



Hypervelocity Sampling Across the Solar System: Retiring Risks for Enceladus, Europa, Titan and Venus - Task 1 Enceladus/Europa

Principal Investigator: Morgan Cable (322); Co-Investigators: Michael Malaska (322), Amy Hofmann (322), Robert Hodyss (322), Sarah Waller (353), Morgan Miller (389), James Lambert (389), Anton Belousov (389), Stojan Madzunkov (389), Nicholas Tallarida (389), Andres Jaramillo-Botero (California Institute of Technology), Robert Continetti (University of California, San Diego)

Program: FY21 R&TD Strategic Initiative

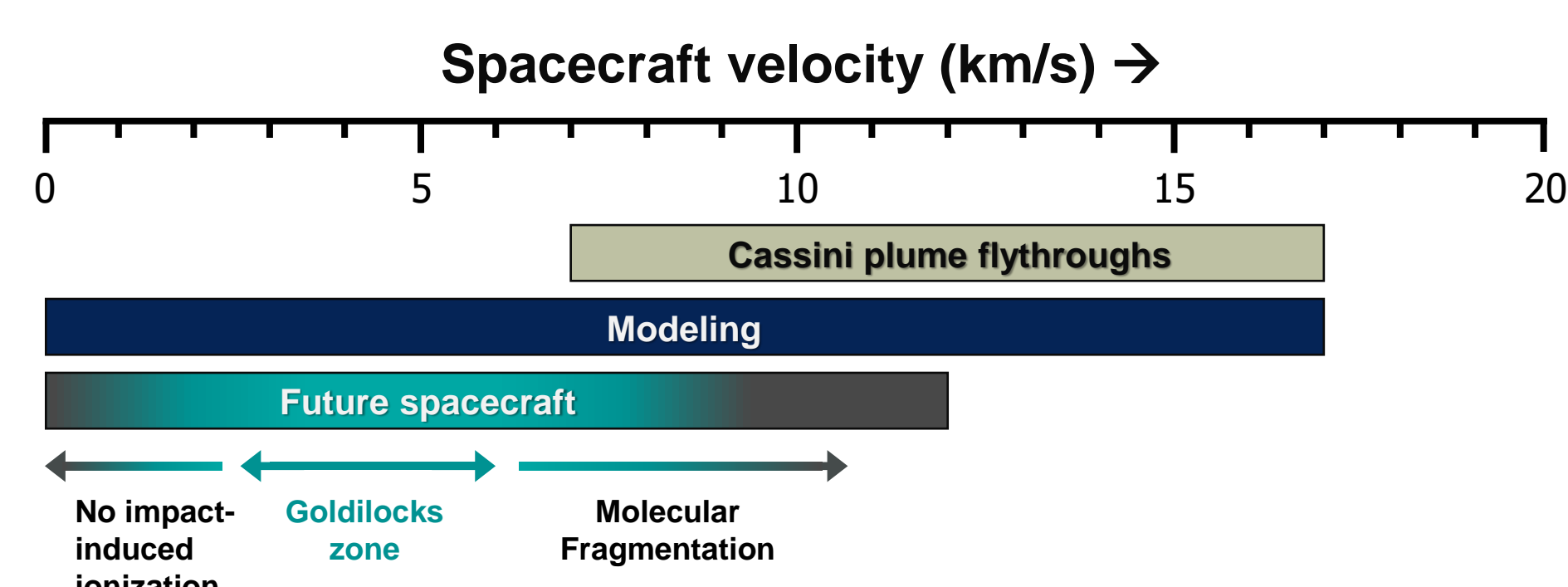
Strategic Focus Area: Hypervelocity Sampling Across Solar System

Objective

The objective of this Strategic RTD is to retire a major weakness received from the Enceladus Life Finder (ELF) New Frontiers 4 proposal, which concerned whether biosignature molecules such as amino acids and fatty acids remain intact following impact of plume ice grains at 5 km/s. Our approach included theoretical and experimental work to demonstrate that ice grains containing amino acids and fatty acids are either intact following impact or that the parent molecules can be effectively reconstructed from fragment analysis.

