Nova
MEDICAL TESTING

Pioneers of Small Molecule Analysis

Metabolomics for Neuroscience

VOL 1

B108 2011 94ST NW, T6N 1H1, Edmonton, AB, Canada | +1 (780) 699-9688 | support@novamt.com

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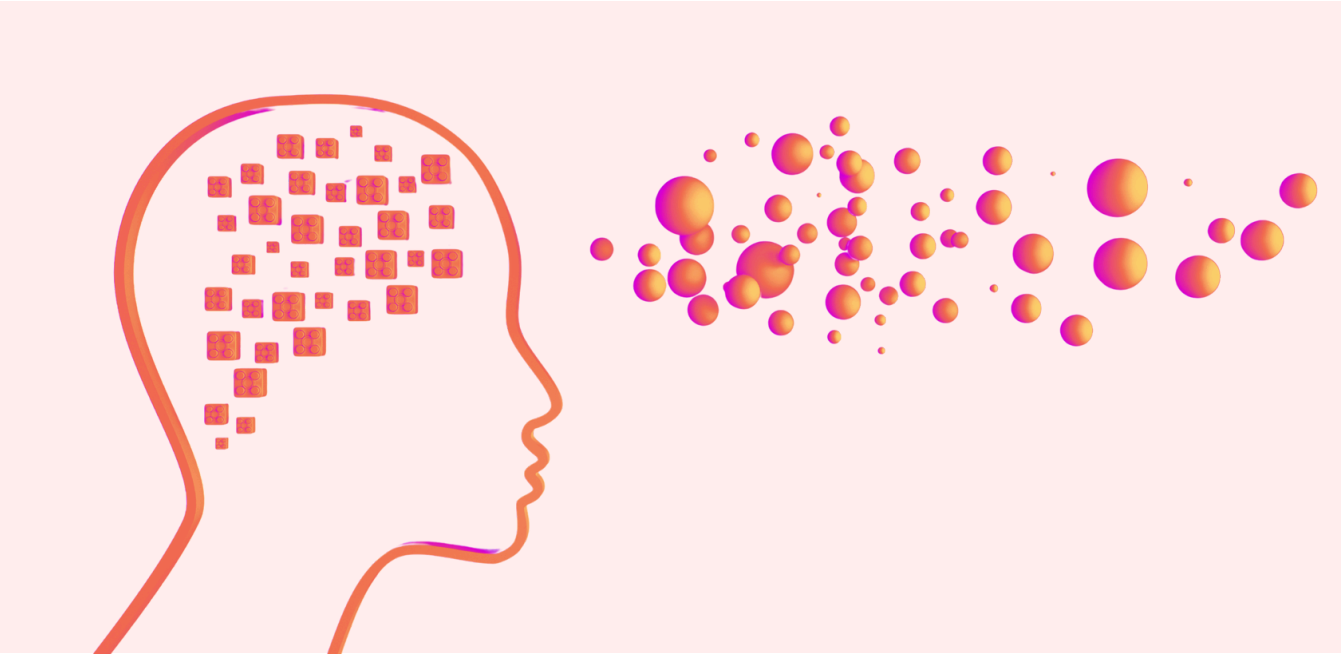
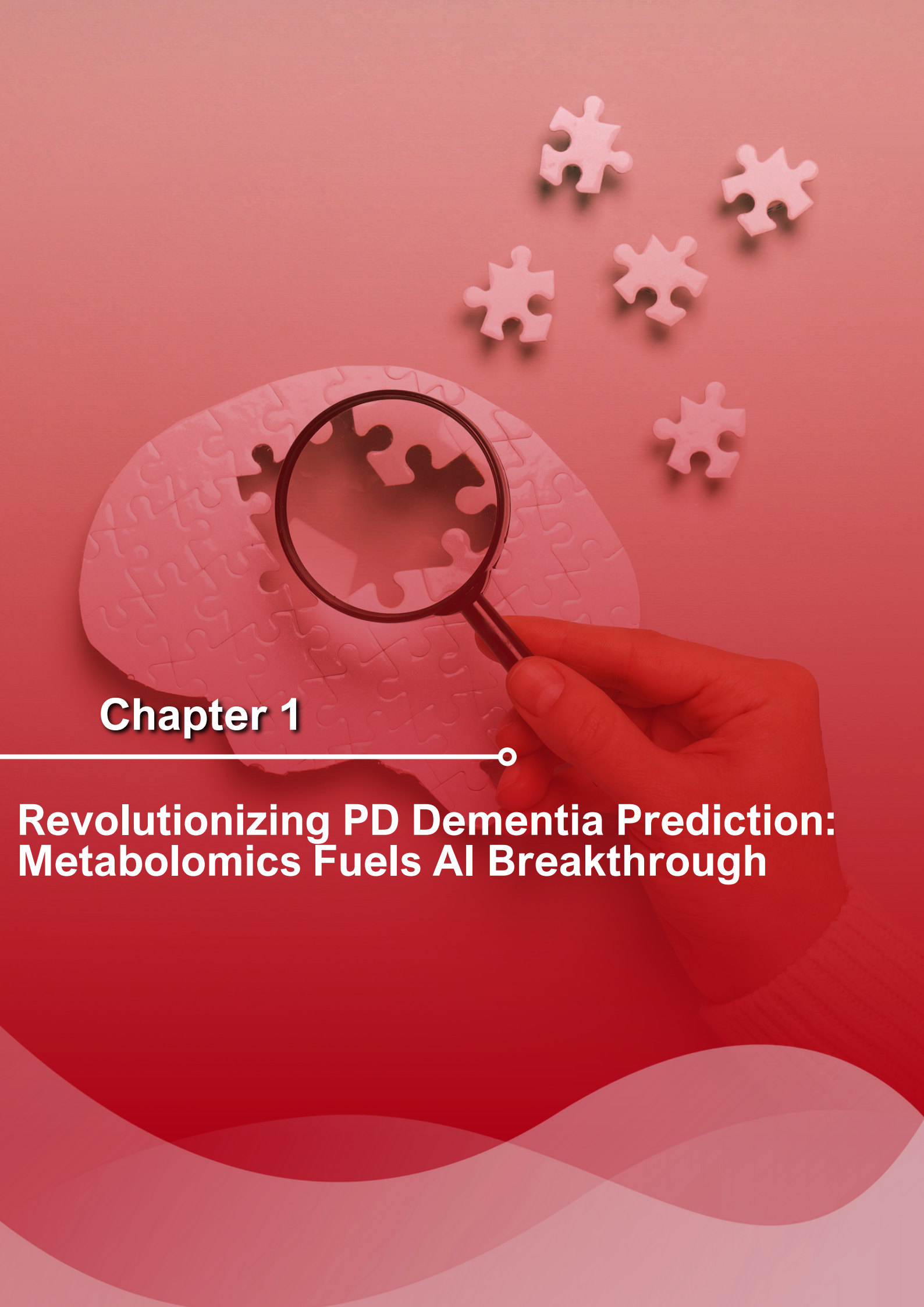


