17TH INTERNATIONAL CONFERENCE OF THE LITHUANIAN NEUROSCIENCE ASSOCIATION

Brain Function, Dysfunction, and Translational Research

28th November 2025, Kaunas, Lithuania

Centre for the Advanced Pharmaceutical and Health Technologies
Lithuanian University of Health Sciences
Hall A-204, Sukileliu av. 13, Kaunas, Lithuania

17th International Conference of the Lithuanian Neuroscience Association
„Brain Function, Dysfunction, and Translational Research"

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PROGRAM

9.00-10.00	**Registration. Coffee/Tea**
10.00-10.10	**Opening and welcome** Prof. **Inga Griškova-Bulanova**, President of the Lithuanian Neuroscience Association Prof. **Arimantas Tamašauskas**, Director, Neuroscience Institute, Lithuanian University of Health Sciences Dr. **Rima Naginienė**, Neuroscience Institute, Lithuanian University of Health Sciences
	I session. Brain Circuits and Neurodevelopment Chair – prof. Inga Griškova-Bulanova, Vilnius University, Lithuania
10.10-10.50	***Keynote lecture:* Dissecting Microcircuits in Neurodevelopmental Disorders for Targeted Therapies** Prof. **Jean-François Perrier**, Department of Neuroscience, University of Copenhagen, Denmark
10.50-11.10	**LINE-1 – an Unexpected Player in Neural Development and Disease** Dr. **Dovydas Širvinskas**, Center on the Biology of Aging, Department of Molecular Biology, Cell Biology and Biochemistry, Brown University, USA
11.10-11.30	**Anxiety-Relieving Circuits in the Hippocampus** Prof. **Cheng-Chang Lien**, Institute of Neuroscience, National Yang Ming Chiao Tung University, Taiwan
11.30-11.50	**Protein N-glycosylation Regulates Dendrite Self-Avoidance and Pruning** Prof. **Cheng-Ting Chien**, Institute of Molecular Biology, Neuroscience Program of Academia Sinica, Taiwan
11.50-12.00	Meeting of the members of Lithuanian Neuroscience Association
12.00-13.00	**Lunch**
13.00-14.00	**Poster session**
	II session. Molecular and Cellular Mechanisms in Brain Disorders Chair – dr. **Giedrius Steponaitis**, Neuroscience Institute, Lithuanian University of Health Sciences, Lithuania
14.00-14.40	***Keynote lecture:* Brain Tumor Microenvironment and Therapy** Prof. **Bożena Kamińska-Kaczmarek**, Nencki Institute of Experimental Biology of the Polish Academy of Science, Poland
14.40-15.00	**BDNF-Mediated Signaling Dysfunction: a Common Mechanism Between Alzheimer's Disease and Epilepsy** Prof. **Maria José Diógenes Nogueira**, Faculty of Medicine, University of Lisbon, Portugal
15.00-15.20	**Neuroimmune Interactions in Obesity: IL-17A and Depression** Prof. **Shun-Fen Tzeng**, Department of Life Sciences, National Cheng Kung University, Taiwan
15.20-15.50	**Coffee/Tea. Poster session**
	III session. Experimental Approaches and Cellular Models Chair – Prof. **Vilmantė Borutaitė**, Neuroscience Institute, Lithuanian University of Health Sciences, Lithuania
15.50-16.10	**Profiling Molecular and Functional Traits of Stress and Depression in Astrocytes** Dr. **Michał Ślęzak**, Centre of Life Sciences and Biotechnology, Łukasiewicz – PORT, Poland
16.10-16.30	**Integration of Progenitor Cells from Adult Brain into Mature Neural Circuits** Prof. **Hwai-Jong Cheng**, Institute of Molecular Biology, Academia Sinica, Taiwan
16.30-16.50	**Uncovering an 'Uncertain' Route to Pain Relief** Prof. **Hau-Jie Yau**, Graduate Institute of Brain and Mind Sciences, National Taiwan University, Taiwan
16.50-17.00	**Concluding remarks, discussions, awards**
17.00-19.00	**Closing party**

Keynote and Invited Presentations

KEYNOTE LECTURE

Dissecting Microcircuits in Neurodevelopmental Disorders for Targeted Therapies

Jean-François Perrier

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Syntaxin-binding protein 1 (STXBP1) is critical for both excitatory and inhibitory neurotransmission. Mutations in STXBP1 cause a severe neurodevelopmental disorder characterized by frequent seizures, for which existing treatments, which focus on seizure management, have limited efficacy. STXBP1 encephalopathy arises because impaired excitatory synapses fail to recruit inhibitory interneurons, disrupting the balance between excitation and inhibition throughout the neocortex. We therefore hypothesized that positive allosteric modulators (PAMs) of glutamate receptors might paradoxically limit hyperexcitability. Indeed, the AMPA receptor PAM CX1739 and the NMDA receptor PAM D-serine mitigated cortical hyperexcitability in brain slices from a *Stxbp1* haploin sufficient mouse model by enhancing recruitment of interneurons. In naturally behaving mice, both CX1739 and the D-serine precursor L-serine augmented interneuron recruitment and reduced spike-wave discharges. These findings reveal that ionotropic glutamate receptor PAMs are a promising mechanism-based therapy for STXBP1 encephalopathy that could be readily translated to clinical trials.

INVITED LECTURE

LINE-1 – an Unexpected Player in Neural Development and Disease

Dovydas Širvinskas

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Long Interspersed Nuclear Element – 1 (abbreviated to LINE-1 or L1) are independent, mobile genomic elements, known as retrotransposons, making up 17% of the human genome. Their insertions into important genomic regions could disrupt delicate processes, therefore, cells have multiple mechanisms of LINE-1 silencing.

Concurrently, it has now been shown that multiple areas of normal embryonic development depend on the expression of LINE-1. Despite prior results showing that LINE-1 was not expressed in Neural Stem Cells (NSC) due to SOX2 silencing, LINE-1 has been especially implicated in neurodevelopment – LINE-1 knockdown impacting cortical organoid size, LINE-1 helping neural progenitors avoid precocious differentiation, and participating in the regulation of the developing human brain.

We confirmed that LINE-1 is robustly expressed in Pluripotent Stem Cells, including H1 human ESC and KOLF2.1J human iPSC lines, by immunofluorescent staining of native LINE-1 ORF-1 protein (ORF1p). We were also able to detect ORF1p in H1 cells differentiated into Neural Stem Cells using the SMADi Neural Induction Kit as well as H1 cells differentiated into neurons using Ngn2-overexpression 12- and 21-days after start of differentiation.

It is therefore important to fully understand the effects of LINE-1 on neurons and neural stem cells, as well as the mechanisms underlying them.

INVITED LECTURE

Anxiety-Relieving Circuits in the Hippocampus

Cheng-Chang Lien

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The dentate gyrus (DG) displays functional specialization along its dorsoventral axis, with dorsal regions linked to spatial processing and ventral regions to emotional control. Using *in vivo* calcium imaging, optogenetics, and behavioral assays, we identified ventral, but not dorsal, mossy cells (MCs) as key modulators of anxiety-like behaviors. Ventral MCs were preferentially activated in anxiogenic contexts and inhibited in safe zones. Circuit mapping showed that MC activation suppresses granule cell and CA1 pyramidal neuron firing through GABAergic recruitment. Enhancing ventral MC excitability reduced anxiety-related behaviors across multiple tests. These results reveal an inhibitory mechanism by which ventral MCs regulate hippocampal output and promote anxiety relief.

INVITED LECTURE

Protein N-glycosylation Regulates Dendrite Self-Avoidance and Pruning

Cheng-Ting Chien

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We systematically screened *Drosophila* mutants with defects in glycosylation pathways to identify those exhibiting impaired dendrite arborization and pruning during metamorphosis. Two complementary studies presented here demonstrate that specific N-glycan modifications on membrane proteins play critical roles in these developmental processes.

The first study reveals that phagocytosis of fragmented dendrites by dendrite-wrapping epidermal cells depends on N-glycosylation of the phagocytic receptor Draper (Drpr)/Ced-1 for proper surface membrane presentation. We further identified two galectins—Crouching tiger (Ctg) and Hidden dragon (Hdg)—that specifically recognize N-glycan-modified Drpr. Upon dendrite injury, Ctg and Hdg are upregulated in macrophage-like hemocytes and recruited to damaged dendrites, where they bridge the "eat-me" signal phosphatidylserine (PS) and N-glycosylated Drpr, thereby facilitating the phagocytosis of fragmented dendrites.

The second study demonstrates that an epidermal cell-derived N-acetylglucosaminidase, Fused lobes (Fdl), regulates dendrite self-avoidance. The cell adhesion molecule Dscam1, which mediates self-recognition between sister branches, carries multiple hybrid- and complex-type N-glycans. Fdl cleaves the GlcNAc moiety from these N-glycans, weakening Dscam1 homophilic interactions and promoting branch separation upon contact.

Collectively, these studies underscore the importance of protein N-glycosylation in epidermal cells as a regulatory mechanism for controlling specific aspects of dendrite development.

INVITED LECTURE

Brain Tumor Microenvironment and Therapy

Bożena Kamińska-Kaczmarek

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Understanding the composition of the tumor microenvironment (TME) and underlying interactions is essential to develop successful anti-cancer immunotherapies. Glioblastoma (GBM) is a deadly brain tumor. Its tumor microenvironment is infiltrated with myeloid cells which support tumor proliferation, diffusive growth and impair responses to treatments.

By employing single cell transcriptomics and Cellular Indexing of Transcriptomes and Epitopes by sequencing (CITE-seq) with 40 protein markers, we dissected identities and functionalities of immune cells in glioma TME of five experimental glioma models with various genetic alterations. Application of spatial transcriptomics allowed us to resolve transcriptional landscape of immune and glial cells in TME. Potential cell-cell and ligand-receptor interactions pointed to myeloid cells as a source of ligands attracting and shaping functionality of T cells and dendritic cells. We demonstrate the unique composition of the specific glioma TME with NRAS gliomas having more activated microglia, less immunosuppressive TME and more T effector lymphocytes than PDGFB gliomas. Isocitrate dehydrogenase (IDH)-mutant gliomas show reduced cytokine/chemokine landscape and lower infiltration, activation and exhaustion of effector T lymphocytes than IDH-wild-type gliomas. Functional subpopulations of reactive astrocytes around the tumors have been characterized. Exploration of human glioblastoma scRNAseq data corroborate findings from experimental gliomas. We discovered glioma-derived osteopontin/SPP1, highly expressed in GBM and glioma stem like cells, as one of the proteins shaping TME and blocking antitumor immunity. Silencing SPP1 expression in human glioma U87-MG cells, which did not affect cell viability/proliferation in vitro, decreased glioma invasion and blocked tumor growth in vivo. We designed the synthetic peptide RGD that blocked SPP1 signaling, reverted tumor effects on myeloid cells, modified immune TME into “a hot” one and normalized neovasculature. When combined with antiPD1 antibody, it restored influx and activity of effector T cells resulting in reduced glioma growth. Further, we developed the humanized peptides, binding specifically to a human SPP1. Intratumoral delivery of the I49 peptide resulted in antitumor activity in the U87-MG xenograft mouse model. Intratumorally delivered peptide overcomes a blood-brain barrier and minimizes non-specific toxicity.

Our results show that exploring TME with single-cell techniques and spatial transcriptomics unravels identities of immune cells that create a tumor specific TME and underlying cell-cell communication networks. The findings led to identification of peptides with a very high specificity and low toxicity which could be used as anti-cancer therapeutics.

Acknowledgements. Work supported by The National Centre for Research and Development PBS3/B7/19/2015 and 2020/39/B/NZ4/02683 from the Polish National Science Center (BK).

INVITED LECTURE

BDNF-Mediated Signaling Dysfunction: a Common Mechanism Between Alzheimer's Disease and Epilepsy

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Brain-derived neurotrophic factor (BDNF) is essential for neuronal survival, differentiation, and synaptic plasticity. In Alzheimer's disease (AD), amyloid β (Aβ) promotes excitotoxicity by increasing intracellular calcium concentration, which activates calpains that cleave its main receptor, TrkB-FL. This calpain-dependent cleavage generates the TrkB-ICD fragment, which may contribute to disease progression. We created a TAT-TrkB peptide to prevent TrkB-FL cleavage. Since epilepsy is also characterized by excitotoxicity, we hypothesized that TrkB-FL cleavage may occur similarly in this context.

This study aimed to investigate the role of TrkB-ICD, determine whether TrkB-FL cleavage occurs in epilepsy, and evaluate the therapeutic potential of TAT-TrkB in AD and epilepsy.

Neurons were transduced with lentiviruses to overexpress TrkB-ICD. Dendritic spine density, synaptic transmission, and gene expression were assessed. In rodents, hippocampal TrkB-ICD overexpression was induced to evaluate memory impairment. TrkB-FL and TrkB-ICD levels were quantified in a rat model of mesial temporal lobe epilepsy (mTLE) induced by kainic acid (KA), both during status epilepticus (SE) and established epilepsy (EE), as well as in brain samples from patients with refractory epilepsy. The efficacy of TAT-TrkB was tested in epilepsy and AD models (5xFAD mice).

TrkB-ICD overexpression resulted in dendritic spine loss, altered synaptic transmission, and changes in the expression of synapse-related genes. Rodents overexpressing hippocampal TrkB-ICD exhibited memory deficits.