Significance

These results help us understand what happens when sampling a plume at hypervelocity. We have achieved >4 km/s with both experimental setups (HIGS and AIS) and have established that organic molecules do indeed survive impacts at these velocities. With modeling, we have fully bounded the velocity range (1-12 km/s) to identify fragmentation pathways and reconstruct mass spectra for organic molecules embedded in ice grains made of pure water-ice as well as containing salts.



These results will feed directly into the next JPL-led mission proposal for Enceladus in New Frontiers 5, which requires better scientific underpinning to justify the plume flythrough velocity and expected limit of detection for key organics (amino acids and fatty acids) at that velocity.

National Aeronautics and Space Administration

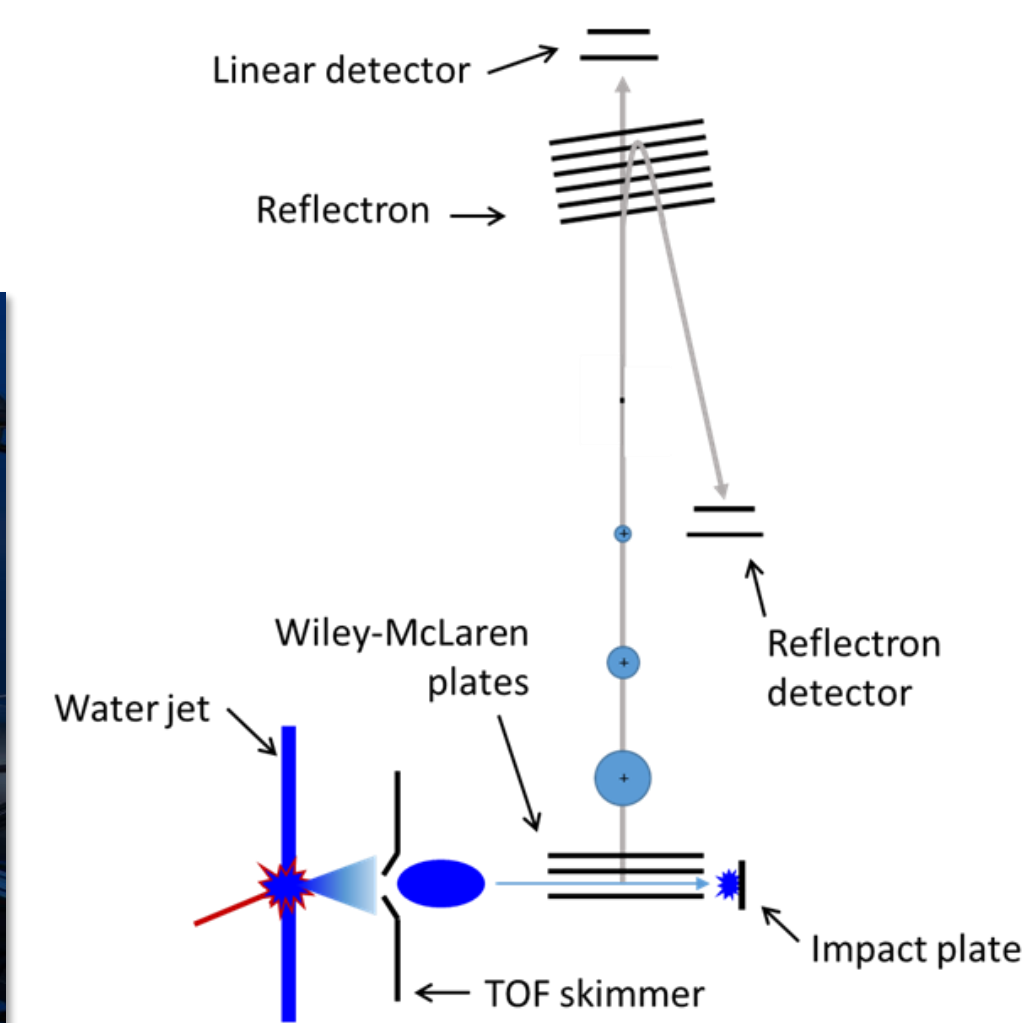
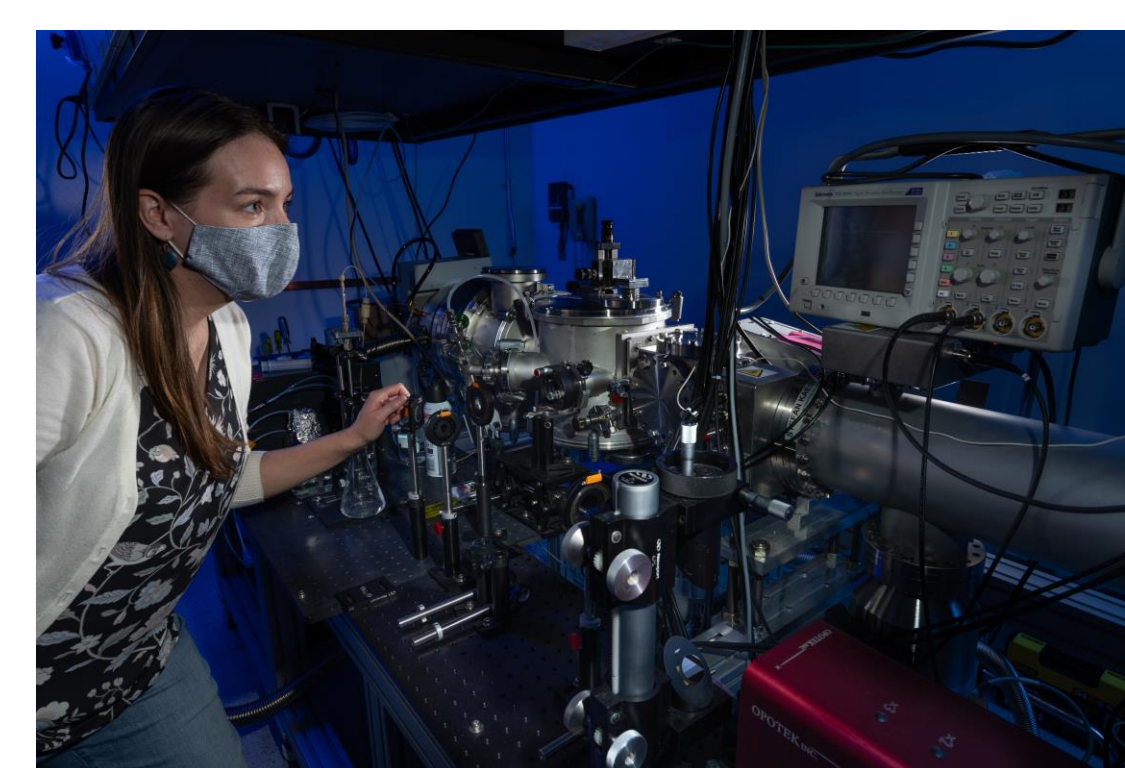
Jet Propulsion Laboratory
California Institute of Technology
Pasadena, California