INTRODUCTION

Neurological disorders represent some of the most complex and devastating conditions affecting human health. From Alzheimer's disease and Parkinson's disease to amyotrophic lateral sclerosis (ALS) and neurodevelopmental impairments, these disorders involve intricate disruptions in cellular metabolism, energy balance, and molecular signaling within the brain. Traditional approaches have only scratched the surface in explaining their root causes or identifying effective, early-stage interventions.

At Nova Medical Testing, we apply meta-omics precision,integrating metabolomics and lipidomics, to illuminate the biochemical foundations of brain function and dysfunction. By capturing a real-time snapshot of small-molecule activity, multi-omics approaches reveal the biochemical imbalances that underlie neurological conditions. This data-rich approach allows researchers to map metabolic pathways linked to brain health, uncovering early indicators of dysfunction and disease progression long before symptoms appear. Powered by advanced LC–MS technologies and AI-driven data analytics, our platforms profile dynamic changes across thousands of metabolites and lipids, providing an unparalleled view into the molecular landscape of neurological disorders. By translating complex metabolic data into actionable biological insight, we help researchers identify early biomarkers, decode disease mechanisms, and evaluate therapeutic efficacy with precision and reproducibility.

This eBook highlights a series of real-world neuroscience applications, showcasing how NovaMT's advanced platforms are helping researchers explore the metabolic signatures of neurological health and disease. Our goal is to empower discovery, support earlier detection, and ultimately contribute to improving the lives of those affected by neurological conditions.



Chapter 1

Revolutionizing PD Dementia Prediction: Metabolomics Fuels AI Breakthrough

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Revolutionizing PD Dementia Prediction: Metabolomics Fuels AI Breakthrough

Our advanced **HP-CIL Metabolomics Platform** was instrumental in establishing a powerful, multi-modal predictive signature for early Parkinson's Disease Dementia (PDD). The data from this study demonstrated how precise metabolic profiling fueled sophisticated machine learning models, leading to the identification of critical metabolite panels that accurately distinguish PD patients at high risk for dementia. The insights gained were crucial for understanding the physiological underpinnings of PDD progression and provide invaluable markers for targeted intervention strategies, ultimately advancing earlier diagnosis and improved patient outcomes.

The Challenge

The study was grappling with a critical challenge in Parkinson's disease (PD): the early identification of individuals at risk for accelerated cognitive decline and dementia. PD is far more than a movement disorder; it is a multisystem condition with a high likelihood of leading to dementia, impacting quality of life and significantly increasing caregiver burden. With long-term dementia conversion rates estimated between 50% and 80%, their goal was to find a way to predict which patients would develop Parkinson's Disease Dementia (PDD) years before its disease onset, enabling early, targeted interventions. The difficulty lay in the disease's heterogeneity and the sheer volume of potential risk factors, making it challenging for traditional analytical methods to evaluate numerous factors simultaneously and comparatively. This complexity underscored the need for advanced machine learning approaches,which require robust, high-quality biomarker data to accurately identify leading predictors and interpret their effects.