Rats showed TrkB-FL cleavage during SE, with hippocampal levels of TrkB-ICD correlating with seizure severity. TrkB-FL cleavage and TrkB-ICD formation were also detected in animals with EE. Brain samples from patients with refractory epilepsy showed increased TrkB-ICD levels.

TAT-TrkB administration improved synaptic deficits and cognitive performance and reduced p-Tau levels and Aβ plaque size in 5xFAD mice. Rats treated with TAT-TrkB 24 hours before KA (mTLE model) developed fewer seizures.

In summary, TrkB-FL cleavage is a shared pathological mechanism in both AD and epilepsy. TrkB-ICD affects neuronal function and synaptic plasticity. TAT-TrkB represents a promising therapeutic strategy, effectively preserving BDNF signaling, reducing neurodegeneration, and mitigating seizures.

INVITED LECTURE

Neuroimmune Interactions in Obesity: IL-17A and Depression

Shun-Fen Tzeng

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Obesity is increasingly recognized as a chronic inflammatory condition, such as that induced by prolonged high-fat diet (HFD) consumption. It not only leads to metabolic dysregulation but also impairs immune-brain communication, contributing to the development of mood disorders. During the early stages of high-fat diet (HFD) exposure, proinflammatory cytokines such as IL-1β, TNF-α, and IL-6 increase markedly, but their levels eventually return to baseline. Despite this, persistent neuroinflammation and gliosis remain, indicating that mediators associated with adaptive immunity may contribute to chronic neuropathology. In our study with male C57BL/6 mice, chronic obesity induced by 12 weeks of HFD feeding increased plasma levels of IL-17A, a key cytokine produced by $CD4^+$ T helper 17 (Th17) cells. It also upregulated IL-17A mRNA expression in the caudate putamen. Peripheral administration of recombinant IL-17A via intraperitoneal injection every two days for one month induced anxiety- and depression-like behaviors, accompanied by enhanced microgliosis in emotion-related brain regions and infiltration of $CD4^+$/$IL\text{-}17A^+$ cells. Intracerebroventricular IL-17A injection activated neurons in the medial prefrontal and insular cortices, implicating its role in emotional circuits. These results highlight IL-17A as a key mediator linking metabolic dysfunction, neuroinflammation, and mood disorders, suggesting its potential as a therapeutic target for obesity-related depression.

INVITED LECTURE

Profiling Molecular and Functional Traits of Stress and Depression in Astrocytes

Michał Ślęzak

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Modern research frameworks aim to deconstruct mental disorders for better understanding of individual symptoms. This approach is particularly important for disorders with large heterogeneity, such as major depression, resulting from the interaction of genetic predisposition rendering an individual susceptible or resilient to environmental factors precipitating the disease. Mounting evidence points to dysfunction of astrocytes as a key neurobiological feature of depression. Astrocytes integrate numerous processes aberrant in depression, such as glucose metabolism and neurotransmitter turnover and their anatomic localization makes them a cellular locus of translating aberrant hormonal signaling, a hallmark of depression, with brain environment.

In my talk, I will summarize our recent work which shows that astrocytes are a key player in depression. We showed that profound transcriptional alterations of glia is the main feature of severe mental neuropathology. Through applying a novel protocol of astrocyte nuclei enrichment we enabled unprecedented insight into astrocyte reprogramming in depression and found glucocorticoid receptor as a key driver of these changes. We found that astrocyte pathological signature can be replicated by chronic social defeat stress (CSDS) in mice. Interestingly, astrocyte-specific elimination of the GR prevented transcriptional, metabolic and behavioral effects of chronic stress in mice. The analysis of human and mice profiles revealed impaired glutamate homeostasis as a hallmark of GR-dependent astrocyte dysfunction.

In the second part of my talk, I will present our current work which focuses on studying the impact of astrocyte-specific gene intervention on sex- and circuit-specific behavioral abnormalities. I will also discuss the importance of developing adequate tools for validation of astrocyte-specific pathways as novel therapeutic strategy of stress-related disorders.

INVITED LECTURE

Integration of Progenitor Cells from Adult Brain into Mature Neural Circuits

Hwai-Jong Cheng

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In the adult mammalian hippocampus, neurogenesis is concentrated in the subgranular zone of dentate gyrus (DG). Adult-born neurons integrate functionally into existing hippocampal circuits, and dysregulation of adult hippocampal neurogenesis (AHN) is linked to disorders of learning, memory, and emotion. AHN declines with age. Our lab investigates how aging alters AHN in mice. We developed an efficient method to culture neurospheres from adult and aged DG neural progenitors, maintaining them as adult hippocampal neural progenitor cells (AHNPCs). We performed single-cell RNA sequencing on AHNPCs to identify intrinsic regulators of age-related changes. We transplanted AHNPCs into the mouse DG in vivo to assess their differentiation and integration in the mature hippocampus. Spatial transcriptomics showed transplanted AHNPCs adopt expression profiles similar to neighboring endogenous granule cells. Ultimately, we aim to determine whether cultured AHNPCs can be used to treat neurological disorders.

INVITED LECTURE

Uncovering an 'Uncertain' Route to Pain Relief

Hau-Jie Yau

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Anterior cingulate cortex (ACC) is well known for its critical role in pain perception. ACC inhibition has a profound pain-relieving effect in several animal models of neuropathic pain. However, whether ACC inhibition can regulate pain through subcortical regions other than the regions mediating conventional descending modulation remains less explored. By employing activity-dependent c-Fos mapping, several brain regions were found to be engaged by ACC inhibition, including the zona incerta (ZI), a largely inhibitory nucleus involved in pain modulation and defense behaviors. By combining *in vivo* optogenetic approach with a robust mouse model of neuropathic pain, we discovered that prolonged photoinhibition of the anterior ACC (aACC) and aACC-to-ZI input respectively induced sustained alleviation of nerve injury-induced mechanical hypersensitivity. In addition, repeated photo-inhibitions daily for a week could delay the development of neuropathic pain. On the other hand, we found that prolonged ZI photoactivation is sufficient to induce similarly sustained alleviation on nerve injury-induced mechanical hypersensitivity. We further showed that ZI involvement was required for prolonged aACC photoinhibition to attenuate nerve injury-induced mechanical hypersensitivity. Moreover, by combining activity-dependent targeting approach, we showed that the ZI cells recruited by repeated aACC photo-inhibitions were required for prolonged aACC photoinhibition to alleviate nerve injury-induced mechanical hypersensitivity. Taken together, our study revealed a novel mechanism that prolonged aACC inhibition engages the ZI to alleviate neuropathic pain.

Poster Presentations

List of poster presentations

P1

The Effect of Bilateral Non-Invasive Vagus Nerve Stimulation on Stress in Healthy Adults

Neringa Burokienė[1], Dovilė Karčiauskaitė[2], Jonė Pukėnaitė[3]

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Stimulation of the vagus nerve influences biomarkers associated with both the hypothalamic-pituitary-adrenal (HPA) axis and the autonomic nervous system. The goal of the study was to evaluate the effect of transcutaneous vagus nerve stimulation (tVNS) on stress biomarkers and related symptoms and compare the effect of unilateral and bilateral stimulation.

Approval was obtained from the Bioethics Committee. 4O healthy subjects were randomly selected from a primary care center. A total of 37 participants (8 men and 29 women) remained throughout the entire study, aged 21-64 years. One-centimeter hair segments from the posterior vertex region of the head, as close to the scalp as possible were taken and analyzed, representing cortisol accumulation over the most recent month. The hair samples were taken before the study and after 4 weeks of stimulation. Three questionnaires (Generalized Anxiety Disorder 7-item scale (GAD-7), Patient Health Questionnaire-9 (PHQ 9), Pittsburgh Sleep Quality Index (PSQI)) were used to evaluate anxiety and depressive symptoms as well as sleep quality during the study. The questionnaires were taken before the study, two weeks in and after four weeks of stimulation. The stimulation was delivered using the non-invasive vagus nerve stimulation device Pulsetto. The stimulation protocol consisted of 8-minute sessions performed twice daily for four consecutive weeks.

Analysis of hair cortisol and cortisone concentrations revealed differential effects of transcutaneous vagus nerve stimulation (tVNS). A Wilcoxon signed-rank test indicated a statistically significant reduction in hair cortisol levels across the full sample (n 37, V 514, p=0.013). Subgroup analyses demonstrated no significant change following unilateral stimulation (n=17, p=0.159), while bilateral stimulation led to a significant decrease in cortisol (n=20, p=0.024). Regarding cortisone, a trend-level reduction was observed in the full sample after four weeks of tVNS (p=0.059), with no significant change in the unilateral group (p 0.431) and a near-significant effect in the bilateral group (p 0.058). Importantly, changes in cortisone were moderately and positively cor-

P1

related with changes in cortisol (Spearman's p = 0.50, p 0.002), suggesting that both markers may reflect a shared modulation of HPA-axis activity, even if cortisone alone did not reach statistical significance. Significant improvements were observed across all self-reported measures following four weeks of tVNS. Depression symptoms (PHQ-9) decreased significantly in the total sample (n = 4O, p<0.001), with strong effects in both unilateral (p<0.001) and bilateral stimulation groups (p<0.001). Anxiety symptoms (GAD-7) also showed significant reductions overall (p<0.001), and in both subgroups (p 0.0004 unilateral; p 0.003 bilateral). Sleep quality, assessed via the PSQI, improved significantly in the full sample (p<0.001), with consistent effects observed in unilateral (p<0.001) and bilateral stimulation conditions (p<0.001).

This study demonstrates that transcutaneous vagus nerve stimulation (tVNS), particularly bilateral stimulation, may effectively reduce physiological stress markers and improve self-reported symptoms of depression, anxiety, and sleep disturbance. The moderate correlation between cortisol and cortisone suggests convergent modulation of HPA-axis activity. These findings support the potential of tVNS as a non-invasive intervention targeting both physiological and psychological aspects of stress-related disorders.

Acknowledgement. This study was funded by UAB Pulsetto as part of an EU-supported project under grant number 05-001-O1-05-O7 and conducted independently by Clinical Trial Center UAB INLITA. The company had no influence on the design, execution, or analysis of the study.

P2

Non-Coding Y RNA Expression in Glioma Cells Following Temozolomide Treatment and in Patient Gliomas

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Glioma is malignant central nervous system tumor, and the most malignant glioma, glioblastoma (GBM) is one of the deadliest tumors that can cause death approximately to 93% of patients within 5 years after diagnosis.

This study aimed to determine the expression of non-coding Y RNAs in glioma cell model after Temozolomide (TMZ) exposure and in patients' tumor samples to assess RNY involvement in glioma therapy resistance in vitro, and diagnostic and prognostic significance in clinical cohort.

Glioblastoma cell lines U251, A172, and LN229 were treated for 2 weeks with the alkylating agent Temozolomide. A number of 32 glioma patient tumor tissues were obtained for analysis: 23 patients had glioblastoma multiforme (grade 4, GBM) and 7 patients had diffuse astrocytoma (grade 2, DA). Total RNA was isolated using TRIzol reagent, and cDNA was synthesised from RNA using reverse transcriptase enzymes. Gene expression analysis of RNY1, 3, 4, and 5 was performed by real-time PCR with SYBR Green detection, enabling quantitative assessment of transcript levels. GAPDH, 18S rRNA, and ACTB were used as reference genes for data normalisation.

A statistically significant upregulation of RNY1 and RNY4 was observed in grade 4 and grade 2 gliomas as compared to normal brain tissue, respectively. RNY4 expression was also higher in patients aged up to 55 years. In treated A172 cells, RNY1 expression was approximately 5-fold higher than in the control cells. In U251 cells treated with TMZ, RNY3 expression was 1.8-fold higher compared with the control. In contrast, in treated LN229 cells, RNY5 expression was approximately 7.7-fold higher than in the control cells.

It was found that RNY1 and RNY4 may represent potential diagnostic biomarkers for gliomas, as their expression in tumor specimens differed significantly between grade 2 and grade 4 tumors. Treatment of different glioblastoma cell lines induced gene- and cell line–specific alterations in RNY expression. The marked increase of RNY1 expression in A172 cells suggests that this gene may be involved in cellular response mechanisms to treatment. Temozolomide-treated cells may be linked to the development and progression of glioma.

P3

Genetic Factors Influencing Pituitary Adenoma in Females: the Role of IL1R3 rs4624606

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Pituitary Adenoma (PA) is a benign tumor arising from the anterior pituitary gland (adenohypophysis). It typically exhibits slow and asymptomatic progression in its early stages. Depending on disease duration and the secretory activity of the adenohypophysis, patients may present with diverse clinical manifestations resulting from hormonal imbalances. The exact etiology and pathogenesis of PA remain unclear. It is believed that multiple factors, including environmental influences, hormonal balance and genetic markers, contribute to the disease development. The disorder is more frequently diagnosed in older individuals. Interestingly, women tend to be diagnosed at a younger age than men, who are typically diagnosed later in life. The IL1R3 gene encodes a co-receptor for IL-1 family cytokines involved in immune response regulation. Overexpression of IL1R3 has been associated with tumor development and poor prognosis.

We aimed to investigate the potential role of the rs4624606 polymorphism in the development of PA among women.

