**Nieminen M**, **Stolpe O**, **Kuhring M**, **Weiner J**, Pett P (2022). “SODAR: enabling, modeling, and managing multi-omics integration studies.” *bioRxiv*. doi:10.1101/2022.08.19.504516

**Ivanov A**, Mattei D, Radscheit K, Compagnion A, Pett J, Herzel H, Paolicelli R, Piwecka M, Meyer U, **Beule D** (2022). “Analyses of circRNA Expression throughout the Light-Dark Cycle Reveal a Strong Regulation of Cdr1as, Associated with Light Entrainment in the SCN.” *Int J Mol Sci*, *23*. doi:10.3390/ijms232012347

Graff P, Wolzopolski J, Voss A, Blimkie T, **Weiner J** (2022). “Extracellular matrix remodeling in atopic dermatitis harnesses the onset of an asthmatic phenotype and is a potential contributor to the atopic march.” *medRxiv*. doi:10.1101/2022.01.17.22269397

Wirges A, Bunse M, Joedicke J, **Blanc E**, Gudipati V, Moles M, Shiku H, **Beule D**, Huppa J, Höpken U, Rehm A (2022). “EBAG9 silencing exerts an immune checkpoint function without aggravating adverse effects.” *Mol Ther*, *30*, 3358-3378. doi:10.1016/j.ymthe.2022.07.009

Hönzke K, **Obermayer B**, Mache C, Fathykova D, Kessler M, Dökel S, Wyler E, Baumgardt M, Löwa A, Hoffmann K, Graff P, Schulze J, Mieth M, Hellwig K, Demir Z, Biere B, Brunotte L, Mecate-Zambrano A, Bushe J, Dohmen M, Hinze C, Elezkurtaj S, Tönnies M, Bauer T, Eggeling S, Tran H, Schneider P, Neudecker J, Rückert J, Schmidt-Ott K, Busch J, Klauschen F, Horst D, Radbruch H, Radke J, Heppner F, Corman V, Niemeyer D, Müller M, Goffinet C, Mothes R, Pascual-Reguant A, Hauser A, **Beule D**, Landthaler M, Ludwig S, Suttorp N, Witzenrath M, Gruber A, Drosten C, Sander L, Wolff T, Hippenstiel S, Hocke A (2022). “Human lungs show limited permissiveness for SARS-CoV-2 due to scarce ACE2 levels but virus-induced expansion of inflammatory macrophages.” *Eur Respir J*, *60*. doi:10.1183/13993003.02725-2021

Freitag K, Sterczyk N, Wendlinger S, **Obermayer B**, Schulz J, Farztdinov V, Mülleder M, Ralser M, Houtman J, Fleck L, Braeuning C, Sansevrino R, Hoffmann C, Milovanovic D, Sigrist S, Conrad T, **Beule D**, Heppner F, Jendrach M (2022). “Spermidine reduces neuroinflammation and soluble amyloid beta in an Alzheimer’s disease mouse model.” *J Neuroinflammation*, *19*, 172. doi:10.1186/s12974-022-02534-7

Schalbetter S, von AA, Cruz-Ochoa N, Dawson K, **Ivanov A**, Mueller F, Lin H, Amport R, Mildenberger W, Mattei D, **Beule D**, Földy C, Greter M, Notter T, Meyer U (2022). “Adolescence is a sensitive period for prefrontal microglia to act on cognitive development.” *Sci Adv*, *8*, eabi6672. doi:10.1126/sciadv.abi6672

Grunert C, Willimsky G, Peuker C, Rhein S, Hansmann L, Blankenstein T, **Blanc E**, **Beule D**, Keller U, Pezzutto A, Busse A (2022). “Isolation of Neoantigen-Specific Human T Cell Receptors from Different Human and Murine Repertoires.” *Cancers (Basel)*, *14*. doi:10.3390/cancers14071842

Dannebaum R, Suwalski P, Asgharian H, Du ZG, Lin H, **Weiner J**, **Holtgrewe M**, Thibeault C, Müller M, Wang X, Karadeniz Z, Saccomanno J, Doehn J, Hübner R, Hinzmann B, Blüher A, Siemann S, Telman D, Suttorp N, Witzenrath M, Hippenstiel S, Skurk C, Poller W, Sander L, **Beule D**, Kurth F, Guettouche T, Landmesser U, Berka J, Luong K, Pa-COVID SG, Rubelt F, Heidecker B (2022). “Highly multiplexed immune repertoire sequencing links multiple lymphocyte classes with severity of response to COVID-19.” *EClinicalMedicine*, *48*, 101438. doi:10.1016/j.eclinm.2022.101438