Discover our HP-CIL Metabolomics Platform

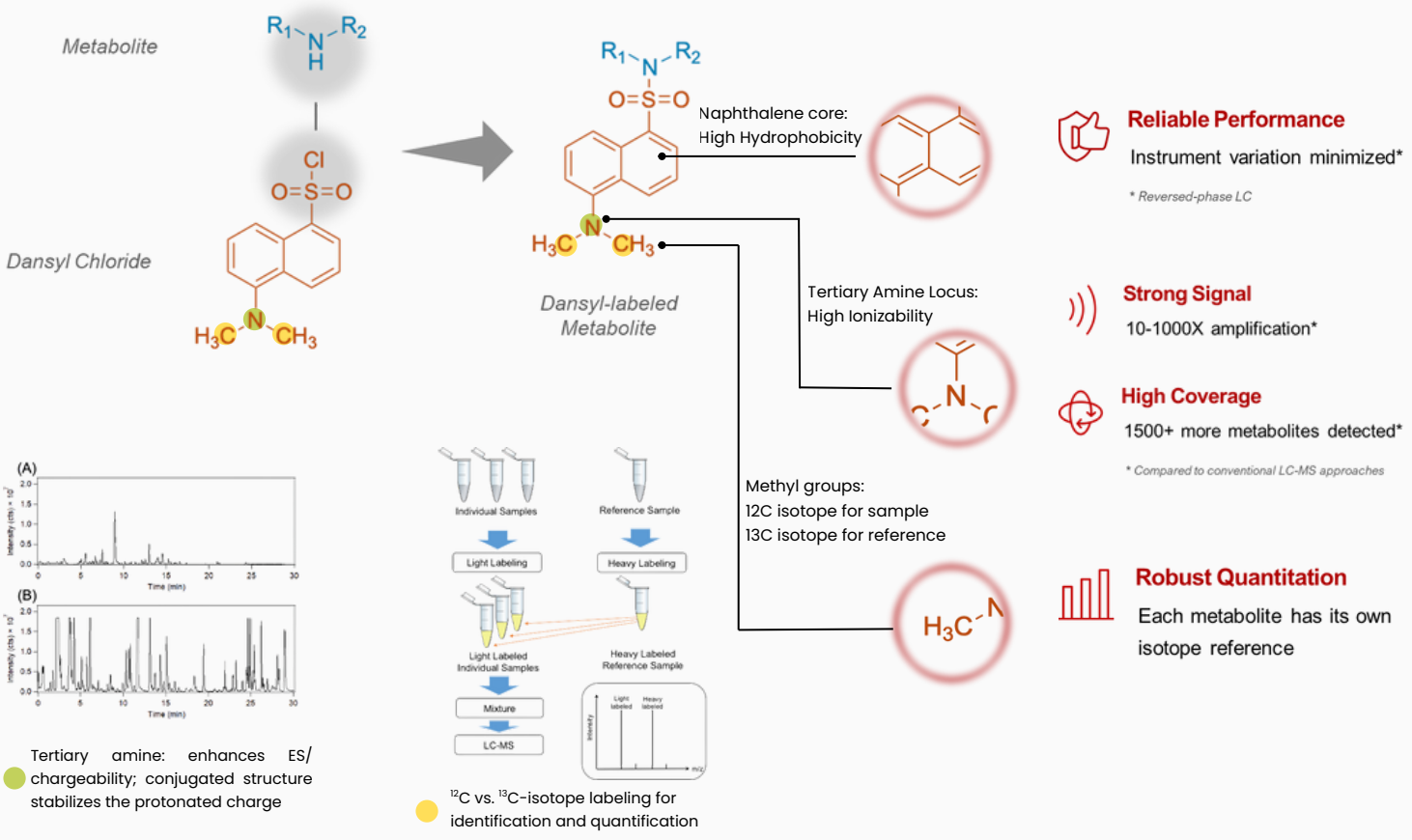
Empower your neuroscience research through advanced metabolomic profiling and biomarker discovery, enabling comprehensive analysis of biochemical pathways and metabolic alterations underlying neurological disorders.

Contact Our Team to Discuss Your Study

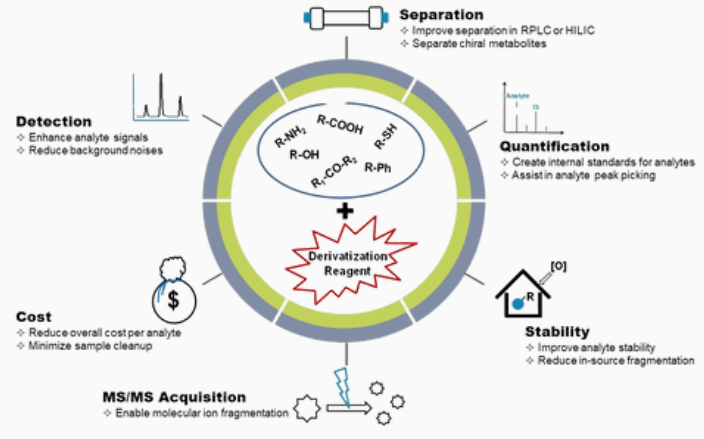
Chapter 1

Technology Used

The High-Performance Chemical Isotope Labeling (HP-CIL) LC–MS technique represents a major advancement in metabolomics, offering a precise and comprehensive solution for complex biological analyses. By leveraging chemical isotope labeling, HP-CIL LC–MS enhances both metabolite detection and quantification. Instead of classifying metabolites by physical properties alone, this method organizes them into four chemical groups (amine/phenol, carboxyl, carbonyl, and hydroxyl) thereby enabling the use of tailored labeling reagents that greatly improve separation and ionization efficiency. As a result, CIL LC–MS achieves far broader metabolome coverage than conventional LC–MS approaches.



A key innovation of CIL LC–MS is differential isotope labeling, in which one sample group is tagged with a heavy isotope and the comparative group with a light isotope. This allows simultaneous LC–MS analysis and generation of paired peaks for each metabolite, enabling highly accurate relative quantification with exceptional sensitivity and reproducibility.



Complementing this platform, IsoMS Pro our proprietary software—delivers advanced data processing and metabolite identification through access to extensive curated databases. Together, HP-CIL LC–MS and IsoMS Pro form a robust and high-throughput solution for metabolomics, empowering biological research and biomarker discovery with unmatched precision and coverage.

Chapter 1

Solution Offered

The high-resolution metabolic biomarker data, crucial for fueling the sophisticated machine learning models, was provided. Leveraging the **GLOBAL Metabolomics Platform,** a comprehensive and unbiased metabolic biomarker profiles were delivered from baseline blood samples of their PD patient cohort. This powerful, LC-MS based technique, enabling high-throughput profiling of thousands of metabolites simultaneously, allowed them to generate the in-depth, nuanced data required for their innovative machine learning approach. This empowered them to discover subtle yet significant differences between patient groups that traditional methods might missed.