The study included 269 women, divided into three groups: 55 patients with active PA, 27 with inactive PA and 187 healthy controls. DNA was extracted from peripheral blood leukocytes using the DNA-salting out method. Genotyping was performed by real-time polymerase chain reaction (RT-PCR). Data were analyzed using IBM SPSS Statistics 29.0 software.

The results showed that the rs4624606 AG genotype, compared to the GG genotype, decreases the odds of developing active PA by 2.2-fold under the codominant genetic model ($p = 0.025$). The combined AG+AA genotypes, compared to GG, reduce the odds of active PA by 2.2-fold under the dominant model ($p = 0.014$). When comparing the AG genotype with the combined GG+AA genotypes, the odds of active PA in women decreased 2 times under the overdominant model ($p = 0.045$). Moreover, the A allele decreased the odds of active PA in women by 1.8-fold under the additive model ($p = 0.022$).

The rs4624606 polymorphism in women is associated with a reduced odds of active PA occurrence, suggesting a potential protective effect of this genetic variant.

P4

Comparative Proteomics of Brain Parenchyma and Vasculature in Mouse and Human Ageing

Austėja Čiulkinytė[1,2,3], Steven Hill[1,2,3], Bethany Geary[4], Blanca Díaz Castro[1,2,3]

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Ageing is the strongest risk factor for various neurodegenerative diseases. In particular, the brain vasculature plays an important role during pre-clinical stages of many neurodegenerative conditions, such as Alzheimer's disease and vascular dementia. Despite numerous efforts, the exact molecular contributions of ageing towards the manifestation of neurodegenerative disease remain incompletely understood. Mouse models are widely used in neurodegeneration and ageing research. However, to ensure the translational potential of mouse models is maximised, there is a need to identify what aspects of ageing are shared between mouse and human. Previous attempts to study the extent of molecular similarities in mice and human ageing have returned conflicting results. Additionally, no direct species comparisons of the ageing brain at the proteome level have been performed. To address this, we have performed a proteomic analysis of cortical brain tissue and isolated vasculature from young and aged mouse and human samples. From this data, we have identified species- and tissue-specific conserved and divergent changes in protein levels and associated functions. These findings will allow us to better evaluate the translatability of mouse models in ageing research and highlight important considerations for future studies.

P5

Associations Between Hippocampal Volume and Working Memory in Ageing: Evidence for a Possible Compensatory Mechanism

Zigmunds Freibergs[1,7], Natālija Hodaseviča[2], Maija Pēce[2], Kristīne Šneidere[1,3], Nauris Zdanovskis[4,5], Ainārs Stepens[1,6]

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Working memory (WM) performance and hippocampal volume decline with aging, but their relationship remains unclear. We aimed to explore the association between verbal digit WM and hippocampal subfield volumes, hypothesizing that they would correlate in older adults and that this association would be stronger in those with mild cognitive impairment (MCI).

Forty-six older adults (65-85 years; M=71.8, SD=5.05; 82.6% female) completed a WM test (Numbers Reversed, Woodcock–Johnson) and the Montreal Cognitive Assessment (MoCA) for cognitive function. Hippocampal volumes were derived from structural MRI, and Spearman correlations and hierarchical regressions were conducted.

In the whole sample, hippocampal heads, particularly the left, explained the largest portion of WM variance (left: 22–24%, right: 19–20%), with several subfields contributing 13-26% of variance after controlling for estimated total intracranial volume and MoCA. In the low MoCA group (MCI), specific hippocampal subfields, rather than whole heads, accounted for 25-58% of WM variance, with the right CA3 head showing the highest contribution (58%). In the high MoCA group (cognitively intact), only a few subfields were associated with WM, explaining 27-33% of variance.

Our results support the idea that the hippocampus may serve as a compensatory mechanism for WM in older adults with MCI. These findings were published in Freibergs et al., 2025, European Journal of Neuroscience.

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P6

Sex Differences in Auditory Gamma Oscillatory Responses

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Auditory steady-state responses (ASSRs) reflect the brain's ability to synchronize with periodic auditory stimulation and are increasingly used as biomarkers in neuropsychiatric research, particularly for gamma-range neural activity. However, sex differences in ASSRs remain poorly understood.

In this study, gamma-range responses were recorded in 80 young adults (42 females; mean age 26.1 ± 4.3 years) using chirp-like auditory stimuli. Female participants were tested during the early follicular phase to control for hormonal influences. Analyses focused on fronto-central EEG channels, evaluating phase-locking and spectral power.

Results revealed stronger gamma synchronization (35–43 Hz) and power (35–46 Hz) in males, while individual gamma frequencies did not differ between sexes. These findings highlight the importance of considering sex-specific factors—hormonal, developmental, and neurobiological—in ASSR research, and underscore the need for sex-specific normative baselines to improve personalized diagnostics and therapeutic approaches.

P7

Effect of the Anticancer Drug Temozolomide on the Stem-Like Phenotype of Glioblastoma Cells

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Primary central nervous system tumors account for less than 1.5 percent of all new cancer cases diagnosed each year, most of which are anaplastic astrocytomas or malignant gliomas. The most aggressive form of glioma, glioblastoma, remains incurable to this day. Gliomas are usually treated with a combination of surgery, radiation therapy, and chemotherapy, which aim to kill cancer cells. Despite the destructive effect of this treatment on cells, there are certain types of cells in glioma tissue, characterized as glioblastoma stem cells (GSCs), which manage to avoid the destructive effects of therapy and are able to infiltrate surrounding CNS tissues and continue to multiply successfully. Currently, there is still a lack of knowledge about the molecular mechanisms that determine the resistance of GSC cells to chemotherapy; therefore it is necessary to study the properties of these cells and their response to therapeutic reagents in more detail.

The aim of this study was to determine the effect of the anticancer drug temozolomide (TMZ) on the stem-like phenotype of glioblastoma cells.

The glioblastoma cell line A172 was used for this purpose, which was cultured in a stemness-inducing medium in non-adherent plates. Under these conditions, the cells form spheroid structures. The expression of the stem cell phenotype was determined by SOX2 expression using the RT-PCR method. In the next stage of the experiment, the stem-like cells (spheroids) and control cells were transferred to conventional plates in a cell differentiation-promoting medium enriched with fetal calf serum and treated with TMZ. The effect of TMZ on the stemness of A172 cells was observed by measuring the expression of the stemness genes SOX2, OCT4, and MYC using the RT-PCR method.

The results revealed that under stemness-promoting conditions, A172 cells showed changes in the expression of SOX2, OCT4, and MYC. These changes were suppressed when the cells were cultured under normal conditions. However, in the case of MYC, this suppression was slower when the cells were treated with TMZ, suggesting that TMZ may help maintain stem-like properties.

P8

Assessment of Catalase Activity and Some Trace Element Concentrations in the Blood of Patients with Astrocytoma

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Glioma is the most common tumor of the central nervous system, originating from glial cells or their precursors, and accounts for approximately 80% of all malignant brain tumors. Astrocytoma develops as a result of mutations in star-shaped astrocyte cells and constitutes about 75% of all gliomas, among which grade IV astrocytoma and glioblastoma are the most frequently diagnosed. The prognosis for patients diagnosed with this grade of brain tumor is extremely poor, with an overall 5-year survival rate of only 5%. Catalase (CAT) is an enzyme predominantly localized in peroxisomes and plays a crucial role in protecting cells against oxidative stress by preventing the accumulation of hydrogen peroxide (H_2O_2). Elevated CAT expression levels have been reported in various cancer tissues compared to their normal counterparts. In gliomas, catalase appears to be constitutively overexpressed relative to astrocytes. However, the molecular mechanisms regulating CAT expression in astrocytoma remain not fully elucidated. Metal homeostasis is essential for the proper functioning of the brain, which is particularly vulnerable to toxic environmental pollutants. The balance of metals within the brain is maintained through the blood-brain barrier (BBB) and the blood-cerebrospinal fluid barrier. Based on the ability of metals to cross the BBB, it has been hypothesized that prolonged exposure to certain metals may increase the risk of brain cancer. Nevertheless, no clear association between metal exposure and brain cancer development has been established.

The aim of the study was to evaluate the correlations between catalase enzymatic activity and the concentrations of selected trace elements in the blood of patients diagnosed with astrocytoma.

The study material consisted of blood and plasma samples obtained from patients diagnosed with astrocytoma. Catalase activity was determined in erythrocytes spectrophotometrically. Copper and zinc concentrations were measured in blood plasma, while selenium concentration was determined in whole blood. Trace element concentrations were determined using inductively coupled plasma mass spectrometry (ICP-MS).

The experiments showed that catalase activity increased significantly - by 12% seven days after surgical removal of the tumor.

P9

Luminance Differences in the Combined Manifestation of Two Geometric Visual Illusions

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This study further explored whether the length misperception induced by cross-shaped distractors, formed by two pairs of oppositely oriented Müller-Lyer wings, can be explained by the combined effects of the Müller-Lyer (MLI) and filled-space (FSI) geometric illusions of extent.

During the psychophysical experiments, one pair of wings randomly altered luminance, while the other pair's luminance stayed constant. Two distractor orientations were used: one with the constant-luminance wings on the right side of the cross, and the other with them on the left side. To independently evaluate the MLI under different luminance settings, in the first series of experiments two distracting crosses of identical orientation were attached to the lateral stimulus terminators. In the next four series, a single distracting cross with different orientations was attached to one lateral stimulus terminator, combining constant and background luminance in various ways.

Applying particular algebraic operations (summation or subtraction) to the data from the experiments enabled us to distinguish the individual effects of two illusion components. These effects are consistent with an analytical interpretation derived from earlier quantitative models of the visual mechanisms underlying the MLI and FSI. A deeper theoretical examination of the model resulted in a proposed revised scheme for the potential merging of MLI and FSI mechanisms, linked to identical neural summation areas at the same stage of visual processing.

It was demonstrated that the theoretical calculations accurately fit the experimental curves for all stimulus variations. This provides strong evidence that the joint effects of the MLI and FSI are among the primary factors influencing the characteristics of the perceptual phenomenon studied.

P10

Neurocognitive Correlates of Internet Use: Psychological Measures and Electrophysiological Signatures from Resting-State and Task-Based EEG in a Sample of Healthy Regular Internet Users

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Problematic Internet Use (PIU) emerges amid ubiquitous connectivity, yet remains conceptually heterogeneous and underrecognized. Nevertheless, the field often evaluates PIU as a binary state (severely expressed versus absent), even though it typically unfolds along a spectrum from minimal involvement to maladaptive, problematic use. The present work examines PIU as a continuum in a non-clinical sample, integrating psychological and behavioral measures alongside EEG indices to identify subtle markers across increasing levels of internet use.

Participants completed self-reports (assessing psychological distress, interoception, and personality), performed an auditory equiprobable Go/NoGo task, and underwent EEG during task and resting-state conditions (to assess ERPs, alpha asymmetry, and microstates).

Interoception–personality–internet use relations were investigated using network analysis, which revealed a link between lower interoceptive awareness (Not-Distracting and Trusting domains) and higher internet use, with neuroticism serving as a bridge between bodily awareness and increased internet engagement. Behavioral Go/NoGo task indices did not differentiate internet use severity, but ERPs showed domain-specific associations (reduced N1 with Gaming; shorter Go-N1 with total use across platforms; longer NoGo-P3 with Information Search domain). Resting EEG indicated greater left parietal activity and increased microstate E occurrence/coverage with increasing severity of internet use.

Converging evidence points to a shift toward externally driven, bottom-up attention and weakened embodied regulation as internet use intensifies. Findings advance early detection targets to prevent maladaptive use from escalating.

P11

Psychedelics Modulate Microglial Function and Extracellular Matrix Uptake

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Synaptic plasticity is the key mechanism allowing learning and memory formation during the critical period in early development. Depression and Alzheimer's disease are associated with reduced number of synapses and decreased synaptic plasticity. The medical treatments for these conditions remain limited. One of the promising ways to tackle Major Depressive Disorder (MDD) is to recreate critical period-like plasticity allowing the reorganization of maladaptive neurocircuits. Psychedelics have already proven to alleviate symptoms of MDD, Posttraumatic Stress Disorder and are trialed for the treatment of addiction. While classical psychedelics such as LSD, psilocybin and DMT have a long-lasting effect on synaptic plasticity by binding to serotonin 2A receptors (5-HT2A), so do the selective serotonin receptor inhibitors (SSRI), that are broadly used for the treatment of MDD. However, the effect of psychedelics lasts way longer, than SSRI's. Recent evidence suggests that by affecting downstream signaling, psychedelics also modulate the remodeling of extracellular matrix (ECM). Growing body of evidence suggests that ECM plays a key role in closing the critical high plasticity period and memory formation. It has been shown that the degradation of ECM, induced by psychedelics is microglia dependent. Microglia are brain immune cells that contribute to synapse plasticity by eliminating synapses, releasing brain derived neurotrophic factor (BDNF) and modulating neuroinflammation.

Brains from control mice, stressed mice (inducing depression), stressed mice treated with psilocybin were collected. Experiments were done using immunostaining and fluorescent microscopy in mice brains treated in vivo. [UN1.1] Data was analysed using Imaris 3D microglia reconstructions.

