

# ATS 2026 Highlights

## Respiratory Structure and Function Early Career Professionals



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### ***Get to know members of the RSF Assembly***

#### ***Is your research clinical, basic science or translational?***

Translational research with a strong clinical focus.

#### ***Tell us about your research?***

My research focuses on identifying metabolic pathways associated with clinical heterogeneity in COPD. Using serum metabolomics integrated with lung function and clinical outcomes, I aim to characterize distinct metabolic phenotypes. This approach seeks to improve risk stratification and support more personalized management strategies in COPD.

#### ***Where do you see yourself in 5 years?***

In five years, I see myself as a clinician-scientist continuing to develop my research career in chronic respiratory diseases, integrating translational research, clinical practice and education to improve respiratory health in my community.

#### ***What do you find is the major benefit of RSF Assembly Membership?***

The RSF Assembly provides an outstanding environment for scientific exchange, mentorship and collaboration, particularly in integrating structure, function and advanced methodologies into clinically meaningful respiratory research.



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If you or someone you know would like to be featured as an ATS RSF ECP please email Carolyn Wang ([carolyn.wang@hli.ubc.ca](mailto:carolyn.wang@hli.ubc.ca))

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### KEY METABOLICS

**Upregulated**  
Compensatory stress responses related to oxidative burden and energy imbalance in COPD.

**Downregulated**  
Systemic metabolic exhaustion, immune dysregulation, and energy disruption, hallmarks of COPD progression.

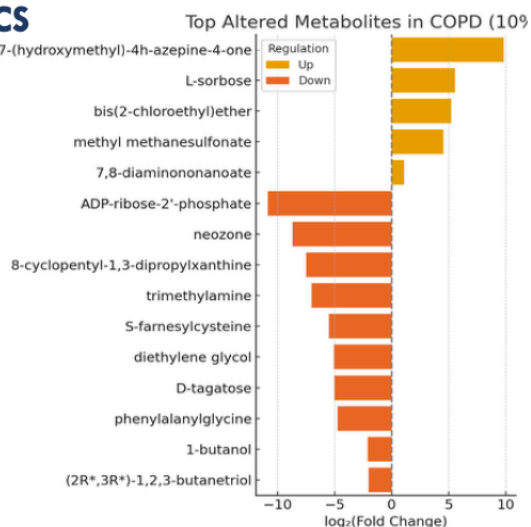


Figure 1: Differentially Expressed Metabolites in COPD vs. Healthy Controls  
Bar chart showing top upregulated (↑) and downregulated (↓) metabolites.  
Positive log<sub>2</sub>FC = higher in COPD; Negative = lower.

### Metabolomic Signatures of COPD: Insights from Comparative Analysis with Healthy Controls

**Objective:** To identify metabolites and metabolic pathways differentially regulated in patients with COPD compared with healthy individuals.

**Methods:** Multicenter cross-sectional study including COPD patients and healthy controls. Clinical, functional and serum samples were analyzed using mass spectrometry, with metabolomic processing and pathway analysis (FDR <10%).

**Results:** Twenty-six metabolic pathways were dysregulated in COPD. Key metabolites included L-sorbose, trimethylamine and an azepine derivative, suggesting activation of the pentose phosphate pathway, altered lipid oxidation, mitochondrial dysfunction and oxidative stress-related signaling.

**Conclusion:** COPD is associated with metabolic reprogramming linked to redox imbalance and energy metabolism. Novel metabolites identified may represent potential biomarkers and therapeutic targets.