Discovery Made

The study identified two distinct metabolite biomarker panels that powerfully differentiate PD patients progressing to dementia (PDID) from those remaining dementia-free (PDND). These panels, comprised of five up-regulated and three down-regulated metabolites, respectively, directly correlated with increased dementia risk. Critically, when integrated into their machine learning model, the metabolomics biomarker data – especially the up-regulated panel – emerged as the fourth most important predictor among 38 multi-modal risk factors, demonstrating significant power to predict PDD within three years. The platform's output, the specific metabolite biomarker panels, proved to be an exceptionally strong component of their multi-modal predictive framework, enabling the machine learning algorithms to discriminate between PDID and PDND with high accuracy (AUC = 0.85) years prior to diagnosis. Far more than just data, these metabolomics biomarkers, combined with machine learning and explainable AI methods, translate complex biochemical information into actionable, interpretable disease insights on risk direction and magnitude.

Adding Value

The GLOBAL Metabolomics Platform transformed this research by providing a critical, high impact data stream that significantly enhanced the predictive power of the machine learning models for early dementia risk in PD patients. Its output, the specific metabolite biomarker panels, proved to be an exceptionally strong component of the multimodal predictive framework. This enabled the machine learning algorithms, combined with explainable AI methods like Tree SHAP, to translate complex biochemical information into actionable, interpretable disease insights regarding the direction and magnitude of risk. This crucial advancement moves them closer to developing targeted interventions and ultimately improving patient outcomes and quality of life.

Reference

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Chapter 2

UNRAVELING METABOLIC DYSREGULATION IN AMYOTROPHIC LATERAL SCLEROSIS

Chapter 2

Unraveling Metabolic Dysregulation in Amyotrophic Lateral Sclerosis

Amyotrophic lateral sclerosis (ALS) is a fatal neurodegenerative disorder characterized by the progressive loss of motor neurons, leading to muscle weakness, paralysis, and respiratory failure. Metabolic dysfunction has emerged as a key feature of ALS pathology, implicating disturbances in energy metabolism, lipid turnover, and amino acid pathways. To explore these biochemical disruptions, the **Focus Metabolomics Platform** was employed to deliver high-resolution metabolic profiling and precise quantification of key metabolites relevant to ALS progression.

Discover our FOCUS Metabolomics Platform

Reveals precise biochemical insight through FOCUS Metabolomics, enabling absolute quantification of metabolites across targeted pathways implicated in neurological disorders. This approach delivers accuracy, reproducibility, and interpretability ideal for validating biomarkers and translating discoveries.

Contact Our Team to Discuss Your Study

The Challenge

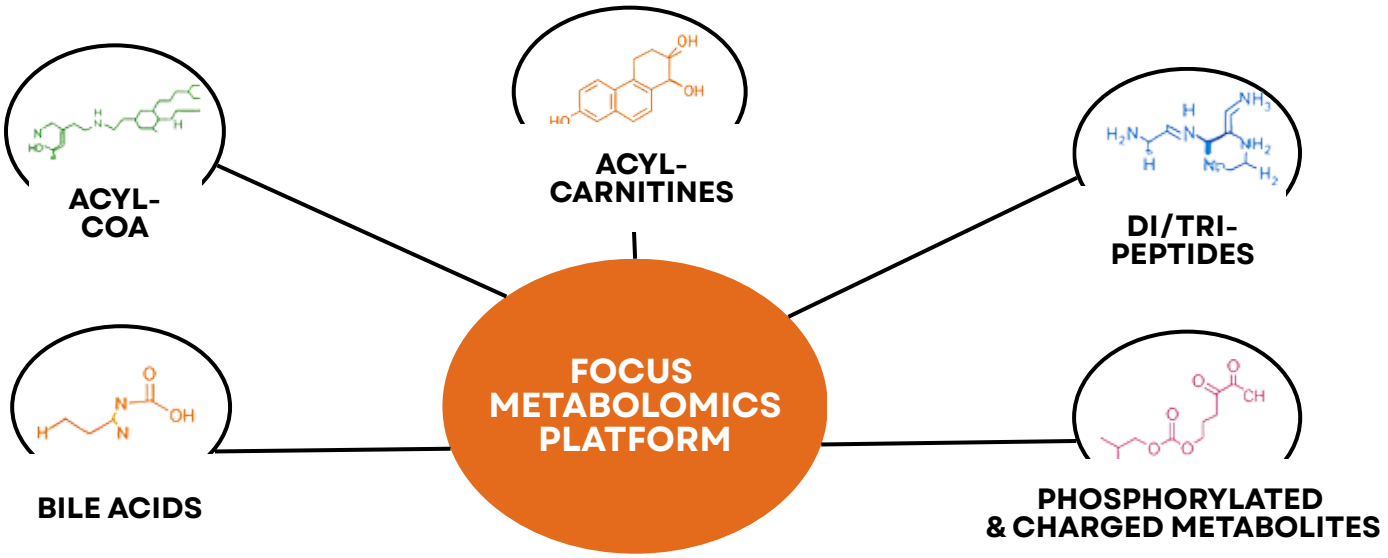
ALS presents a major challenge due to its multifactorial nature and rapid disease progression. Despite decades of research, the molecular mechanisms linking motor neuron degeneration to metabolic imbalance remain poorly understood. Traditional biochemical methods lack the sensitivity and coverage to capture the subtle yet widespread alterations occurring across metabolic networks in ALS. This limitation hinders the identification of reliable biomarkers for early diagnosis, disease monitoring, and therapeutic evaluation. Our **FOCUS Metabolomics Platform** provides an unparalleled opportunity to deeply investigate these crucial neurometabolic changes. By offering precise, unbiased, quantitative metabolomic profiling, we enable researchers to unravel these complex metabolic networks, gain critical insights into ALS mechanisms and ultimately identify actionable therapeutic targets.

Chapter 2

Technology Used

The FOCUS Metabolomics Platform features five targeted LC–MS assays for high-precision detection and quantification of biologically significant metabolites - acyl-carnitines, acyl-CoAs, di/tri-peptides, bile acids, and ionic (phosphorylated & charged metabolites) ones, with optional absolute quantification of selected compounds. These molecules play central roles in neurobiology and physiology, yet remain analytically challenging due to extreme polarity, structural diversity, and low ionization efficiency under conventional analytical approaches.