This study present that psilocybin has induced statistically significant increase in EMC uptake by microglia cells. However, they did not induce lysosomal volume or count. The interplay between modulating microglial activity together with ECM degradation and synaptic plasticity might be the underlying fundamental molecular pathways explaining prolonged therapeutic effects of psychedelics. Understanding how psychedelics mediate metaplasticity through microglia could help create novel therapeutic options as well as understand microglia cell physiology more thoroughly.

P12

Hidden Messages in Vesicles: Unveiling miRNA Biomarkers for Parkinson's Disease through Next-Generation Sequencing

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Parkinson's disease (PD) is a progressive neurodegenerative disorder characterized by the gradual loss of dopaminergic neurons in the substantia nigra. PD usually leads to hallmark motor symptoms such as bradykinesia and resting tremor. Although current therapies can alleviate symptoms, the disease remains incurable. MiRNAs derived from extracellular vesicles (EV-derived) have shown great potential as biomarkers for various diseases, including PD. Therefore, finding miRNA biomarkers could enable early disease detection and support personalised treatment strategies.

We aimed yo profile EV-derived miRNAs in Parkinson's disease patients and healthy controls using next-generation sequencing (NGS) to identify potential biomarkers for the disease.

EV-derived miRNAs were isolated from the blood serum of five PD patients and five healthy controls. The samples were then subjected to NGS. Sequencing data were analysed using principal component analysis (PCA), DESeq2 for differential expression and KEGG pathway analysis.

PCA revealed two distinct clusters corresponding to healthy controls and PD patients. Differential expression analysis using DESeq2 identified ten miRNAs significantly deregulated in PD patients compared to controls. KEGG pathway analysis showed that these miRNAs are involved in pathways, like PD, Alzheimer's disease, dopaminergic synapse, MAPK signaling, suggesting potential links to molecular mechanisms underlying PD.

We identified ten miRNAs as potential biomarkers for Parkinson's disease. These miRNAs were found to be involved in neurodegeneration-related pathways, suggesting their possible role in PD pathogenesis. Further studies with larger sample sizes are required to validate these findings and better characterize the expression patterns of these miRNAs.

P13

Serotonergic Modulation of Auditory Steady State Responses

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Brain's ability to synchronize with periodic gamma band auditory stimulation relies on excitatory and inhibitory neurotransmission balance by involving pyramidal neurons and GABAergic interneurons interaction. It is also has been shown that auditory steady state responses (ASSR) are sensitive to neuropsychiatric disorders, consciousness states, glutamatergic and GABAergic systems pharmacological modulation, thus emphasizing potential of gamma band auditory response as a translational biomarker of cortical circuitry integrity. However, several methods for evoking ASSR exist which raise question whether all ASSR are generated equally given the possibility of partly distinct mechanisms, dependences on pharmacological agents and attentional modulations. To answer these questions, we directly compared ASSR evoked by flutter-amplitude modulation and click based stimulus.

Fifteen healthy subjects completed psilocybin (0.26 mg/kg) and placebo EEG recording sessions. During each session FAM (440Hz carrier with 40Hz modulation) and Click (1.5ms white noise bursts at 40Hz) stimulations where presented 150 times each. Stimuli length was 0.5s and inter-stimulus interval 0.7-1s. Auditory stimulation was binaural at 60 dB SPL. EEG was time-frequency transformed in 1-100 Hz range with 1 Hz step, by using complex-Morlet wavelets and Phase-locking index (PLI), evoked amplitude (EA) and mean resultant length (MRL) measurements were calculated. Measurements were averaged over fronto-central electrodes and over time-frequency window of 38-42 Hz, 200-500 ms. Absolute (subtraction) and relative (division) baseline corrections where used.

We showed that ASSR evoked by FAM was weaker relative to click. This result was stable in both conditions (Placebo vs Psilocybin). In addition, the effect of weaker ASSR after psilocybin relative to placebo was found with all three employed measurements regardless of the baseline correction method. However, absolute baseline correction method yielded larger effect sizes and achieved power. Taken together, our results show that Psilocybin attenuates ASSR emphasizing its use as a translational biomarker of cortical circuitry integrity, however the methodological choices such as baseline type also play an important role in shaping the ASSR.

P14

Supplementation with Fructooligosaccharides and Galactooligosaccharides Modulates High-Fat Diet-Induced Morphological Changes of Microglia in Aged Mice

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Chronic high-fat diet (HFD) consumption and ageing are both associated with metabolic stress and sustained neuroinflammation, processes that influence microglial function in the brain. Microglia undergo distinct morphological changes in response to inflammatory cues, and these structural changes are closely linked to their functional state.

In this study, we examined how prebiotic supplementation with galactooligosaccharides and fructooligosaccharides (GOS+FOS) modulates microglial morphology in aged mice exposed to long-term HFD. Aged C57BL/6J mice were assigned to four dietary conditions (control diet, control - GOS+FOS, HFD, and HFD - GOS+FOS). Sagittal brain sections were stained with Iba1 and imaged using confocal microscopy. Three-dimensional branching architecture and two-dimensional shape descriptors were quantified.

Microglia in HFD-fed conditions showed increased branching complexity and enlarged soma profiles, consistent with an activated or metabolically primed state. HFD supplementation with GOS+FOS partially reduced these HFD-induced structural alterations, reducing branch number and branch length and diminishing soma enlargement. In contrast, microglial morphology in CD - GOS+FOS group remained comparable to control diet.

In summary, we demonstrate that long-term consumption of HFD induces pronounced microglial remodeling in the aged mice, while supplementation with FOS and GOS mitigate several neuroinflammatory morphological alterations.

P15

The Perceived Size of a Part Changes When it is Separated from the Whole

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This study investigates the visual phenomenon of increasing stimulus size [Bertulis & Bielevicius. Expansion of perceived size. J. Perception, 2025]. In psychophysical experiments, observers adjusted the test distance to match the length of the entire stimulus—the pentagon—and its components: the apex and the rectangular segment, which can be called the pedestal, both when separated and combined. The shape of the pentagon changed during presentations due to three simultaneous variables: a) the length of the apex gradually increased from 30 to 180 arc minutes, b) the horizontal edges of the pentagon decreased from 150 to 0 arc minutes; and c) the apex angle narrowed from 100 to 23 degrees, while the pentagon's length and height remained constant at 180 and 72 arc minutes, respectively. Based on the averages of the experimental results, the pentagonal-shaped stimulus demonstrated an expansion effect, which, due to shape changes, ranged from 2 to 19 arc minutes. For the isolated apex with increased length and narrowed opening angle, expansion values were higher and, ranging from 10 to 33 arc minutes, showed a consistent upward trend without reaching a peak. In the pentagon's structure, the apex with similar shape and size dynamics displayed a different expansion profile. The expansion value gradually increased from about 9 to 35 arc minutes (its maximum), then decreased to 30 and 19 arc minutes. Similarly, the pedestal displayed different patterns when viewed as a separate object and as part of the pentagon. The isolated pedestals showed expansion (7 to 30 arc min) throughout. Inside the pentagon, narrow pedestals (30, 60 arc min) did not even exhibit expansion and instead showed a negative error sign. Wider pedestals produced relatively weak expansion, peaking at 8 arc minutes before decreasing to 1.5 arc minutes. The combined curves of the isolated apex and pedestal did not match the experimental curve of the whole pentagon.

Based on the data, the perceived shape seems to be a key factor in determining perceived size and, therefore, the expansion effect. During the visual size-matching process, the spatial proportions within the perceived shape are likely to change when combined with another shape, even though the geometry remains unchanged. The representation of a shape (such as a pentagon) in higher neural networks is not simply a sum of its parts' representations (apex and pedestal).

P16

Coupling Between EEG Oscillations and Biological Markers in Treatment-Resistant Depression

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Repetitive transcranial magnetic stimulation (rTMS) is a promising intervention for treatment-resistant depression (TRD), yet its neurophysiological and inflammatory/trophic correlates remain poorly understood. This study integrated EEG, peripheral blood cytokines, growth factors, and clinical assessments to characterise biological signatures associated with rTMS treatment.

Seventeen patients with TRD underwent rTMS using the iTBS protocol. Depressive symptoms were assessed through the Hamilton Depression Rating Scale (HAM-D) and the Montgomery-Åsberg Depression Rating Scale (MADRS). Blood serum levels of TNF-α and VEGF-A were measured using an ELISA assay, and resting-state EEG was recorded both before and after treatment. Paired t-tests were used for clinical scale evaluation, and Wilcoxon signed-rank tests for biomarker changes. Correlation analyses explored relationships between baseline EEG activity, blood biomarkers, and symptom severity.

Significant clinical improvement was observed following rTMS, as indicated by decreases in HAM-D scores (approx. -37%) and MADRS scores (approx. -29%). Analysis showed no significant pre-/post- changes in blood serum concentrations of TNF-α ($W = 48$, $p = 0.496$) or VEGF-A ($W = 40$, $p = 0.433$). EEG analyses revealed non-significant increases in beta and decreases in theta/alpha power post-treatment. Two significant EEG–biomarker associations emerged: baseline alpha power correlated positively with baseline VEGF-A ($r = 0.563$, $p = 0.029$) and baseline TNF-α ($r = 0.535$, $p = 0.033$). Additionally, baseline gamma power correlated with baseline depression severity, as measured by the MADRS scale ($r = 0.509$, $p = 0.037$), indicating that a higher symptom burden was associated with elevated gamma activity.

In conclusion, while rTMS resulted in significant clinical improvement, no substantial changes in biomarkers or EEG frequency bands were detected post-treatment. Nevertheless, significant correlations between baseline EEG oscillations (alpha and gamma) and peripheral biomarkers/symptom severity suggest that intrinsic electrophysiological states may reflect inflammatory and clinical profiles in TRD. These findings underscore the potential of EEG-cytokine and growth factor coupling as a biological marker framework and highlight the need for more thorough mechanistic studies.

P17

Studies of Extracellular Vesicles miRNA-21-5p and miRNA-106a-5p in Patients with Multiple Sclerosis

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Multiple sclerosis (MS) is a chronic autoimmune disease of the central nervous system that causes inflammatory and neurodegenerative lesions. Ectracellular vesicles are small membrane-bound structures secreted by all types of cells and found in various biological fluids. Currently, the diagnosis of MS is based on clinical, radiological and laboratory criteria, but especially in the early stages, these markers are often non-specific. For this reason, additional diagnostic markers are being sought that can increase diagnostic accuracy and complement existing MS diagnostic methods. One of the significant molecules that can increase diagnostic accuracy is microRNA (miRNA). MiRNAs are small, non-coding RNA molecules that regulate gene expression and can be used as circulating biomarkers for various diseases, including MS.

MiRNAs were isolated from serum extracellular vesicles from 49 MS patients and 49 controls using „ExoRNeasy Midi Kit“. MiRNA concentration and quality were assessed by using „NanoDrop 2000“ and cDNA synthesis was performed using the “TaqMan® Advanced miRNA cDNA Synthesis Kit“. MiRNA expression was detected by using RT-PCR method. RT-PCR results were analyzed with „QuantStudio™ Design & Analysis Software“. The obtained data were processed and statistically evaluated using the „IBM SPSS Statistics 29.0.2.0“ program.

It was found that the expression of both studied miRNAs was significantly different between the MS and control groups of neurologically healthy individuals (p0.05). ROC curve analysis revealed the diagnostic and prognostic potential of the studied miRNAs, assessed by AUC values.

The results obtained indicate that the studied miRNA-21-5p and miRNA-106a-p may be suitable as potential biomarkers in multiple sclerosis.

P18

MiRNA Expression Associated with the Remyelination Process in Multiple Sclerosis

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Multiple sclerosis (MS) is an autoimmune disorder characterized by demyelination of neurons in the central nervous system, resulting in axonal damage and subsequent motor, sensory, and cognitive dysfunctions. Current therapeutic strategies primarily aim to suppress immune activation and infiltration. Consequently, elucidating the biological mechanisms underlying myelin repair – remyelination – has become a central focus of MS research. One of the potential regulators of the remyelination process is microRNAs, which are involved in the differentiation of oligodendrocyte precursor cells into mature oligodendrocytes. It remains unclear whether disease-modifying therapies influence the expression of miRNAs associated with remyelination in the blood.

The aim of this study is to investigate the expression of miR-204-5p and miR-17-5p involved in the remyelination process – both before and after treatment – and healthy controls, in order to identify treatment-related differences.

The expression of miRNAs were analyzed in extracellular vesicles isolated from the blood serum of three groups: a control group (n=25), untreated MS patients (n=18), and MS patients treated with second-line disease-modifying therapies prior to the study (n=24). MiRNA isolation was performed using the ExoRNeasy Midi Kit (Qiagen), and cDNA synthesis was conducted with the TaqMan Advanced miRNA cDNA Synthesis Kit (AB). QPCR was performed using the QuantStudioTM 3 System. Statistical analyses were performed using GraphPad Prism and SPSS software.

A statistically significant difference in miR-17-5p expression was observed between the control group and MS patients treated with second-line disease-modifying therapies (p=0.0415). The diagnostic performance of miR-17-5p for distributing these two groups was moderate (AUC=0.6719; 95% CI: 0.5154-0.8283). MiR-17-5p expression was significantly higher in MS patients treated with second-line disease-modifying therapies compared with the control group. These findings suggest a potential association between miR-17-5p expression and treatment-induced modulation of remyelination processes in MS.