Horak P, Griffith M, Danos A, Pitel B, Madhavan S, Liu X, Chow C, Williams H, Carmody L, Barrow-Laing L, Rieke D, Kreutzfeldt S, Stenzinger A, Tamborero D, **Benary M**, Rajagopal P, Ida C, Lesmana H, Satgunaseelan L, Merker J, Tolstorukov M, Campregher P, Warner J, Rao S, Natesan M, Shen H, Venstrom J, Roy S, Tao K, Kanagal-Shamanna R, Xu X, Ritter D, Pagel K, Krysiak K, Dubuc A, Akkari Y, Li X, Lee J, King I, Raca G, Wagner A, Li M, Plon S, Kulkarni S, Griffith O, Chakravarty D, Sonkin D (2022). “Standards for the classification of pathogenicity of somatic variants in cancer (oncogenicity): Joint recommendations of Clinical Genome Resource (ClinGen), Cancer Genomics Consortium (CGC), and Variant Interpretation for Cancer Consortium (VICC).” *Genet Med*, *24*, 986-998. doi:10.1016/j.gim.2022.01.001

**Weiner J**, **Obermayer B**, **Beule D** (2022). “Venn Diagrams May Indicate Erroneous Statistical Reasoning in Transcriptomics.” *Front Genet*, *13*, 818683. doi:10.3389/fgene.2022.818683

Gloaguen Y, Kirwan J, **Beule D** (2022). “Deep Learning-Assisted Peak Curation for Large-Scale LC-MS Metabolomics.” *Anal Chem*, *94*, 4930-4937. doi:10.1021/acs.analchem.1c02220

Chopra A, Mueller R, **Weiner J**3, Rosowski J, Dommisch H, Grohmann E, Schaefer A (2022). “BACH1 Binding Links the Genetic Risk for Severe Periodontitis with ST8SIA1.” *J Dent Res*, *101*, 93-101. doi:10.1177/00220345211017510

Bischoff P, Trinks A, Wiederspahn J, **Obermayer B**, Pett J, Jurmeister P, Elsner A, Dziodzio T, Rückert J, Neudecker J, Falk C, **Beule D**, Sers C, Morkel M, Horst D, Klauschen F, Blüthgen N (2022). “The single-cell transcriptional landscape of lung carcinoid tumors.” *Int J Cancer*, *150*, 2058-2071. doi:10.1002/ijc.33995

Georg P, Astaburuaga-García R, Bonaguro L, Brumhard S, Michalick L, Lippert L, Kostevc T, Gäbel C, Schneider M, Streitz M, Demichev V, Gemünd I, Barone M, Tober-Lau P, Helbig E, Hillus D, Petrov L, Stein J, Dey H, Paclik D, Iwert C, Mülleder M, Aulakh S, Djudjaj S, Bülow R, Mei H, Schulz A, Thiel A, Hippenstiel S, Saliba A, Eils R, Lehmann I, Mall M, Stricker S, Röhmel J, Corman V, Beule D, Wyler E, Landthaler M, **Obermayer B**, von SS, Boor P, Demir M, Wesselmann H, Suttorp N, Uhrig A, Müller-Redetzky H, Nattermann J, Kuebler W, Meisel C, Ralser M, Schultze J, Aschenbrenner A, Thibeault C, Kurth F, Sander L, Blüthgen N, Sawitzki B, PA-COVID-19 SG (2022). “Complement activation induces excessive T cell cytotoxicity in severe COVID-19.” *Cell*, *185*(3), 493-512.e25. ISSN 0092-8674, doi:10.1016/j.cell.2021.12.040

Zinnall U, Milek M, Minia I, Vieira-Vieira C, Müller S, Mastrobuoni G, Hazapis O, Del GS, Schwefel D, Bley N, Voigt F, Chao J, Kempa S, Hüttelmaier S, Selbach M, Landthaler M (2022). “HDLBP binds ER-targeted mRNAs by multivalent interactions to promote protein synthesis of transmembrane and secreted proteins.” *Nat Commun*, *13*(1), 2727. doi:10.1038/s41467-022-30322-7