Assay	ID NO	Internal Standards
Bile Acid	79	Taurodeoxycholic acid, Taurolithocholic acid, Taurocholic acid, Glycolithocholic acid, Glycoursodeoxycholic acid, Taurochenodeoxycholic acid, Cholic acid-3-sulfate,Taurocholic acid-3-sulfate, Glycodeoxycholic acid, β-muricholic acid
Ionic Metabolite	85	D-(+)-Trehalose, D-Glucose 6-Phosphate, D-Sorbitol, DL-Phenyl-5-alanine, L-Lysine
Acyl-Carnitine	24	C18:0 L-carnitine, L-Carnitine, C4:0 L-carnitine, L-Carnitine
Acyl-CoA	27	Acetyl-CoA, Butyryl-CoA, Octanoyl-CoA, Palmitoyl-CoA
Di-/Tripeptide	1,300	Carnosine, Anserine, Glycyl-Glycine , Valyl-Proline, etc



- Acyl-carnitines transport fatty acids into mitochondria for β-oxidation, sustaining neuronal energy and membrane function.
- Acyl-CoAs are activated fatty acids essential for lipid metabolism and signaling; their dysregulation links to neuro-metabolic disorders.
- Di/tri-peptides act as neuromodulators and amino acid reservoirs but are difficult to detect due to low abundance and diversity.
- Bile acids regulate brain-gut signaling and neuroinflammation, though their numerous isomers complicate identification.
- Phosphorylated & charged metabolites drive energy transfer and signal regulation, yet high polarity and multiple charge states hinder detection.

Chapter 2

Solution Offered

To navigate the complex neurometabolic changes in ALS, this study leveraged our **FOCUS Metabolomics Platform**, powered by advanced LC-MS/MS technology, enabling them to conduct unbiased quantitative metabolomic profiling on cortical tissue from hFUSR521G mice and post-mortem spinal cord tissue from ALS-FUS cases. The precision of our targeted LC-MS/MS analysis allowed them to accurately measure the effect of arimoclomol on acylcarnitine levels in treated mouse cortices. This comprehensive approach facilitated a detailed analysis of various metabolite classes, with a particular focus on crucial lipid-related species, which were key to their hypothesis. With rigorous compound identification through accurate mass, retention time, and MS/MS spectra, alongside relative quantification normalized to internal standards, our client gained a robust and comprehensive understanding of the metabolic landscape within their ALS models.

Discovery Made

Pronounced metabolic alterations were revealed in ALS patients and disease models compared to healthy controls. Significant disruptions in **amino acid metabolism** — including glutamate, arginine, and branched-chain amino acids, which suggested excitotoxicity and impaired nitrogen balance. **Lipid metabolism** was also markedly affected, with dysregulation of phospholipids and acylcarnitines indicating mitochondrial energy defects.

In cortical tissue from **hFUSR521G mice**, elevated levels of **acylcarnitine species** were identified, including carnitine (C0:0), short-chain (C2:0–C4:0), and long-chain (C14:0–C18:2) forms. This is consistent with mitochondrial β-oxidation dysfunction. Treatment with **arimoclomol** reduced several acylcarnitine species in both mutant and control mice, demonstrating its potential to restore lipid composition and improve mitochondrial efficiency. Together, these findings highlight **mitochondrial and lipid metabolic dysregulation** as key biochemical features of ALS and underscore the role of **Focus Metabolomics Platform** in elucidating disease mechanisms and therapeutic effects.

Adding Value

The **Focus Metabolomics Platform** transformed complex metabolic data into actionable biological insights, enabling a deeper understanding of ALS pathology. Its high quantitative accuracy and reproducibility provided confidence for biomarker validation and therapeutic monitoring. By uncovering pathway-specific disturbances in energy, lipid, and amino acid metabolism, this approach bridged discovery and translational research - offering researchers and clinicians a reliable tool for biomarker discovery, patient stratification, treatment evaluation, and empowering the ALS research community to move closer to identifying measurable biomarkers and understanding the metabolic foundation of neurodegeneration.