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P19

Research on miRNAs Involved in the Remyelination Process in Patients with Multiple Sclerosis

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Multiple sclerosis (MS) is an inflammatory, demyelinating disease of the central nervous system that leads to progressive neurodegeneration and diverse neurological symptoms, most commonly affecting young and middle-aged women. MicroRNAs play key regulatory roles in immune function and myelin repair, making them potential markers of disease mechanisms and treatment response. MS is managed with disease-modifying therapies classified as first-line agents (e.g., interferon beta, glatiramer acetate) and second-line agents (e.g., natalizumab, fingolimod). However, reliable biomarkers capable of objectively assessing treatment effectiveness in individual patients are still lacking, underscoring the need to identify molecular indicators of therapeutic response.

RNA was extracted from blood using the "MirVana™ miRNA Isolation Kit". Nucleic acid concentration and purity were determined using a NanoDrop 2000 spectrophotometer. Complementary DNA was synthesized with "TaqMan® Advanced miRNA Assays", and miRNA expression was quantified by real-time PCR. Resulting data were processed using "QuantStudio™ Design & Analysis Software", and statistical analyses were performed in SPSS.

Significant differences in the expression of both examined microRNAs were observed between treatment groups, with the highest levels detected in patients receiving second-line therapy ($p < 0.05$). A significant positive correlation between miR-204-5p and miR-17-5p expression was also identified, most pronounced in the second-line treatment group ($p < 0.05$).

MiR-204-5p and miR-17-5p showed distinct expression patterns across treatment groups, with both microRNAs most highly expressed in patients receiving second-line therapy. When comparing expression levels before and after both first-line and second-line treatment, miR-204-5p showed a slight increase, while miR-17-5p showed a slight decrease. However, these changes were not statistically significant. It was found that the interaction between the two microRNAs involved in the remyelination process was significant in patients treated with second-line therapies.

P20

LncRNA ANRIL Polymorphisms Association with Pituitary Adenomas Hormonal Activity

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Pituitary adenomas (PAs) are common non-metastatic tumours that develop in the pituitary gland. PA can be divided into hormonally active, secreting excess hormones, and inactive forms, non-functioning. Although the exact mechanisms of PA development remain unclear, genetic factors, including single-nucleotide polymorphisms (SNPs), are thought to play a significant role in its development. Certain SNPs may increase the risk of developing PA, while others may have a protective effect. However, although several studies have examined genetic variants associated with PA, the influence of specific SNPs such as lncRNA ANRIL rs1333045 and rs1537373 has not yet been investigated.

We aimed to determine associations between lncRNA ANRIL (rs1333045, rs1537373) polymorphisms and PA hormonal activity.

The study involved 404 subjects: 180 patients with PA and 224 healthy subjects. SNPs were determined by real-time polymerase chain reaction (RT-PCR). The Akaike Information Criterion (AIC) was used for optimal model selection. Statistical data analysis was performed using the IBM SPSS Statistics 29.0.2.0 program.

The lncRNA ANRIL rs1333045 and rs1537373 T allele is statistically significantly more frequent in the group of patients with active PA compared to healthy individuals ($p=0.005$ and $p=0.033$, respectively). We found that, according to the AIC, each T allele of rs1333045 was associated with 1.5-fold increased odds of developing active PA under the additive model ($p=0.010$). Also, we determined that each G allele of the rs1537373 SNP decreases the odds of active PA occurrence by 1.4-fold under the additive model ($p=0.049$). Additionally, analysis revealed that the rs1537373 GT genotype, compared with the TT and GG genotypes, was associated with a 1.8-fold increased likelihood of developing inactive PA under the overdominant model ($p=0.029$).

LncRNA ANRIL rs1333045 T allele suggests a potential risk of developing hormonal functioning PA, whereas the rs1537373 G allele may suggest a potential protective effect. The lncRNA ANRIL rs1537373 GT genotype may contribute to a higher likelihood of developing non-functioning PA.

P21

Comparison of the Accuracy in Identifying the Geometric Center of Figures with Different Spatial Structures

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This study examined the accuracy of locating the geometric center of visual stimuli, represented by different parts of the contour, using eye-tracking equipment.

Two methods of stimulus representation were employed. In one, geometric shapes – rectangles, rhombuses, pentagons, and horizontal bars – were composed of lines 2 px thick (1 px = 1.8 arcmin) with a brightness of 300 cd/m ^{2} on a grey background of 25 cd/m ^{2}. In the other, the shapes were marked by bright spots 5 px in diameter positioned at the corners. The experiment included three sizes of shapes: large (800 × 400px or 800 × 800 px), medium (400 × 400 px), and small (200 × 400 px or 200 × 200 px). Method Stimuli were presented singly in random order on a 117 cm diagonal, 1920 × 1080 px resolution "Samsung LE 46 B 652" screen. The participant was seated 1 m from the screen, with head movements stabilized using a mount. Eye movement tracking, stimulus presentation, and data collection were performed using the ViewPoint PC-60 system (Arrington Research, Inc.). After calibration, the participant viewed each stimulus for 6 seconds, during which their eye movements were tracked and displayed in real-time. Seven university students, with an average age of 26 years, took part in the study. Analysis Data from the final second of each of the 11 experimental runs were collected to estimate the perceived location of the centroid. Analyses and visualizations were carried out using Python (custom scripts) and MS Excel.

According to the average data of all observers, differences in the representation of geometric shapes did not significantly affect the accuracy of center finding. For large rhombuses represented by lines, compared with same figures predicted by corners, the center difference in the X axis was 14 pixels, and along the Y axis – just 3 pixels; for medium shapes, the X difference was 44 pixels, Y – 13 pixels; for small shapes, the X difference was –31 pixels, Y – 4 pixels, for large rectangle X – 19, Y – -21; medium X – -11, Y – -3; small X – -10, Y – 40, for large pentagon X – 35, Y – 19; medium X – -21, Y – -8, small X – -8, Y – 3, for large horizontal bar X – -11, Y – 1, medium X – -82, Y – -10, small X – 43, Y – -3.

The variations in perceived locations of the geometric centers of differently depicted shapes were not statistically significant.

P22

Emotion Regulation in Healthy Young Males is Moderated by Cortisol and Testosterone-to-Cortisol Ratio

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Cognitive reappraisal (CR) is an emotion regulation strategy that involves cognitive effort to reinterpret emotional stimuli. Accordingly, the application of CR alters emotional response to the stimuli. Numerous studies have shown that cortisol is linked to improved performance of CR tasks. However, there are no studies investigating links between CR and testosterone levels, although indirect studies suggest that higher testosterone levels are associated with impaired emotion regulation abilities. Moreover, both cortisol and testosterone inhibit each other's activity, therefore, it is crucial to investigate these hormones together to understand a broader perspective of how they might influence emotional behavior.

In this study, 140 males (27.5 ± 9.0 years) performed an emotion regulation task in which they either watched or reappraised emotional visual stimuli depending on the cue shown before the image. If the word "View" was present, participants simply watched neutral or negatively valenced images. If the word "Regulate" was shown, participants had to down-regulate negative emotions by reinterpreting the stimulus positively or imagining a better outcome of the shown situation. After each stimulus, participants self-reported negativity of the image. Before the task, each participant completed an emotion regulation questionnaire to assess their habitual use of CR. Thereafter, each participant provided a saliva sample, which was used to evaluate cortisol and testosterone concentrations.

The findings revealed that self-reported negativity differed across conditions, being highest in view, lower in regulated, and lowest in neutral, indicating a successful CR implementation during the study. Moreover, higher habitual use of CR was linked with more effective cognitive emotion regulation task performance (lower self-reported negativity scores in regulate condition) when cortisol levels were high and when the cortisol-to-testosterone ratio was low (i.e., closer to zero).

Although testosterone was not directly associated with task performance, these findings suggest that higher cortisol levels have a positive effect on cognitive emotion regulation, with testosterone inhibiting this relationship.

P23

Exploring the Association Between IKBKB And IKBKG Protein Levels and the Occurrence of Relapsing-Remitting Multiple Sclerosis

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Multiple sclerosis (MS) is a chronic immune-mediated inflammatory disorder that targets and degenerates myelinated neurons within the central nervous system (CNS), ultimately resulting in nontraumatic neurological disability. Approximately 80% of individuals diagnosed with MS exhibit the relapsing-remitting form (RRMS). The etiology of MS is attributed to a sustained disruption of immune homeostasis arising from intricate interactions between genetic predisposition and environmental determinants. The IKK2 (IKBKB) acts as a key mediator in activating the nuclear factor kappa-light-chain-enhancer of activated B cells (NF-κB) signaling pathway. This activation boosts NF-κB signaling activity, leading to functional dysregulation in both T and B lymphocytes. Likewise, the NEMO/IKKγ (IKBKG) is essential for activating the NF-κB pathway and is involved in a wide range of physiological and cellular processes, including immune regulation, inflammatory response, cell proliferation, and survival. The NF-κB signaling pathway has been extensively linked to the development of numerous human disorders, especially those marked by chronic inflammation.

This study aimed to determine the associations between IKBKB and IKBKG protein concentrations and the occurrence of relapsing-remitting multiple sclerosis.

The concentrations of IKBKB and IKBKG proteins in blood serum were determined using the enzyme-linked immunosorbent assay (ELISA) method. Statistical data analysis was performed using SPSS software.

It was found that IKBKB serum concentration was statistically significantly higher in RRMS patients compared with the control group (median (IQR): 1.78 (1.44) vs. 1.37 (0.81), $p = 0.002$). IKBKB analysis showed no statistically significant differences between RRMS patients and control groups (median (IQR): 0.21 (0.14) vs. 0.17 (0.10), $p = 0.110$).

The study demonstrated that serum IKBKB concentration was significantly elevated in RRMS patients compared with healthy controls, suggesting a potential involvement of IKBKB in disease mechanisms. In contrast, IKBKG levels showed no statistically significant differences between the groups.

P24

The Impact of Instructional Content Enhancement Elements on Neurotypical Students' Cognitive Processes and the Evaluation of Neurodivergent Students' Reading Strategies Using Eye-Tracking Technology

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With the rapid integration of digital technologies in education, a key question arises regarding how different methods of instructional content presentation influence students' cognitive processes, attention, and information retention. The research problem stems from limited clarity about how enhancement elements affect younger students' cognitive functioning, complicating the development of effective learning materials. The study hypothesized that diverse enhancement elements increase cognitive load, impair information retention, and hinder knowledge application. The study aimed to identify which enhancement factors influence cognitive functioning and how they relate to the learning process.

The study employed a literature review, an experimental eye-tracking approach, student surveys on subjective cognitive load, and statistical analysis. The experiment involved 46 students from grades 5–8, using a within-subjects design with repeated measures after one month.

Findings showed that instructional content featuring infographics and decorative images increased cognitive load, reduced information retention, and hindered practical knowledge application, even though students rated these formats as less demanding. In contrast, plain (control) and highlighted text were more effective, decreasing extraneous cognitive load and improving performance in retention and transfer tasks. Correlational analysis indicated that shorter saccade lengths were associated with more intensive information processing, while higher perceived cognitive load correlated with shorter fixation durations, possibly signaling attentional diversion. Additionally, 4 students with learning disorders (dyslexia, writing difficulties, attention disorder) were excluded from the main analysis and examined separately, visually comparing their scan paths across the same four conditions. Neurotypical reading patterns were efficient, with short saccades and minimal regressions, whereas neurodivergent students showed fragmented attention and higher cognitive load, especially in visually enhanced formats. Highlighted and plain text supported more focused reading, while infographic and decorative formats disrupted reading flow. These findings provide practical guidance for designing instructional materials aligned with students' cognitive capacities.

P25

Genetic Predictors of Pituitary Adenoma Size: Insights from CXCL13 Genetic Variants

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Pituitary adenoma (PA) is one of the most common brain tumors, yet its pathogenesis remains unclear. PA can be categorized by size into microadenomas (<10 mm) and macroadenomas (≥10 mm). While microadenomas usually present with mild or isolated endocrine abnormalities, macroadenomas are more likely to cause visual impairment, headache, hypopituitarism, and local invasiveness due to mass effect on surrounding structures. Molecular biomarkers indicate biological and pathological processes or therapeutic responses, offering valuable insights for diagnosis and prognosis. CXCL13, a homeostatic chemokine, primarily induces B-cell chemotaxis, lymphoid tissue organization, and the recruitment of immune cells. CXCL13 gene variants, particularly those affecting expression or function, may influence PA risk, size, invasiveness, and treatment response. Understanding the genetic role of CXCL13 could support personalized treatments and improve prognostic tools for PA management.

A case-control study enrolled 170 PA patients and 230 healthy controls. DNA samples from peripheral blood leukocytes were purified by the DNA salting-out method. Single-nucleotide variants (rs355689, rs355687) were determined using real-time polymerase chain reaction (RT-PCR). Statistical data analysis was performed using the "IBM SPSS Statistics 30.0" program.

