ISTAART Immersives: Genome Engineering for High-Resolution Drug Target Mapping in Human Microglia

Saturday, July 11, 2026 | 1 p.m. - 5 p.m.
Cutty Sark — InterContinental — London, United Kingdom
All times are in British Summer Time
In-person attendance only

Overview

Genome engineering has moved beyond simple gene disruption and now enables high-resolution interrogation of protein structure, function, and therapeutic potential. This workshop introduces participants to next-generation CRISPR dense mutagenesis approaches for rational drug target mapping, with a particular focus on applying these strategies in human microglia and other advanced cellular models. Attendees will learn how to design and implement saturating mutational libraries, engineer precise domain-level perturbations, and uncover functional hotspots within disease-associated proteins and multi-protein complexes. Building on recent innovations in iPSC-derived microglial systems, the session demonstrates how genetically tractable human models can be used to generate high-content functional readouts that directly inform target selection and therapeutic prioritization. Participants will explore experimental design principles, editing modalities (Cas9, base editing, prime editing), scalable phenotyping strategies, and computational frameworks for mapping mutational fitness landscapes. Comparative examples from neuronal and glial lineages will highlight how these approaches generalize across CNS biology, while insights derived from clinical genome editing applications will provide a framework for evaluating precision, safety, and translational relevance. By the end of the workshop, attendees will have a practical understanding of how high-resolution CRISPR mutagenesis can be integrated into functional genomics pipelines to systematically dissect protein function, reveal druggable vulnerabilities, and accelerate target discovery in neuroimmune and neurodegenerative research contexts.

Organizing Committee

- Falak Sher
- Marta Olah, PhD

Target Audience

This ISTAART immersive workshop is designed for…

Learning Objectives

- Design and evaluate CRISPR dense mutagenesis strategies to interrogate protein function at amino-acid resolution, including approaches for tiling, domain mapping, and saturating mutational scanning.
- Apply next-generation genome engineering tools (Cas9, base editing, prime editing) to construct high-resolution mutational libraries tailored to disease-associated proteins and multi-protein complexes.
- Implement iPSC-derived microglia and associated human cellular models as functional genomics platforms for phenotypic screening, perturbation analysis, and mechanistic discovery.

Registration

Pre-conferences are offered for in-person attendance only. Preconferences require a separate registration fee in addition to AAIC full conference registration, or they may be purchased as stand-alone events. Visit alz.org/AAIC.

Agenda: Friday, July 11, 2026 | 1 p.m. - 5 p.m.

Time	Session Details	Speakers and Moderator
1:00 p.m. - 1:15 p.m.	Welcome, Introductions, and Goals	
1:15 p.m. - 1:45 p.m.	Mini-Lecture: - Foundations of High-Resolution CRISPR Mutagenesis Dense mutagenesis principles, library design strategies, editing modalities - Live annotation exercise using example protein domains	
1:45 p.m. - 2:15 p.m.	Demonstration - Designing Saturating Mutational Libraries Real-time walk-through using design tools	
2:15 p.m. - 2:30 p.m.	**Break**	

2:30 p.m. - 3:00 p.m.	Interactive Module - Applying Mutagenesis in Human Microglia Models iPSC-derived microglia workflow overview	
3:00 p.m. - 3:30 p.m.	Hands-On Analysis, Mapping Functional Hotspots - Walkthrough of example datasets	
3:30 p.m. - 4:00 p.m.	Case Studies & Translational Insights	