Mothes R, Pascual-Reguant A, Koehler R, Liebeskind J, Liebheit A, Bauherr S, Dittmayer C, Laue M, Manitius R, Elezkurtaj S, Durek P, Heinrich F, Heinz GA, Guerra GM, **Obermayer B**, Meinhardt J, Ihlow J, Radke J, Heppner FL, Enghard P, Stockmann H, Aschman T, Schneider J, Corman V, Sander LE, Mashreghi M, Conrad T, Hocke A, Niesner RA, Radbruch H, Hauser AE (2022). “Local CCL18 and CCL21 expand lung fibrovascular niches and recruit lymphocytes, leading to tertiary lymphoid structure formation in prolonged COVID-19.” *medRxiv*. doi:10.1101/2022.03.24.22272768

https://www.medrxiv.org/content/early/2022/03/27/2022.03.24.22272768.full.pdf,

Yerinde C, Keye J, Durlanik S, Freise I, Nowak F, Hsiao H, Letizia M, Schlickeiser S, **Obermayer B**, Huck A, Friedrich M, Wu H, Kunkel D, K”uhl AA, Bauer S, Thiel A, Siegmund B, Glauben R, Weidinger C (2022). “HDAC7 controls anti-viral and anti-tumor immunity by CD8+ T cells.” *bioRxiv*. doi:10.1101/2022.09.18.508452

https://www.biorxiv.org/content/early/2022/09/19/2022.09.18.508452.full.pdf,

Dörr D, **Obermayer B**, **Weiner JM**, Zimmermann K, Anania C, Wagner LK, Lyras EM, Sapozhnikova V, Lara-Astiaso D, Prósper F, Lang R, Lupiáñez DG, **Beule D**, Höpken UE, Leutz A, Mildner AMA (2022). “C/EBPβ regulates lipid metabolism and Pparg isoform 2 expression in alveolar macrophages.” *Science Immunology*, *7*(75), eabj0140. doi:10.1126/sciimmunol.abj0140

https://www.science.org/doi/pdf/10.1126/sciimmunol.abj0140,

Kedziora S, **Obermayer B**, Sugulle M, Herse F, Kräker K, Haase N, Langmia I, Müller D, Staff A, **Beule D**, Dechend R (2022). “Placental Transcriptome Profiling in Subtypes of Diabetic Pregnancies Is Strongly Confounded by Fetal Sex.” *Int J Mol Sci*, *23*(23). ISSN 1422-0067, doi:10.3390/ijms232315388

Pennitz P, Kirsten H, Wyler E, Goekeri C, **Obermayer B**, Heinz GA, Mashreghi MF, Trimpert J, Landthaler M, Suttorp N, Hocke AC, Hippenstiel S, T”onnies M, Scholz M, Kuebler WM, Witzenrath M, Hoenzke K, Nouailles G (2022). “Integrational approaches for cross-species analysis of lung pathologies at single-cell resolution.” *Pneumologie*, *76*(S 01), FV 285. FV 285.

Hoffmann K, **Obermayer B**, Hönzke K, Fatykhova D, Demir Z, Löwa A, Alves L, Wyler E, Lopez-Rodriguez E, Mieth M, Baumgardt M, Hoppe J, Firsching T, Tönnies M, Bauer T, Eggeling S, Tran H, Schneider P, Neudecker J, Rückert J, Gruber A, Ochs M, Landthaler M, **Beule D**, Suttorp N, Hippenstiel S, Hocke A, Kessler M (2022). “Human alveolar progenitors generate dual lineage bronchioalveolar organoids.” *Commun Biol*, *5*(1), 875. ISSN 2399-3642, doi:10.1038/s42003-022-03828-5

Neitzel H, Varon R, Chughtai S, Dartsch J, Dutrannoy-Tönsing V, Nürnberg P, Nürnberg G, Schweiger M, Digweed M, Hildebrand G, Hackmann K, **Holtgrewe M**, Sarioglu N, Schulze B, Horn D, Sperling K (2022). “Transmission ratio distortion of mutations in the master regulator of centriole biogenesis PLK4.” *Hum Genet*, *141*(11), 1785-1794. doi:10.1007/s00439-022-02461-w