We found that CXCL13 rs355689 TT genotype vs. CC+CT was associated with about 2.5-fold decreased odds of PA occurrence under the recessive model (OR = 0.406, 95% CI: 0.169-0.974, p = 0.043) and CXCL13 rs355687 CA genotype vs. CC+AA was associated with about 1.5-fold increased odd of PA occurrence under the overdominant model (OR = 1.552, 95% CI: 1.041-2.312, p = 0.031). Binary logistic regression analysis revealed that CXCL13 rs355687 CA genotype vs. CC+AA was associated with about 1.8-fold increased odds of macro PA occurrence under the overdominant model (OR = 1.751, 95% CI: 1.114-2.751, p = 0.015). Conclusions: Our findings show that the CXCL13 rs355689 TT genotype significantly reduces the odds of PA occurrence, suggesting a potential protective effect. In contrast, the rs355687 CA genotype increases the risk of PA development and demonstrates an even stronger association with macroadenoma formation. These results indicate that CXCL13 genetic variation, particularly rs355687 CA, may contribute to PA susceptibility and tumor growth dynamics.

P26

The Effect of Viral RNA-Mimetics on Microglia Cell Cultures and Mitochondrial Network Formation

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The main causes of development of neurodegenerative diseases, such as Parkinson's and Alzheimer's are neuronal damage and loss, often associated with neuroinflammatory processes. Neuroinflammation can be caused by various factors, including bacterial and viral infections, leading to activation of cells of the brain immune system, including microglial cells, which play a crucial role in the development of neurodegenerative diseases and can have a negative effect on neurons. Viral components can activate microglial cells via pattern recognition receptors, such as TLR3 and TLR7, modulating inflammatory processes. Some research papers suggest that changes in mitochondrial metabolism and dynamics can modulate neuroinflammatory responses in microglia, however, this is under investigated and poorly understood.

In this study, using various methods including fluorescence microscopy, BrdU assay, polymerase chain reaction (PCR), we investigated effects of viral RNA-mimetics Loxoribine and Poly (I:C) on microglial BV-2 cells and mitochondrial dynamics. We found that Loxoribine and Poly (I:C) significantly increased expression of mitochondrial fission factor (Mff) fission marker compared to the control group but had no effect on expression of fusion marker mitofusin 1 (Mfn1) in BV-2 cell cultures. Loxoribine and Poly (I:C) had no effect on microglial viability, proliferation or mitochondrial content.

Our results suggest that viral RNA-mimetics may affect structures of mitochondrial networks in microglial cells through increased expression of fission proteins.

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P27

TLR3 Activator Poly(I:C) Induces Pro-Inflammatory Microglial Changes Leading to Neuronal Loss

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Viral infections of central nervous system can trigger persistent neuroinflammatory responses driven by activated brain immune cells – microglia. As a result, virus-induced pro-inflammatory activation may accelerate neurodegenerative processes and contribute to disease progression. However, actual molecular mechanisms underlying microglia-induced activation and subsequent neuroinflammatory responses remain poorly understood.

To address this question, primary rat neuronal–glial co-cultures and pure microglial cultures were treated with poly(I:C), a Toll-like receptor 3 agonist that mimics viral RNA, providing a model for studying neuronal–microglial interactions during viral inflammation.

We have found that poly(I:C) induces microglia-mediated neuronal loss. Moreover, poly(I:C) induces phosphatidylserine exposure on neuronal membrane leaflet and enhances uptake of phosphatidylserine coated beads by microglial cells. These processes were accompanied by lactadherin release promoting phosphatidylserine recognition by microglial cells. Overall, our data show that synthetic TLR3 agonist poly(I:C) promotes neuronal loss through microglial phagocytic uptake.

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P28

Landscape of m6A mRNA Methylation and Expression Signatures in Human Glioma

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Glioblastoma (GB) are highly aggressive and genetically complex brain tumors that infiltrate surrounding brain tissue, making them extremely difficult to treat effectively. Recent research has revealed that m6A modification is abnormally activated in glioma, underscoring its key role in various processes of glioma development.

m6A modifications in mRNA of glioma stem cells NCH421k (GSCs) and in glioblastoma tumor tissues were investigated using methylation-based RNA immunoprecipitation (MeRIP) and direct Nanopore RNA sequencing (dRNA-seq). Data analysis amongst GSCs demonstrated 740 hypermethylated and 830 hypomethylated genes after MeRIP-seq. dRNA-seq data presented 4,340 RRACH motifs associated with hyper-methylated up-regulated genes and 9,106 motifs associated with hyper-methylated down-regulated genes across samples taken from glioma patients. We identified eight statistically significant RRACH motifs across seven genes — AAACA|2129|OS9, AGACA|1210|PAGR1, GGACA|2173|OS9, GGACT|2187|TOB1, AAACC|3283|PIK3R2, GAACC|3068|GP1BB, GGACA|3110|RETREG1, and GGACT|3122|LUC7L3 — to narrow down potential gene candidates.

Findings indicated that m6A in target motifs is modified approximately 3.4-fold more in LGG than in GB, distinguishing patient samples by pathology. Next, we found that global m6A methylation score was significantly lower in GB cluster compared to LGG cluster ($p=0.0002$). Furthermore, lower m6A methylation scores were associated with shorter survival in glioma patients ($p=0.016$) while the expression levels did not differ among m6A-based clusters ($p=0.08$) or in a Kaplan-Meier survival analysis ($p=0.79$).

In summary, m6A modifications in mRNA may emerge as future-defining biomarkers capable of reshaping gliomas biology.

P29

Functional Characterization of Serotonergic Tryptamine Analogs via Calcium Imaging: Potency and Efficacy Profiling at the 5-HT_2A Receptor

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The 5-HT_2A receptor, a Gq-coupled GPCR, plays a central role in perception, cognition, and mood and is a key target for understanding psychedelic mechanisms and developing novel neuropsychiatric therapies.

Here, we functionally characterized three serotonergic compounds—serotonin, psilocin, and a synthetic analogue (X1) — using calcium imaging in U2OS HiTSeeker cells stably expressing 5-HT_2A and transfected with the genetically encoded calcium indicator jGCaMP8m. Intracellular calcium responses ($\Delta F/F_0$) were recorded following compound application at increasing concentrations, normalized to a 60-second baseline, and analyzed using a four-parameter logistic model in R.

Serotonin exhibited the highest potency (EC_{50} = 3.2 nM), followed by psilocin (15.4 nM) and X1 (23.0 nM). Dose–response curves for psilocin and X1 were right-shifted relative to serotonin, reflecting lower potency. Maximum efficacy was similar for serotonin and psilocin (~1.70 $\Delta F/F_0$), while X1 showed a reduced response (~1.25 $\Delta F/F_0$), consistent with partial agonism. Hill slopes (–0.32 to –0.50) indicated low receptor cooperativity. Comparison of calcium indicators demonstrated superior sensitivity and reproducibility of jGCaMP8m. Notably, X1, while active in vitro, failed to induce behavioral responses *in vivo*, suggesting pharmacokinetic or pathway-specific limitations.

This study highlights the utility of calcium imaging for detailed functional profiling of 5-HT_2A ligands, reveals biased agonism among tested compounds, and provides a framework for rational development of selective neuropsychiatric therapeutics.

P30

Analysis of miRNA Expression Profiles Using an Integrated DESeq2 and sPLS-DA Approach to Identify Potential Multiple Sclerosis Biomarkers

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Multiple sclerosis (MS) is a complex autoimmune disorder driven by diverse molecular, genetic, and immunological processes, and characterized by diverse clinical course forms. The identification of reliable biomarkers is essential for improving our understanding of MS disease mechanisms and for developing more advanced diagnostic and prognostic strategies. microRNA expression profiling represents one of the most promising approaches for revealing molecular alterations associated with MS pathogenesis.

The aim of this study was to identify potential MS biomarkers by applying sequencing-based expression analysis and machine-learning methods using untreated samples.

MiRNA sequencing was performed on samples from 9 MS patients and 13 healthy controls. Following data quality control, principal component analysis (PCA) was applied to evaluate sample structure and group separation. Differential expression analysis was conducted using DESeq2, with results visualized through a volcano plot and heatmap. In parallel, sPLS-DA was employed to identify features contributing most strongly to group discrimination. Molecules overlapping between DESeq2 and sPLS-DA results were further evaluated using boxplots and univariate logistic regression models.

PCA analysis showed a clear separation between the MS and control groups based on miRNA expression. DESeq2 identified miRNAs that were significantly differentially expressed. sPLS-DA further narrowed down the set of features with strong ability to distinguish the groups. All miRNAs selected by sPLS-DA overlapped with those found by DESeq2, supporting their stability and biological relevance. Logistic regression showed that even single miRNAs from this set could significantly separate the two groups.

The integrated DESeq2 and sPLS-DA analysis identified a group of miRNAs that were statistically different between MS patients and healthy controls and showed strong discriminatory ability. The overlapping miRNAs represent strong candidates for potential diagnostic or prognostic MS biomarkers. The analysis was performed using untreated samples, making the results more reliable and providing a solid basis for future validation studies.

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P31

Comparing In Silico and Sequencing-Based miRNA Expression in Multiple Sclerosis

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Multiple sclerosis (MS) is a chronic inflammatory demyelinating disease of the central nervous system characterized by considerable clinical heterogeneity. Its diagnosis and prognosis remain challenging – although clinical, radiological, and laboratory criteria are applied, reliable biomarkers capable of enabling earlier detection, predicting relapses, or assessing therapeutic efficacy are still lacking. Moreover, treatment effectiveness is often limited by inter-individual variability in therapeutic response and the complexity of disease progression. One promising class of biomarkers is microRNAs (miRNAs), small non-coding RNA molecules that regulate gene expression at the transcriptional or post-transcriptional level. However, due to their broad diversity, identifying biologically relevant miRNAs requires integration of in silico and experimental approaches.

Our study consisted of two major stages: (1) in silico miRNA modeling and (2) an experimental sequencing phase. In the silico phase, we computationally derived predicted miRNA expression profiles in the context of MS. MiRNA sequencing was performed using the Illumina platform on extracellular vesicle samples isolated from blood (9 MS patients and 13 healthy controls). Differential expression analysis was conducted using the DESeq2 package to evaluate miRNA expression profiles between MS patients and healthy individuals. Overlapping miRNAs identified through both in silico prediction and sequencing were compared to assess their biological relevance to MS.

Four miRNAs predicted in silico were confirmed in sequencing data. Among them, hsa-miR-19a-3p showed the highest expression change ($\log_2$FoldChange > 1), while hsa-miR-17-5p, hsa-miR-139-5p, and hsa-miR-20a-5p exhibited moderate but signifi-

cant alterations. KEGG analysis revealed enrichment in pathways of neurodegeneration – multiple diseases, amyotrophic lateral sclerosis (ALS), and the MAPK signaling pathway, suggesting shared molecular mechanisms between MS and other neurodegenerative disorders.

The integration of in silico modeling with high-throughput sequencing analysis effectively identifies biologically relevant miRNAs in multiple sclerosis and highlights their potential as biomarkers involved in neurodegenerative and inflammatory signaling pathways.

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P32

reaDream: Towards Objective Dream Decoding

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reaDream is a multifaceted project with the aim of objective nighttime dream decoding. Dreams impact our emotional state and memory and can hint at certain medical conditions (Nielsen 2013, Siclari et al. 2020). However, most dreams are forgotten upon awakening. Dream researchers collect dream reports from people after awakening, though these subjective reports can be unreliable and incomplete. Without dream reports, "dream experience becomes decoupled from the primary sort of evidence" (Windt 2013). The reaDream project taps into a new form of evidence to decode multimodal dream content in real time. The system comprises a comfortable EEG/EMG recording device, and a deep learning model to classify dream components in real time, such as emotions, movements, visuals, and sounds.

P33

Investigating the Behavioral Effects of Monosodium Glutamate in Cockroaches (*Blaberus giganteus*)

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Monosodium glutamate (MSG) is a widely used flavor enhancer that acts on glutamatergic signaling pathways. Although MSG is considered safe for human consumption, its potential to influence neural signaling and behavior remains insufficiently characterized. Investigating these effects in invertebrate models provides an ethical and tractable approach to study glutamatergic signaling and behavioral outcomes in a simplified nervous system.

This study aimed to assess the influence of dietary MSG on the behavior and physiological parameters of *Blaberus giganteus*.

Fifteen nymphs were randomly assigned to three groups: a control group receiving water, a 1% MSG-treated group, and a 4% MSG-treated group. Each group received 12 mL of its respective solution over ten days in custom-built enclosures maintained in darkness. Group body weights were measured at the start and end of the exposure period, followed by behavioral assessment using a Y-maze choice test.

All groups exhibited weight gain, indicating suitable physiological conditions during exposure. The control group demonstrated the greatest mean weight increase (4 g), whereas both MSG-treated groups showed comparatively smaller gains (3 g each). Behavioral analysis revealed altered locomotor activity in MSG-exposed cockroaches. By the 10th day total mobility duration reached 33 hours in the control group. In contrast, the 1% MSG group exhibited only 6 hours, and the 4% MSG group – 12 hours of mobility. In the Y-maze assay, the control and 1% MSG groups exhibited a preference for the water arm, but all individuals in the 4% MSG group selected the MSG arm.

These findings indicate that MSG exposure modulates both locomotor and preference behaviors in B. giganteus in a concentration-dependent manner. The results support the hypothesis that MSG can induce hypersensitive and preference-related behavioral changes in invertebrates, providing insight into glutamatergic signaling and the potential neurobehavioral effects of dietary additives across species.