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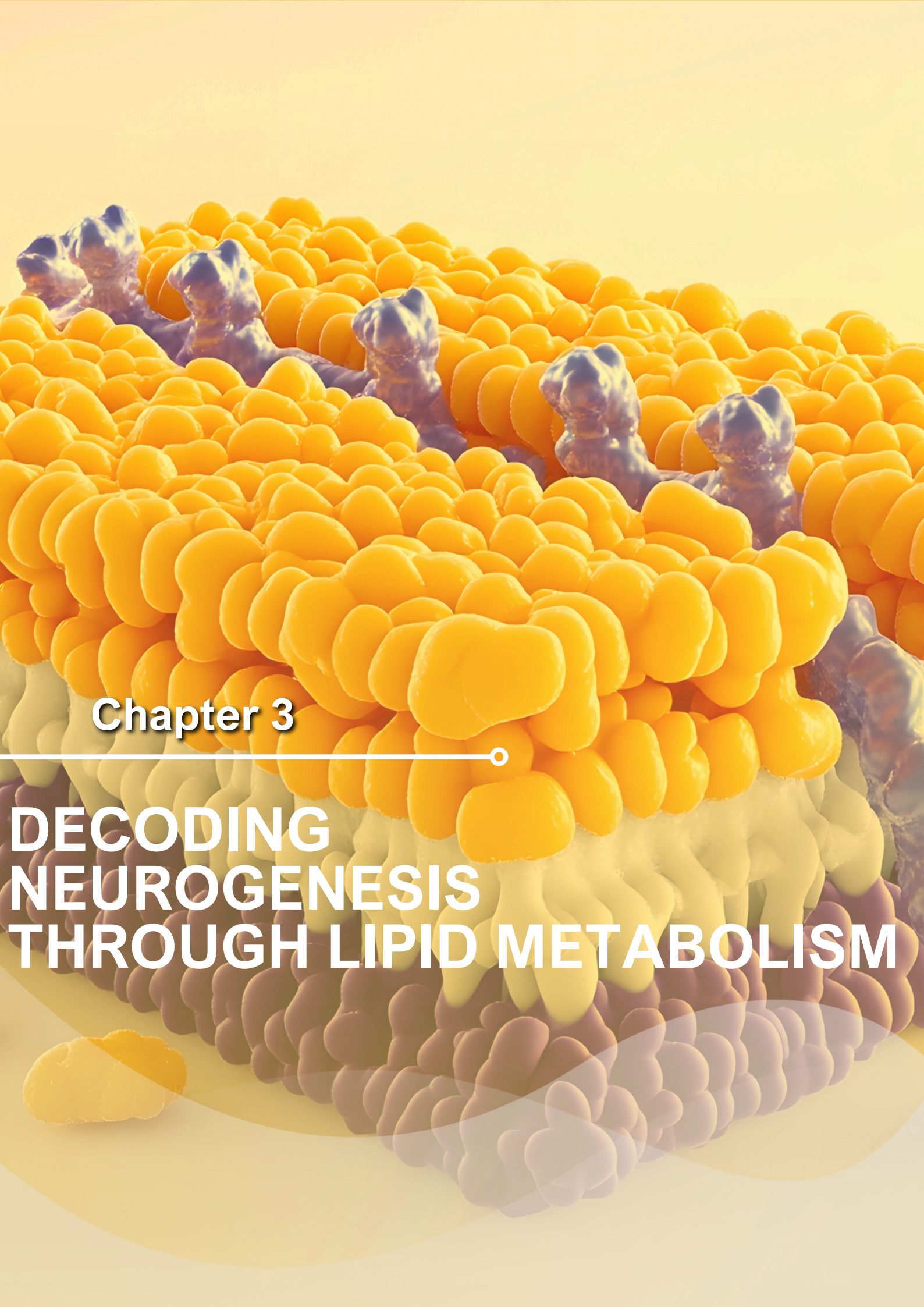


Chapter 3

DECODING NEUROGENESIS THROUGH LIPID METABOLISM

Chapter 3

Decoding Neurogenesis through Lipid Metabolism

Neurogenesis in the adult brain's subventricular zone (SVZ) relies heavily on coordinated metabolic regulation, particularly lipid synthesis. In this collaborative study led by researchers at **Johns Hopkins University**, lipidomic profiling powered by **GLOBAL Lipidomics Platform** revealed how serine racemase (SR) - an enzyme converting L-serine to D-serine - plays a central role, in maintaining lipid homeostasis essential for neural stem cell proliferation and differentiation. By integrating lipidomic data with molecular and genetic analyses, the study established a direct connection between serine metabolism, fatty acid synthesis, and neurogenesis in the adult brain.

The Challenge

Adult neurogenesis is a metabolically demanding process, requiring precise coordination of amino acid and lipid metabolism. Although serine metabolism has been studied in the context of neurotransmission, its influence on lipid biosynthesis and neural stem cell function was not well understood. The loss of serine racemase disrupted this metabolic balance, leading to reduced fatty acid synthesis and impaired neuronal formation in the SVZ. Deciphering these lipid alterations demanded an advanced analytical approach, capable of resolving subtle yet biologically significant lipidomic changes in complex brain tissue.

Discover our GLOBAL Lipidomics Platform

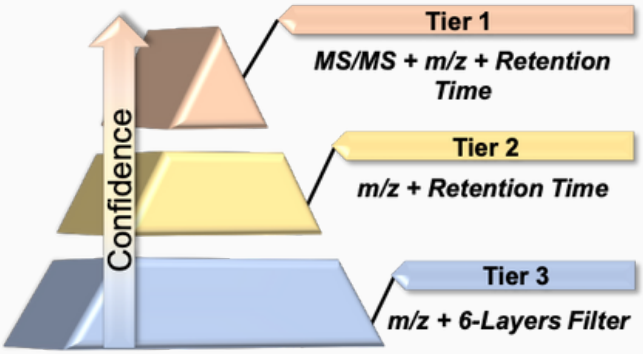
Explore the complex landscape of lipid metabolism to uncover new perspectives on neuroinflammation, membrane integrity, and signaling dysregulation. Our GLOBAL Lipidomics Platform delivers comprehensive, quantitative lipid analysis to support breakthrough discoveries in neurological research.