www.nasa.gov

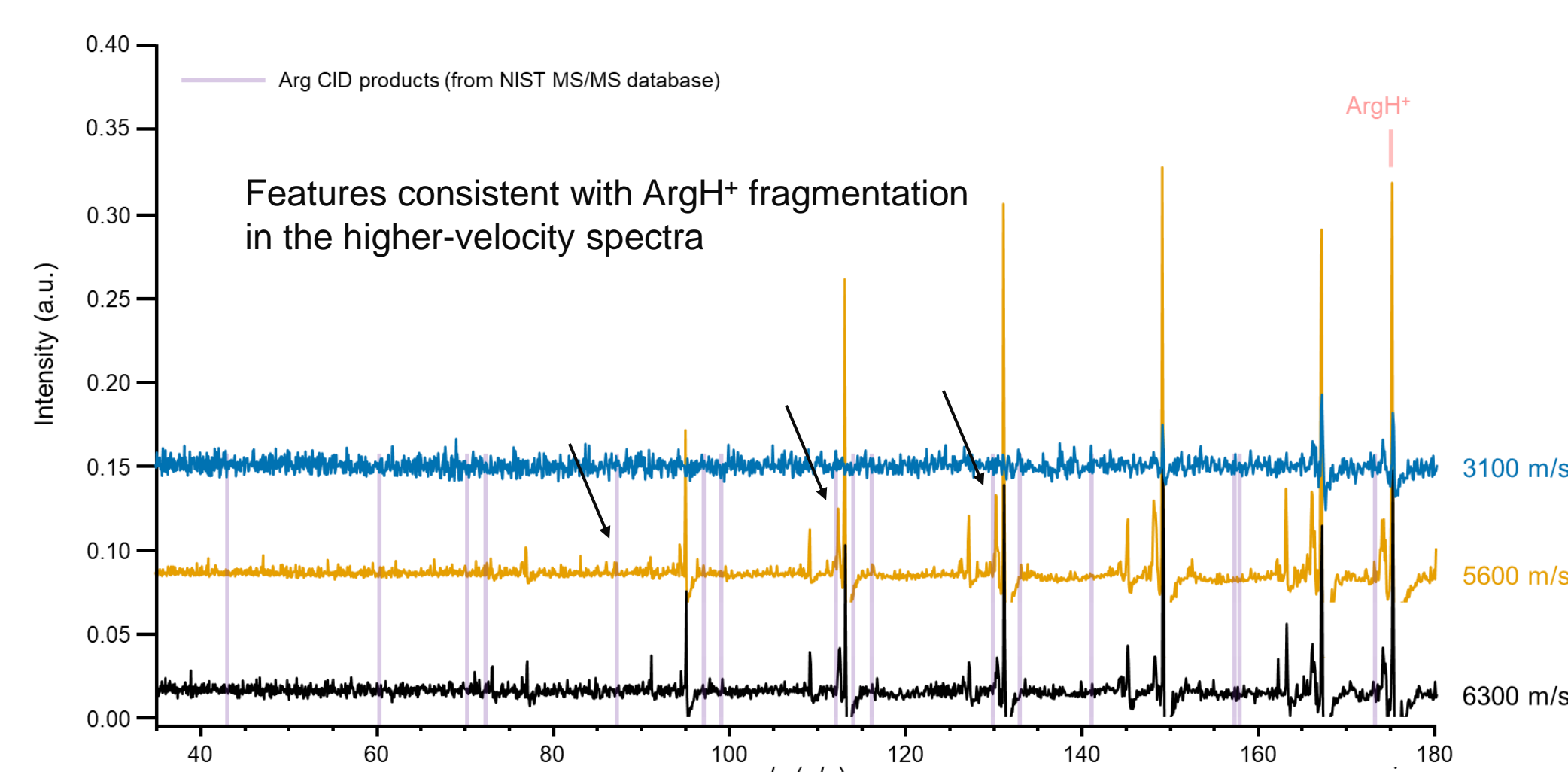


Hypervelocity Ice Grain System (HIGS)