P34

Association Analysis Between IL-33 rs1157505 Polymorphism and Multiple Sclerosis Risk in Women from Lithuania

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Multiple sclerosis (MS) is an immune-mediated disorder affecting the central nervous system, marked by inflammation, demyelination, and progressive neurodegeneration. The disease involves complex interactions between genetic susceptibility and environmental triggers leading to immune system dysregulation and neuronal injury (Portaccio et al., 2024). Importantly, MS disproportionately affects women, who are two to three times more likely to develop the disease than men, highlighting potential sex-specific genetic and immunological factors (Coyle, 2021). Interleukin-33 (IL-33), a cytokine involved in immune regulation and tissue repair, plays a significant role in modulating inflammatory responses in MS (Augustine et al., 2019). Although the *IL-33* gene polymorphism rs1157505 has been primarily studied in Alzheimer's disease, IL-33's involvement in immune pathways supports exploring this variant's association with MS susceptibility, particularly in women (Chapuis et al., 2009).

We aimed to investigate the association between *IL-33* gene polymorphism rs1157505 and susceptibility to multiple sclerosis in women within the Lithuanian population.

The study enrolled 145 patients with MS and 145 healthy controls. DNA was extracted from peripheral blood leukocytes using the DNA salting-out method. Genotyping was carried out using the real-time polymerase chain reaction (RT-PCR) method. Statistical analysis was performed with „SPSS version 30.0".

Logistic regression revealed that the G allele is associated with a 1.6-fold increase in the odds of developing MS under the additive model (OR = 1.575; 95% CI: 1.042–2.381; p = 0.031). The CG genotype was linked to a 1.8-fold increase in odds under the co-dominant model (OR = 1.801; 95% CI: 1.107–2.931; p = 0.018), as were the combined CG + GG genotypes under the dominant model (OR = 1.773; 95% CI: 1.105–2.845; p = 0.018). The CG genotype alone also showed a 1.8-fold increase under the overdominant model (OR = 1.756; 95% CI: 1.186–2.840; p = 0.022).

Our results showed that the *IL-33* rs1157505 polymorphism is linked with higher odds of MS development, but further research is required.

P35

Differential Effects of Organic and Inorganic Selenium on Oxidative Stress and Metal Homeostasis in Mouse Brain and Liver

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This study aimed to evaluate and compare the effects of different selenium compounds on levels of glutathione and metallothionein levels, as well as on markers of lipid peroxidation and micronutrient status, in brain and liver tissues of mice. Mice were orally administered either inorganic sodium selenite or organic L-selenomethionine at a dose of 0.4 mg Se/kg body weight for eight weeks. Blood, brain, and liver tissues were collected for analysis. Antioxidant markers: content of reduced glutathione (GSH), metallothioneins (MT), and malondialdehyde (MDA) from lipid peroxidation were evaluated spectrophotometrically; micronutrient levels (Se, Zn, Cu, and Fe) determined by inductively coupled plasma mass spectrometry. SeMet supplementation significantly reduced liver MT concentration compared to control. Na_2SeO_3 lowered blood GSH levels. Both selenium compounds significantly increased MDA, with SeMet raising blood and liver levels, and Na_2SeO_3 having a stronger effect. Substantial Se accumulation was observed in both groups: SeMet elevated liver and brain Se as well as liver Fe, while Na_2SeO_3 boosted liver and brain Se. Additionally, Na_2SeO_3 reduced brain Cu, Zn, and Fe, yet increased liver Fe compared to controls.

Overall, the findings suggest that prolonged selenium supplementation, whether organic or inorganic, can have complex and sometimes adverse effects on antioxidant defenses and trace element homeostasis. These results underscore the critical role of selenium form, dose, and exposure duration in determining its benefits, as excessive intake may lead to oxidative stress rather than protection.

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Non Eco-friendly Ad Stickers on Retail Store Floors from Shoppers' Eyes

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Non Eco-friendly Ad Stickers on Retail Store Floors from Shoppers' Eyes Retailers set high expectations for non-eco-friendly ad stickers on floors for quick installations and relatively low costs. As smartphones are increasingly used by customers while shopping in stores, their gaze is also expected to go down. Hence, some retailers may assume this is an opportunity to install these ad stickers on floors. These stickers might capture shoppers' attention as they walk through the store in high-traffic areas or near promoted product shelves.

Recently, many EU and US retailers' floors have been increasingly equipped with various designs of ad stickers that advertise products/services, enhance brand visibility, or convey important information to shoppers. Moreover, retail stickers can cover different content types, such as informational (e.g., social distancing, navigation), promotional (e.g., sales), decorative (e.g., seasonal themes), and social/interactive (e.g., taking a photo and sharing it on social media). Thus, stickers can be designed in 2D or 3D formats. Despite the increasing number of ad stickers on retail stores' floors, their effectiveness is not revealed in academia or business literature. It appears that businesses use eco-friendly ad floor stickers for in-store marketing campaigns, but their effectiveness is not defined. This research aims to explore the effectiveness of ads on retail store floors through shoppers' eye-gaze behavior. Two ad stickers for two distinctive stores (stores: X food brand and beauty Y brand) were created and covered promotional and informative content types. It was sought to enhance the visibility of ad stickers. Hence, all ad stickers were near tested product shelves. Self-report and ML-empowered mobile eye trackers were used. In total, 43 participants were involved. For the eye tracking analysis, Blickshift analytics was run. This research shows that most shoppers do not notice both ad stickers on floors. Only one participant paid attention to an ad sticker in a food store and was considered an outlier because the shopper was a marketing specialist. It confirms that non-eco-friendly ad stickers on retail store floors are not effective, and retailers are encouraged to avoid them.

Future research is needed to investigate diverse formats (e.g., 3D) and content types of ad stickers on retail store floors.

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Detection and Quantification of Synaptic Events in Mouse Hippocampal Ca1 Neurons During Postnatal Development Using "miniML" Machine Learning-Based Analysis

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The early stages of postnatal development in hippocampal pyramidal neurons are characterized by both morphological and electrophysiological changes, which are crucial for the development of neural networks and the functional maturation of neurons (Ben-Ari, 2001; Hensch, 2005). During this period, synaptic pruning plays a vital role in optimizing the processing and transmission of signals within the neuronal network. Synaptic activity is typically measured by the frequency and amplitude of synaptic events recorded electrophysiologically; however, detecting and quantifying these events in hippocampal pyramidal neurons is complicated by noisy signals, variability, and the large number (>1000) of synaptic events.

The aim of this study was to improve the detection and quantification of synaptic events in electrophysiological recordings from mouse hippocampal CA1 neurons by adapting a machine learning–based approach called "miniML" (Wang et al., 2024).

In this study "miniML" detects and quantifies synaptic events with slight parameter adjustments, even in recordings characterized by high noise levels and complex event patterns. By implementing this machine learning approach, we provide an automated, precise, and efficient method for the analysis of large-scale electrophysiological data, enabling comprehensive investigations into synaptic function and neuronal development.

P38

Decoding the Impact of Glioblastoma EVs on Neural Stem Cells via Calcium Dynamics and Transcriptomics

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Glioblastoma (GBM) is an aggressive brain tumor marked by rapid growth, frequent recurrence, and resistance to treatment. Emerging research shows that GBM cells interact with neural stem cells (NSCs) through extracellular vesicles (EVs). Understanding how GBM-derived EVs influence NSCs is key to revealing tumor–microenvironment dynamics and identifying novel therapeutics. Because calcium signaling governs cell proliferation, migration, and differentiation, changes in intracellular calcium may provide an early indicator of EV-driven NSC reprogramming. This study examined how GBM cell lines from different origins affect NSC behavior, focusing on calcium-signaling changes and validating findings with next-generation sequencing (NGS).

Human neural stem cells (NSC H9 line) were treated with EVs isolated from GBM cell lines A172 and U87-MG conditioned media using 12% polyethylene glycol (PEG) precipitation. Cells were exposed to GBM-derived EVs (~1250 EVs per cell) for 17 h for Ca2+ signalling analysis and for 24 h for NGS. For Ca^{2+} imaging, NSCs were loaded with 2 μM Oregon Green-488 BAPTA-1 dye and imaged at 2 Hz for 200 s using a 40× objective. Nifedipine (2 μM) and caffeine (5 mM) were applied sequentially to assess L-type Ca^{2+} channel activity and ryanodine receptor (RyR)-mediated Ca^{2+} release, respectively.

The pilot study revealed that GBM EVs influence Ca^{2+} signaling in NSCs, with effects dependent on the cell line. A172 EVs increased Ca^{2+} signal frequency in affected NSCs, which was blocked by nifedipine, suggesting elevated L-type Ca^{2+} channel activity. In U87 EV–treated NSCs, signal amplitude increased with nifedipine and further rose with caffeine, indicating enhanced RyR activity. NGS analysis revealed changes in RyR, SLC8B1 and LETM1 gene expression, suggesting increased Ca^{2+} concentration in mitochondria leading to augmented metabolic activity in mitochondria. Changes in Ca^{2+} signaling induced by EVs point to potential cross-talk between cytosolic and mitochondrial Ca^{2+} pathways.

The study shows that A172 EVs enhance Ca^{2+} signaling, potentially promoting NSC proliferation and differentiation, whereas U87-MG EVs strongly elevate RyR levels, increasing NSC sensitivity to environmental cues such as growth factors or inflammatory interleukins. These functional effects are further supported by NGS analysis, which confirms the underlying molecular changes driving these EV-mediated responses.

P39

Machine Learning Analysis of Acoustic Features for Colour Prediction in Sound–Colour Synaesthesia

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Sound–colour synaesthesia is an uncommon condition in which sounds automatically trigger consistent and vividly perceived colour sensations. The purpose of this study was to examine whether the colours most often reported by a synesthete can be reliably predicted from objective acoustic features of voice recordings.

A classification experiment of using sets of acoustic features and machine learning approaches demonstrated that the models obtained extremely good performance – 97–100% Accuracy for binary and 89–90% for multi-class problem.

The results provide novel insights into how specific sound components might relate to the imagery of the human subconsciousness. Moreover, the findings highlight the potential of computational methods to objectively characterise synaesthetic perception, offering a foundation for future research.

P40

Epilepsy-Specific Features of the Glycobiology of Human Brain Tissue and Synaptosomes

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Glycoconjugates play vital roles in neurobiological processes, including tissue patterning, neural development, synaptic formation, and neuronal network remodelling. Sialic acid, a monosaccharide often found at the ends of sugar chains on neuronal glycoproteins and glycolipids, is of particular importance. In the mouse brain, the presence of sialic acid has been shown to promote excitability of neuronal circuits and to cause seizures, a common feature of the epileptic brain. However, whether this is caused by a global increase in sialylation across all brain glycoproteins or synapse-specific changes, and whether there are other significant alterations in the glycosylation of neuronal proteins in epileptic human brain remains to be determined. Therefore, this study used surgically resected human brain tissue to investigate glycobiology in healthy and epileptic human brain tissue and neural connections, the synaptosomes.

Multiomics – transcriptomic and glycomic analysis of epileptic human brain tissue and isolated synaptosomes uncovered new molecular signatures. This study identified new players influencing synaptic protein function, neuronal signalling, and network excitability – processes disturbed in epilepsy. Results uncovered new glycan structures in epileptic brain that may pave the way for innovative therapies, offering hope for patients with drug-resistant epilepsy.

This research bridges the gap between neurobiology and glycoscience, opening new avenues for understanding and treating epilepsy.

P41

Precision Genome Editing and Targeted Delivery Strategies for Aceruloplasminemia

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Aceruloplasminemia (ACP) is a rare, autosomal recessive neurodegenerative disorder caused by mutations in the ceruloplasmin (CP) gene, leading to iron buildup in the brain, liver, and pancreas. Current therapies, including iron chelation and enzyme replacement, offer limited clinical benefits. To tackle these challenges, we aim to develop a comprehensive gene therapy approach tailored for ACP. Our strategy employs patient-derived induced pluripotent stem cells (iPSCs) and mouse organotypic brain slices to investigate and correct CP deficiency.

We aim to restore CP function using two complementary delivery platforms: neurotropic, non-replicating HSV-1 vectors for targeted delivery of genome editing tools to neural tissue, and lipid nanoparticles (LNPs) for delivering CRISPR prime editing components. Prime editors enable precise correction of point mutations in the CP gene, overcoming limitations of earlier CRISPR technologies. Lipid compositions for LNP formulations will be optimized to enhance delivery efficiency and tissue targeting, with a focus on the brain.

Our study evaluates HSV-mediated delivery of gene editing components into patient-derived iPSCs and explores LNP-mediated delivery in mouse organotypic brain slices. By comparing these delivery platforms, we aim to determine the best strategy that combines the most effective genome editing method with the most efficient delivery system, allowing for the assessment of therapeutic potential at both molecular and functional levels.

P42

Role of CB2 Receptor in β-Hydroxybutyrate Mediated Microglial Anti-inflammatory Phenotype

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The cannabinoid receptor type 2 (CB2R), primarily expressed in microglia, the brain's resident immune cells, acts as a central regulator of neuroinflammatory responses. When CB2R is activated it triggers anti inflammatory signaling, making it a promising target for modulating microglial function in neuroinflammatory diseases. The ketone body, β-hydroxybutyrate (BHB), is gaining attention as a therapeutic agent for neurodegenerative disorders due to its ability to modulate neuroinflammation and preserve blood–brain barrier integrity. One mechanism by which BHB exerts anti-inflammatory effects is through regulation of microglial function; however, the precise mechanisms remain unclear.