Foddis M, Blumenau S, **Holtgrewe M**, Paquette K, Westra K, Alonso I, Macario M, Morgadinho A, Velon A, Santo G, Santana I, Mönkäre S, Kuuluvainen L, Schleutker J, Pöyhönen M, Myllykangas L, Pavlovic A, Kostic V, Dobricic V, Lohmann E, Hanagasi H, Santos M, Guven G, Bilgic B, Bras J, **Beule D**, Dirnagl U, Guerreiro R, Sassi C (2022). “TREX1 p.A129fs and p.Y305C variants in a large multi-ethnic cohort of CADASIL-like unrelated patients.” doi:10.1016/j.neurobiolaging.2022.11.013

Boschann F, Moreno D, Mensah M, Sczakiel H, Skipalova K, **Holtgrewe M**, Mundlos S, Fischer-Zirnsak B (2022). “Xq27.1 palindrome mediated interchromosomal insertion likely causes familial congenital bilateral laryngeal abductor paralysis (Plott syndrome).” *J Hum Genet*, *67*(7), 405-410. doi:10.1038/s10038-022-01018-z

Seidel F, Laser K, Klingel K, Dartsch J, Theisen S, Pickardt T, **Holtgrewe M**, Gärtner A, Berger F, **Beule D**, Milting H, Schubert S, Klaassen S, Kühnisch J (2022). “Pathogenic Variants in Cardiomyopathy Disorder Genes Underlie Pediatric Myocarditis-Further Impact of Heterozygous Immune Disorder Gene Variants?” *J Cardiovasc Dev Dis*, *9*(7), 216. doi:10.3390/jcdd9070216

May V, Koch L, Fischer-Zirnsak B, Horn D, Gehle P, Kornak U, **Beule D**, **Holtgrewe M** (2022). “ClearCNV: CNV calling from NGS panel data in the presence of ambiguity and noise.” *Bioinformatics*, *38*(16), 3871-3876. doi:10.1093/bioinformatics/btac418

Schöpflin R, Melo U, Moeinzadeh H, Heller D, Laupert V, Hertzberg J, **Holtgrewe M**, Alavi N, Klever M, Jungnitsch J, Comak E, Türkmen S, Horn D, Duffourd Y, Faivre L, Callier P, Sanlaville D, Zuffardi O, Tenconi R, Kurtas N, Giglio S, Prager B, Latos-Bielenska A, Vogel I, Bugge M, Tommerup N, Spielmann M, Vitobello A, Kalscheuer V, Vingron M, Mundlos S (2022). “Integration of Hi-C with short and long-read genome sequencing reveals the structure of germline rearranged genomes.” *Nat Commun*, *13*(1), 6470. doi:10.1038/s41467-022-34053-7

Rieke D, de BT, Horak P, Lamping M, **Benary M**, Jelas I, Rüter G, Berger J, Zettwitz M, Kagelmann N, Kind A, Fabian F, **Beule D**, Glimm H, Brors B, Stenzinger A, Fröhling S, Keilholz U (2022). “Feasibility and outcome of reproducible clinical interpretation of high-dimensional molecular data: a comparison of two molecular tumor boards.” *BMC Med*, *20*, 367. ISSN 17417015, doi:10.1186/s12916-022-02560-5

Richter G, Wagner G, Reichenmiller K, Staufenbiel I, Martins O, Löscher B, **Holtgrewe M**, Jepsen S, Dommisch H, Schaefer A (2022). “Exome Sequencing of 5 Families with Severe Early-Onset Periodontitis.” *J Dent Res*, *101*(2), 151-157. doi:10.1177/00220345211029266

Coutelier M, **Holtgrewe M**, Jäger M, Flöttman R, Mensah M, Spielmann M, Krawitz P, Horn D, **Beule D**, Mundlos S (2022). “Combining callers improves the detection of copy number variants from whole-genome sequencing.” *Eur J Hum Genet*, *30*(2), 178-186. doi:10.1038/s41431-021-00983-x

Vogt G, Verheyen S, Schwartzmann S, Ehmke N, Potratz C, Schwerin-Nagel A, Plecko B, **Holtgrewe M**, Seelow D, Blatterer J, Speicher M, Kornak U, Horn D, Mundlos S, Fischer-Zirnsak B, Boschann F (2022). “Biallelic truncating variants in ATP9A cause a novel neurodevelopmental disorder involving postnatal microcephaly and failure to thrive.” *J Med Genet*, *59*(7), 662-668. doi:10.1136/jmedgenet-2021-107843