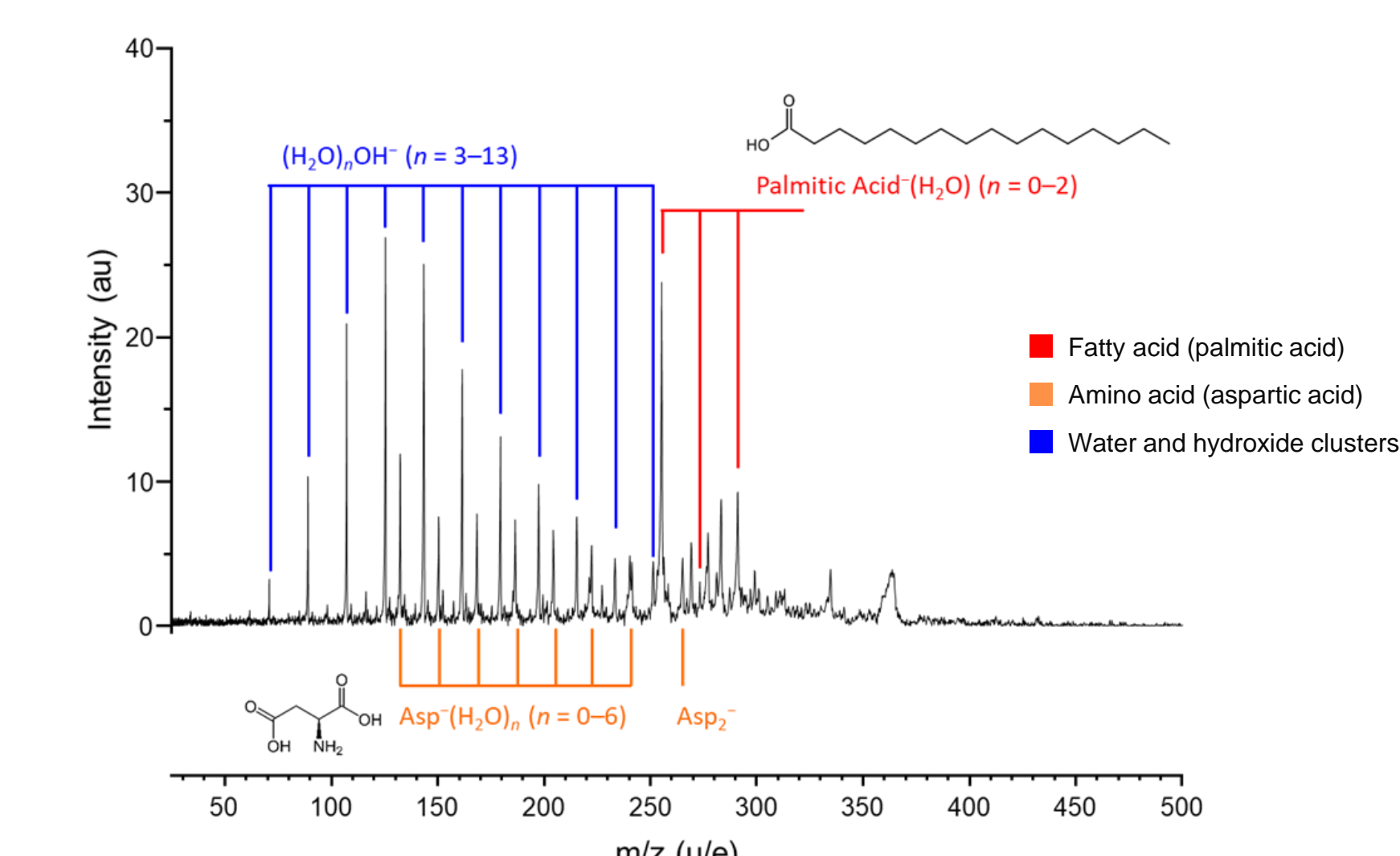
HIGS uses an infrared laser beam impacting a water jet (15 μm diameter) to create a distribution of charged molecules and clusters up to $\sim\mu\text{m}$ in size, traveling at speeds up to 6.3 km/s. Biomolecules and salts can be added to the water jet to reproduce plume particle composition. The advantage of this system is that it generates many ice grains of different sizes at once, which is likely to be more representative of the plume of Enceladus or Europa.



Left: Photo of HIGS with Co-I Waller (Credit: JPL Photolab). Right: Schematic of HIGS showing ice grain generation, impact, and analysis by MS.