Since the role of BHB in this context is unexplored, we used two neuroinflammation models to test the hypothesis that BHB effects are mediated by CB2R. In a mouse model of diet-induced obesity (DIO), characterized by chronic low-grade neuroinflammation, BHB treatment promoted ramified microglial morphology and enhanced debris clearance while sparing synaptic elements. These changes coincided with increased CB2R signaling tone. When primary microglial cultures were challenged with lipopolysaccharide (LPS), BHB helped restore their function. However, that benefit disappeared when CB2R was pharmacologically blocked. Moreover, BHB suppressed nuclear factor kappa-light-chain-enhancer of activated B cells (NF-κB) signaling, and this effect was negated by CB2R inhibition, suggesting a mechanistic link between BHB and CB2R-dependent pathways.

Collectively, our findings demonstrate that BHB's anti-inflammatory effects are mediated, at least in part, through CB2R signaling, providing new insight into its therapeutic potential for neuroinflammation.

P43

Expression of IRG1 in Microglia and its Effects on Hif1α and IRF7

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Upon exposure to LPS and IFNγ, IRG1 (immune-responsive gene 1) expression highly increases in macrophages and microglia. It regulates immunometabolism in the cell and so is involved in metabolic and inflammatory changes cells go through under inflammatory conditions. Some of the major transcription factors that regulate cell metabolism and inflammatory response are Hif1α (hypoxia inducible factor 1 subunit alpha) and IRF7 (Interferon regulatory factor 7) and the relationship between these transcription factors and IRG1 is not well understood. The aim of our study was to investigate whether IRG1 has an effect on the expression of Hif1α and IRF7.

BV-2 mouse microglia cells were stimulated with TLR4, TLR3, and TLR7 agonists (LPS, loxoribine, and poly-(I:C) respectively) IRG1 expression was measured by western blot. To test the effect of IRG1 on the expression of Hif1a and IRF7 we utilized siRNA to silence IRG1. Expression of Hif1α and IRF7 were detected by immunofluorescence.

IRG1 expression was significantly upregulated in microglia, stimulated by LPS and loxoribine. LPS also increased the expression of Hif1α and IRF7 while loxoribine only increased the expression of Hif1α. IRG1 silencing also shows a tendency to decrease Hif1α expression but has no effect on IRF7 expression.

IRG1 is upregulated in BV-2 microglia after TLR4 and TLR7 stimulation. Hif1α but not IRF7 expression is partially controlled by IRG1 in BV-2 cells during inflammation.

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Dissecting Cortical Contributions to Gamma-Range Entrainment and Ketamine-Induced Deficits

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Cortical circuits exhibit spontaneous rhythmic activity and entrainment to periodic sensory stimulation. In the auditory system, rhythmic sounds elicit the Auditory Steady-State Response (ASSR), which is typically strongest in the gamma range, around 40 Hz (Pictone et al., 2003; Jasinskyte et al., 2023; Kozono et al., 2019). Although this preferred entrainment frequency is well described in humans and rodents, it remains unclear whether it emerges from cortical network dynamics or is already predetermined in subcortical auditory structures. ASSR deficits are a promising biomarker for neuropsychiatric disorders, particularly schizophrenia, where 40-Hz entrainment is reduced in patients and high-risk individuals (Grent-'t-Jong et al., 2023; Tada et al., 2016; Thuné et al., 2016). Comparable impairments in cortical entrainment are observed in rodent schizophrenia-like models where NMDA receptors are systemically suppressed (Cizus et al., 2025; Jasinskyte et al., 2025), yet the primary neural targets of NMDA antagonists remain unresolved.

Here, we aimed to determine (1) whether optimal entrainment is set by cortical networks or inherited from subcortical inputs, and (2) whether NMDA antagonists directly disrupt cortical network dynamics underlying neural entrainment. LFPs were recorded from A1 in C57BL/6 mice using implanted electrodes.

Thalamocortical inputs were optogenetically activated by expressing ChR2 in MGB neurons and delivering light pulses via an optic fibre over A1. Chirp trains (5–100 Hz, 3 s) of clicks or light pulses evoked ASSRs and dSSRs. Recordings were obtained before and 5 min after sub-anesthetic ketamine (20 mg/kg). Time–frequency analysis (Morlet wavelets) measured power and inter-trial coherence.

Under baseline conditions, cortical entrainment to auditory chirps showed reduced responses in the high-frequency range, whereas direct optogenetic activation of thalamocortical projections preserved high-frequency entrainment. Ketamine administration impaired gamma-range entrainment during both auditory and optogenetic stimulation, reducing power and ITC across high frequencies.

These findings indicate that (1) the optimal entrainment to gamma frequency is imposed by subcortical auditory processing before reaching auditory cortex, and (2) ketamine directly disrupts cortical network dynamics governing entrainment. These results provide mechanistic insight into ASSR generation and its disruption in NMDA antagonist-based models of schizophrenia.

P45

Implementation of a Cortico-Thalamic Transformer for understanding Language Processing

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Transformer networks (Vaswani et al., 2017) have revolutionized artificial intelligence with their powerful capabilities, yet it remains unknown if they process information in a way that is similar to the human brain. Recent theories suggest that the transformer's attention mechanism may mimic the brain's cortico-thalamic circuits (Granier & Senn, 2025). However, a working computational model is needed to test this idea against real-world brain data.

This study aimed to build and train a cortical transformer model, which is a transformer based on the proposed cortico-thalamic architecture, which maps the mathematical components of the self-attention mechanism—queries, keys, and values—directly onto the biological dynamics of specific cortical layers and thalamic loops (Granier & Senn, 2025). The goal was to create a tool that can generate internal activity patterns for direct comparison with human brain recordings during a language task.

A cortical transformer was built in PyTorch, using a 4-layer, 6-head design. The model, containing 11.71 million parameters, was trained for 34 epochs on the Multi30k dataset (Elliott et al., 2016) to complete an English-to-German translation task. A data pipeline was developed to extract the model's internal activations (Query, Key, and Value vectors) in response to linguistic input.

The cortical transformer was successfully trained, achieving a BLEU score of 25.29. While not state-of-the-art, this result serves as a critical proof of concept, demonstrating that the cortico-thalamic architecture is computationally viable and capable of learning a complex language task. The system is now prepared for future neuroscientific studies that will correlate its activations with human brain recordings, providing a framework to investigate the biological basis of attention and cognition.

P46

Modulation of Brain Activity via Deep Brain Stimulation: an EEG-Based Assessment with Personalized Models in Parkinson's Disease

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Parkinson's disease (PD) is a neurodegenerative disorder marked by motor impairments, often accompanied by pathological oscillations in brain networks (notably excessive beta-band activity). Understanding these alterations is crucial for improving diagnosis and guiding therapies such as deep brain stimulation (DBS). In this study, we combined a computational model with source-reconstructed EEG to examine how dopaminergic modulation and DBS affect brain network activity in PD.

We created a neural mass model that accounts for dopamine-driven modulation. The model suggests that increasing dopamine reduces pathological oscillations and promotes more stable brain activity. To test this prediction, we analyzed high-density EEG from a PD patient recorded before DBS (on/off medication) and six months after DBS implantation (on/off stimulator, on/off medication). EEG signals were source-reconstructed using the patient's MRI, and functional connectivity metrics (amplitude envelope correlation, AEC; phase-locking value, PLV) were calculated across standard frequency bands.

Our results showed that beta-band functional connectivity was markedly reduced after DBS – the largest change among all frequency bands. Beta-band coupling between cortical regions (especially frontal and temporal areas) significantly decreased post-DBS, whereas changes in delta, theta, alpha, and gamma bands were minor. This reduction in pathological beta synchrony aligns with our model's prediction that enhanced dopaminergic signaling suppresses excessive network oscillations and corresponds to

improved motor function with DBS therapy. These findings highlight beta-band connectivity as a key biomarker of PD network changes and demonstrate that integrating computational modeling with EEG connectivity analysis yields mechanistic insight into DBS effects, informing personalized neuromodulation strategies.

To further support clinical translation, these models will be embedded into The Virtual Brain platform to create individualized digital twins of Parkinson's disease patients.

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Association Between Persistent Organic Pollutants and Steroid Hormone Levels in Baltic Grey Seal Pups

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The Baltic Sea is one of the world's most polluted aquatic environments, primarily due to Persistent Organic Pollutants (POPs). Because these pollutants are fat-soluble (lipophilic), they accumulate readily in the thick blubber of marine mammals like Grey Seals, making them highly vulnerable.

This investigation determined the concentrations of the following pollutant groups in free-ranging (Innarahu, Estonia) Grey Seal pups (n=20; 10 females, 10 males): ΣPCB (IUPAC numbers 101, 153, 138, 180, 194, 170, 156, 149, 52), ΣDDTs (p,p′-DDE, p,p′-DDT, p,p′-DDD), ΣHCHs (β-HCH, α-HCH), HCB, trans – nonanchlor, ΣPBDE (IUPAC numbers 28, 47, 99), ΣPAHs (PAE, ANT, 4CPP, FAE, PYR), TPP, BPN, BB, DPS, HOM, BCS. Comparing the 2024 data to 1998 showed a dramatic reduction in pollutant levels ΣPCB was down 83%, HCB was down 82%, ΣDDTs down 67%, ΣHCH down 74% and trans-nonachlor down 84%. Plasma concentrations of key steroid hormones were also determined, targeting compounds related to stress, metabolism, and reproduction: adrenal stress and metabolic hormones: Cortisol (COR), Cortisone (CORNE), Corticosterone (COS), 11-Deoxycortisol, and 11-Deoxycorticosterone (precursor).Reproductive and precursor steroids: Progesterone (Prog), Pregnenolone (Preg), 17-OH-Pregnenolone (17-OH-preg), 17-OH-Progesterone (17-OH-prog), and Dihydroprogesterone (Dihydro – prog) (progesterone metabolite).The influence of POP exposure on hormone levels was assessed using a Generalized Linear Model (GLM).

Despite this major decrease in contamination, the Likelihood-Ratio Chi-Square Test demonstrated a significant influence ($p < 0.05$) of these pollutants on several circulating hormones: 11-deoxycos, CORNE, Prog, Preg, 17OH-preg, Dihydro-prog. This study demonstrates that the current POP burden in Grey Seal pups remains high enough to significantly influence the endocrine system, affecting pathways related to stress, lipid metabolism, and steroid synthesis.

P48

Retinal Age Prediction in Lithuanian Population

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Ageing changes are heterogenous, with substantial variation in health impacts of ageing across populations, individuals and tissues [Grimbly MJ, et al. BMJ Open Ophth 2024;9:e001794. doi:10.1136/bmjophth-2024-001794]. Biological ageing markers have emerged to better represent the ageing process and predict the risk of diseases. Retinal age is an imaging-based biomarker for biological age assessment from retinal fundus photographs. Accelerated ageing, or Retinal age gap (RAG) – the difference between calculated retinal age and chronological age, provides a valuable metric for quantifying the risk of vascular, neurodegenerative, metabolic diseases and even assessing the risk of mortality. However, an undisclosed controversy remains whether generated retinal age models are accurate predictors of biological age. Moreover, further clinical trials exploring their applicability across diverse healthy populations are warrant.

We aimed to determine the accuracy of retinal age prediction models and evaluate their ability to reflect age-related parameters from retinal images exploring their estimation to chronological age of healthy Lithuanian population subjects.

Color fundus images from 92 patients were analyzed for age prediction, allocating 80% of patients (n = 74) for training and 20% (n = 18) for validation. Images were split into training and validation sets at the patient level to avoid data leakage. Each patient contributed 8 images, except for one patient who had 6 images, resulting in a total of 734 fundus images included in the analysis. Preliminary experiments using grayscale OCTA images resulted in insufficient prediction performance, therefore the analysis focused exclusively on color fundus data. A convolutional neural network based on EfficientNet-B2 was adapted for regression by replacing the classification head with a single linear output unit predicting normalized age values.

EfficientNet-B2 was selected based on findings from our previous study, in which several convolutional and transformer-based architectures were compared for classifying fundus images of healthy versus pathological images. The evaluated models in-

cluded ResNet-18, ResNet-50, DenseNet-121, EfficientNet-B0, InceptionV3, as well as transformer-based models Swin Transformer, DeiT, ConvNeXt, and a standard Vision Transformer. EfficientNet-B2 demonstrated the strongest overall performance in that classification task, motivating its use in the present regression study.

Image preprocessing included resizing, padding to a fixed resolution, and common data augmentations (rotation, flips, brightness/contrast adjustment, hue–saturation changes, CLAHE, Gaussian noise/blur). Intensities were normalized using ImageNet statistics. The model was trained using the AdamW optimizer and a CosineAnnealingLR learning-rate schedule. Regression was optimized using an L1 loss (MAE loss) applied to normalized age labels. Evaluation metrics included MAE, RMSE, and the coefficient of determination (R^2) computed on denormalized predictions.

On the validation set, the model achieved a mean absolute error (MAE) of 2.43 years, a mean squared error (MSE) of 9.76, a root mean squared error (RMSE) of 3.12 years, and a coefficient of determination (R^2) of 0.836.

Predicted versus true age values demonstrated a strong linear association across the examined range.

These findings highlight the potential of EfficientNet-B2 as an applicable model for retinal age assessment in healthy Lithuanian population.

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