Regions Using Long-Read Trio Sequencing and Allele-Specific Transcriptomics (A-340) <i>Joshua Bopp, Wuerzburg (Germany)</i>	
11:00 AM – 11:15 AM	From enhancer variant to bone phenotype: functional modeling in iPSC-derived cells (A-357) <i>Regina Grün, Goettingen (Germany)</i>	

36th GfH Annual Conference

March 4-6, 2026 | Science Congress Center Munich



11:15 AM – 11:30 AM	The Value of Epigenetic Signatures as Key to Diagnosis in Neurodevelopmental Disorders (A-378) <i>Teresa Neuhan, Munich (Germany)</i>	
11:30 AM – 11:45 AM	Light inducible FLPase reconstitution (LIFR) enables temporal control of gene expression for human genetic disease modelling in Drosophila (A-373) <i>Roman Praschberger, Innsbruck (Austria)</i>	
11:45 AM – 12:00 PM	High-throughput differentiation of human blood vessel organoids to model vascular diseases (A-192) <i>Dariusz Skowronek, Greifswald (Germany)</i>	
10:30 AM – 12:00 PM	Workshop 9 Bioinformatics / Biostatistic Chair: Bernt Popp, <i>Nuremberg (Germany)</i> & Axel Schmidt, <i>Bonn (Germany)</i>	Taurus 1+2, Ground Floor
10:30 AM – 10:45 AM	Bone2Gene: Deep Phenotyping of Rare Bone Diseases (A-284) <i>Eike Bolmer, Bonn (Germany)</i>	
10:45 AM – 11:00 AM	NGPsuite: Privacy-preserving integration of GestaltMatcher face analysis and PubCaseFinder HPO-based phenotype matching (A-259) <i>Tzung-Chien Hsieh, Bonn (Germany)</i>	
11:00 AM – 11:15 AM	Prediction and exploration of ReNU syndrome by facial image analysis (A-314) <i>Alexander Hustinx, Bonn (Germany)</i>	
11:15 AM – 11:30 AM	Disentangling Familial and Syndromic Facial Features Using Latent Embedding Analysis (A-140) <i>Carolin Kaffiné, Bonn (Germany)</i>	
11:30 AM – 11:45 AM	Predicting Functional Effects of Ion Channel Variants Using Deep Learning and Protein Language Models (A-313) <i>Francesca Rissom, Potsdam (Germany)</i>	
11:45 AM – 12:00 PM	Exploring the boundaries of the diagnostic spectrum of FSHD - Genetic and epigenetic profiling for FSHD diagnosis using nanopore sequencing (A-279) <i>Florentine Scharf, Munich (Germany)</i>	
12:00 PM – 01:30 PM	Lunch / Meetingtime / Poster Viewing / Lunch Symposium	Foyer 0 +1 +2
12:15 PM – 01:15 PM	DFG-Fördermöglichkeiten Lea Berg, Bonn (Germany)	Hörsaal, Ground Floor

36th GfH Annual Conference

March 4-6, 2026 | Science Congress Center Munich



12:15 PM – 01:15 PM	GHGA-Workshop: 10.000 Genomes and Counting: Experiences, Interfaces and Perspectives from the genomDE Model Project <i>Organised by: Jan Eufinger (GHGA/DKFZ), Andreas Till (genomDE/BfArM), Tatjana Hübner (genomDE/BfArM).</i>	Taurus 1+2, Ground Floor
12:15 PM – 12:25 PM	<i>Opening: On the Path to Modern Genomic Medicine: Status of the genomDE Model Project</i> <i>Andreas Till, Bundesinstitut für Arzneimittel und Medizinprodukte (BfArM)</i>	
12:25 PM – 12:35 PM	Data Handling in GRZ and GHGA <i>Christian Mertes, TUM & TUM Klinikum</i>	
12:35 PM – 12:45 PM	A central trust centre at the Robert Koch Institute: Gateway for Secure Genomic Research and Health Care <i>Anna Lübbe, Robert Koch-Institut (RKI)</i>	
12:45 PM – 12:55 PM	Clinical Perspective on genomDE - first impact in clinical practice of genomDE <i>Malte Spielmann, Charité – Universitätsmedizin Berlin</i>	
12:55 PM – 01:15 PM	Joint Discussion with all speakers of the session <i>Chair: Jan Eufinger (GHGA/DKFZ)</i>	
01:30 PM – 02:30 PM	Symposium 6 Gene therapies Chair: Nataliya Di Donato, Hannover (Germany) & Peter Krawitz, Bonn (Germany)	
01:30 PM – 02:00 PM	Tailoring AAV vectors for in vivo gene therapy <i>Hildegard Bühning, Hannover (Germany)</i>	
02:00 PM – 02:30 PM	Optogenetic therapies: opportunities and challenges Tobias Moser, Goettingen (Germany)	
01:30 PM – 02:30 PM	Symposium 7 Pangenome Chair: Birte Kehr, Hannover (Germany) & Martin Kircher, Bonn (Germany)	Hörsaal, Ground Floor
01:30 PM – 02:00 PM	Pangenome based analysis of structural variation <i>Tobias Marschall, Duesseldorf (Germany)</i>	
02:00 PM – 02:30 PM	Population sampling in the human pangenome reference <i>Eimear Kenny, New York (USA)</i>	
01:30 PM – 02:30 PM	Symposium 8 GfH-SFGH Joint-Symposium	Venus 1+2, Third Floor

36th GfH Annual Conference

March 4-6, 2026 | Science Congress Center Munich



	Chair: Juliane Winkelmann, Munich (Germany) & Markus Nöthen, Bonn (Germany)	
01:30 PM – 02:00 PM	Impact of genetic diversity on HLA and KIR imputation <i>Nicolas Vince, Nantes (France)</i>	
02:00 PM – 02:30 PM	France Médecine Génomique Plan (PFMG) <i>Jean-François Deleuze (France)</i>	
02:30 PM – 02:45 PM	Closing remarks and Awards Ceremony	Audimax, First Floor