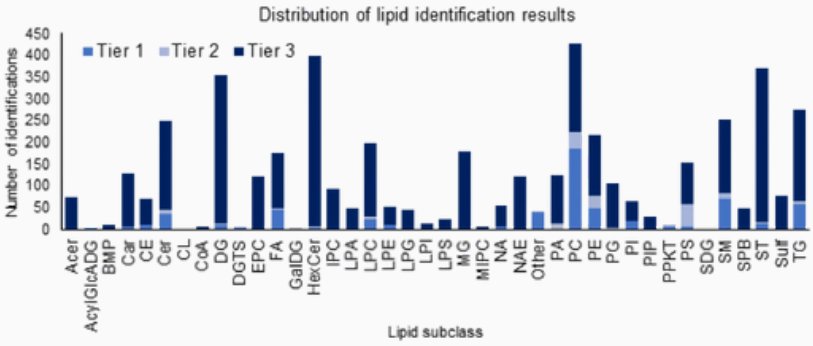
Contact Our Team to Discuss Your Study

Chapter 3

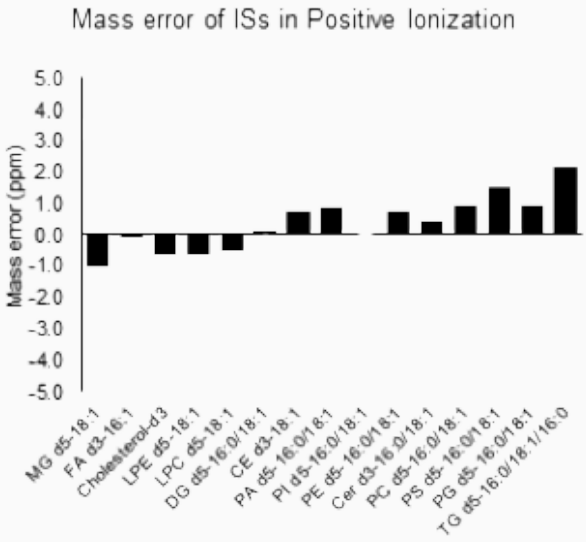
Technology Used

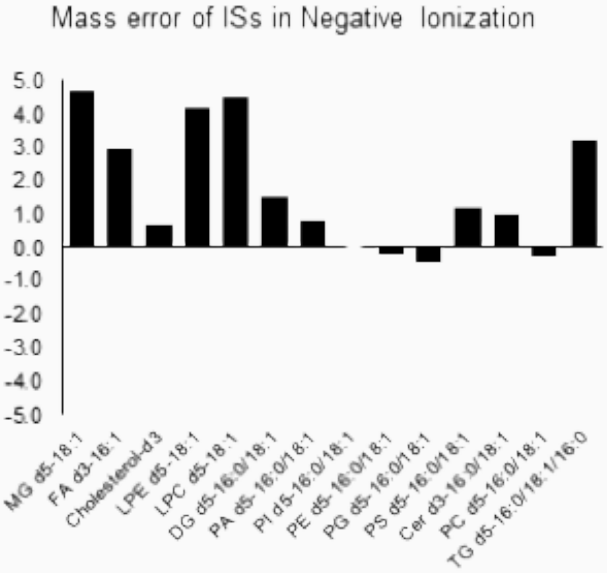
The GLOBAL Lipidomics Platform employs advanced LC-MS/MS technology to deliver exceptional sensitivity and specificity for profiling complex lipid mixtures. Through liquid chromatography, lipids are separated by polarity and molecular weight, ensuring clear resolution of individual species. The separated lipids are then ionized in both positive and negative electrospray modes (ESI) and analyzed by tandem mass spectrometry, which fragments the molecules to reveal detailed structural information such as head-group composition, acyl-chain length, and degree of unsaturation.

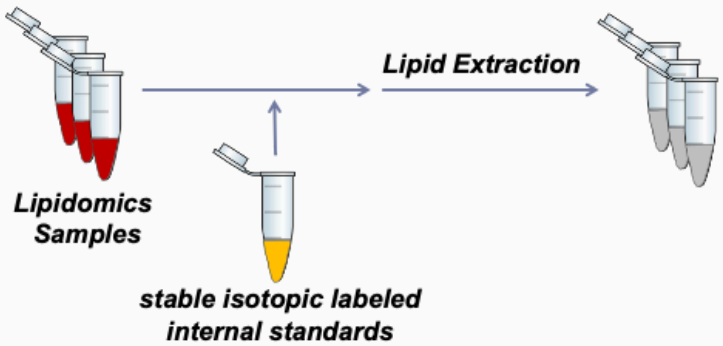




Complemented by Lipid Screener, our proprietary software, the platform combines powerful data processing with access to curated lipid databases for three-tiered identification. Its optimized workflow minimizes sample loss, enhances coverage, and maintains quantitative precision using stable isotope–labeled internal standards (SIL-IS). Rigorous lipid class-matched normalization and quality control protocols ensure reproducibility, defining a robust and reliable system for high-precision lipidomics.







Chapter 3

Solution Offered

Leveraging the **GLOBAL Lipidomics Platform**, a comprehensive lipidomic analysis was performed using **high-resolution LC–MS**. This platform provided quantitative coverage across major lipid subclasses - including phospholipids, sphingolipids, acylglycerols, and acyl-carnitines, while offering exceptional accuracy and reproducibility in the simultaneous profiling of up to **5,000 lipid species**. The resulting lipidomic data delivered a systems-level view of metabolic shifts in SR-deficient brain tissue, revealing the molecular mechanisms underlying disrupted fatty acid synthesis and impaired neurogenesis.

Discovery Made

Lipidomic analysis revealed extensive remodeling of lipid metabolism in SR-deficient mice. More than 300 lipid species were significantly altered across multiple classes. Marked reductions in sphingomyelins, phosphatidylcholines, and ceramides. Key components of neuronal membranes and signaling pathways were observed, alongside upregulation of phosphatidic and lysophosphatidic acids. These results pointed to suppressed de novo fatty acid synthesis, as evidenced by reduced malonyl-CoA and FASN expression, and altered ACC regulation independent of AMPK signaling. Importantly, supplementation with L- and D-serine restored malonyl-CoA levels and rescued neurogenesis, confirming the metabolic link between serine availability and lipid synthesis in the brain.

Adding Value

Through the lipidomic analysis performed with the **GLOBAL Lipidomics Platform**, researchers at **Johns Hopkins University** gained critical biochemical insights into how amino acid metabolism governs neurogenesis via lipid regulation. The approach provided high-sensitivity quantification and broad lipid coverage, transforming complex datasets into clear biological interpretations. Beyond identifying lipid biomarkers of impaired neurogenesis, this work demonstrated that restoring serine-dependent lipid metabolism can rescue neural development, and reinforcing the power of precision Lipidomics in advancing neurodevelopmental and neurodegenerative research.

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NEUROTRANSMITTERS COMPOUND LIST

Nova Medical Testing's Neuroscience solution offers five targeted pathway panels—Dopaminergic, Serotonergic, Cholinergic, Glutamatergic, and GABAergic—capturing over 1,660 metabolites and lipids central to brain signaling and health. These pathways are among the most biologically significant in neuroscience, underpinning cognition, neurotransmission, and neuroinflammation.

PANEL	COMPOUND LIST
Dopaminergic (350+ compounds)	Dopamine Dopamine 3-O-sulfate Phenethylamine Tyramine Tyramine O-sulfate Tyramine O-glucuronide N-Methyltyramine p-Octopamine 3-Methoxytyramine Adrenaline Noradrenaline Cholesterol 3-Iodothyronamine 3,4-Dihydroxyphenylethanol (DOPET) 3,4-dihydroxyphenylalanine (DOPA) 3,4-Dihydroxyphenylacetaldehyde (DOPAL) 3,4-Dihydroxyphenylacetic acid (DOPAC) 3-Methoxytyramine (3-MT) Homovanillic Acid (HVA) Tetrahydrobiopterin (BH4) Pyridoxal-5-phosphate (PLP) Anandamide (AEA) Tyrosine Metabolism (47 metabolites) Phosphatidylserine (PS) (72 lipids) Fatty Acids (67 lipids) Di-/Tripeptides (100+ peptides)
Cholinergic (380+ compounds)	Choline Acetyl-CoA Acetylcholine (ACh) Acetic acid Phosphatidylcholine (PC) (222 lipids) lysophosphatidylcholine (LPC) (53 lipids) Di-/Tripeptides (100+ peptides) Phosphorylated & charged metabolites

PANEL	COMPOUND LIST
Serotonergic (600+ compounds)	Serotonin (5-HT) 5-Hydroxyindoleacetaldehyde (5-HIAL) 5-Hydroxyindoleacetic Acid (5-HIAA) Melatonin (N-acetyl-5-methoxytryptamine) Sphingosine-1-phosphate (S1P) Ceramide Tryptamine Histamine Prostaglandin (PGA 2 , PGB 2 , PGC 2 , PGD 2 , PGE 2 , PGG 2 , PGH 2 , PGI 2 , PGJ 2) Tryptophan Metabolism (66 metabolites) Phosphatidylethanolamine (PE) (164 lipids) Ceramide Phosphoethanolamine (PE-CER) (53 lipids) Sphingomyelin (205 lipids) Di-/Tripeptides (100+ peptides) Phosphorylated & Charged Metabolites
Glutamatergic (120+ compounds)	Glutamic & Aspartic Acid Metabolism (15 metabolites) Glutamine Glutathione α-Ketoglutarate (α-KG) 24S-hydroxycholesterol (24-OHC) Phosphatidylinositol-3,4,5-trisphosphate (PIP 3) Di-/Tripeptides (100+ peptides) Phosphorylated & Charged Metabolites
GABAergic (110+ compounds)	Gamma-Aminobutyric acid (GABA) Succinic Semialdehyde (SSA) Succinic acid (SA) γ-Hydroxybutyric Acid (GHB) Hypotaurine Allopregnanolone Pregnanolone Pregnanolone 3-O-sulfate Pregnanolone 3-O-glucuronide Di-/Tripeptides (100+ peptides) Phosphorylated & Charged Metabolites

PANEL	TECHNOLOGY	ADD ON VALUE
Dopaminergic	1. HP-CIL Metabolomics (Elevated) 2. GLOBAL Lipidomics 3. FOCUS Metabolomics • Di-/Tripeptides • Ionic Metabolite Assay	Lipid Metabolism (2500+) Amino Acid Metabolism (400+) Energy Metabolism (40+) Nutrient Metabolism (20+)
Serotonergic		
Cholinergic		
Glutamatergic	1. HP-CIL Metabolomics (Comprehensive) 2. FOCUS Metabolomics • Di-/Tripeptides • Ionic Metabolite Assay	Steroid Metabolism (30+) Amino Acid Metabolism (550+) Energy Metabolism (70+) Nutrient Metabolism (40+)
GABAergic		

CORPORATE PROFILE

ABOUT US

Nova Medical Testing Inc. (NovaMT) is a Canada-based metabolomics company simplifying small-molecule analysis for health and research innovation. Founded in 2017 by Dr. Liang Li, Professor of Chemistry at the University of Alberta, NovaMT develops cutting-edge mass spectrometry-based solutions for diagnostic and biomedical applications.

Located in Edmonton Research Park, we specialize in high-quality, accessible metabolomic and lipidomic analysis that support researchers across healthcare, nutrition, life sciences, and disease research.

Our Partnership

We are excited to highlight the robust partnership between NovaMT and the TMIC Li Node. Our collaboration with TMIC is built on a foundation of mutual trust and seamless integration. Many of our services are closely integrated, ensuring that clients benefit from a cohesive and comprehensive approach to metabolomics. We are proud to work hand-in-hand with TMIC to deliver top-tier insights and solutions.

Our Vision

NovaMT is a world leader in large-scale small-molecule analysis and metabolome-based health risk detection for deeper insights and better outcomes. By combining advanced mass spectrometry with AI-driven omics analytics, we provide scalable solutions and services that empower academia, biopharma, and healthcare to generate transformative insights into health and disease.

Our Experience

40,000+	10+	120+	350+	500+
ANALYZED SAMPLES	LC-MS INSTRUMENTS	PAPERS PUBLISHED	SERVICE PROJECTS	CLIENTS

Nova
MEDICAL TESTING
Pioneers of Small Molecule Analysis

METABOLOMICS BEYOND LIMITS

From Insight To Impact

Contact Information

B108 2011 94 ST NW, T6N 1H1,
Edmonton, AB

+1 (780) 699-9688

support@novamt.com

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