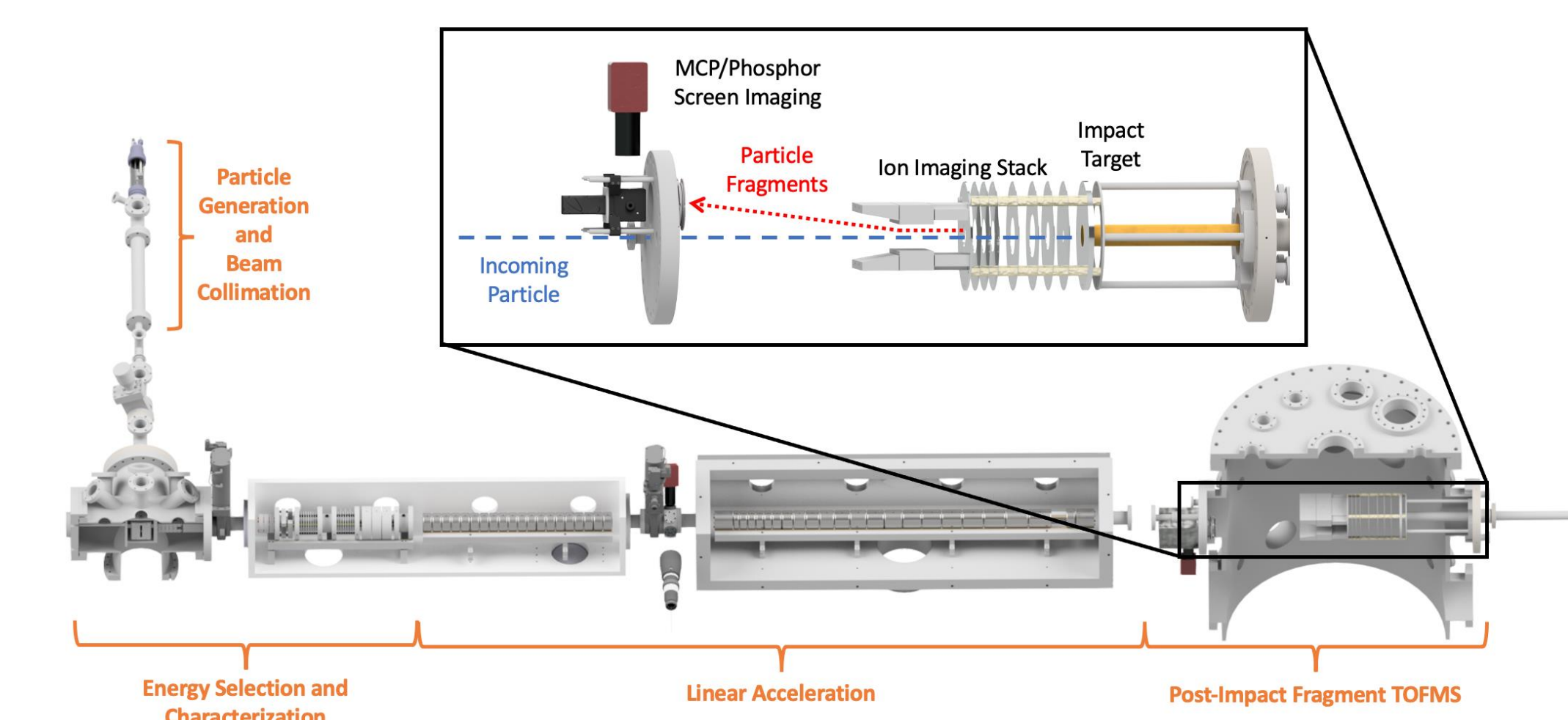
Above: Hypervelocity impacts of arginine (an amino acid) in water clusters up to $\sim\mu\text{m}$ in diameter indicate this biomolecule is still intact at 4.6 km/s (not shown), and starts to fragment at 5.6 km/s. Below: Analysis of mixtures of biomolecules (such as amino acids and fatty acids) enables deconvolution



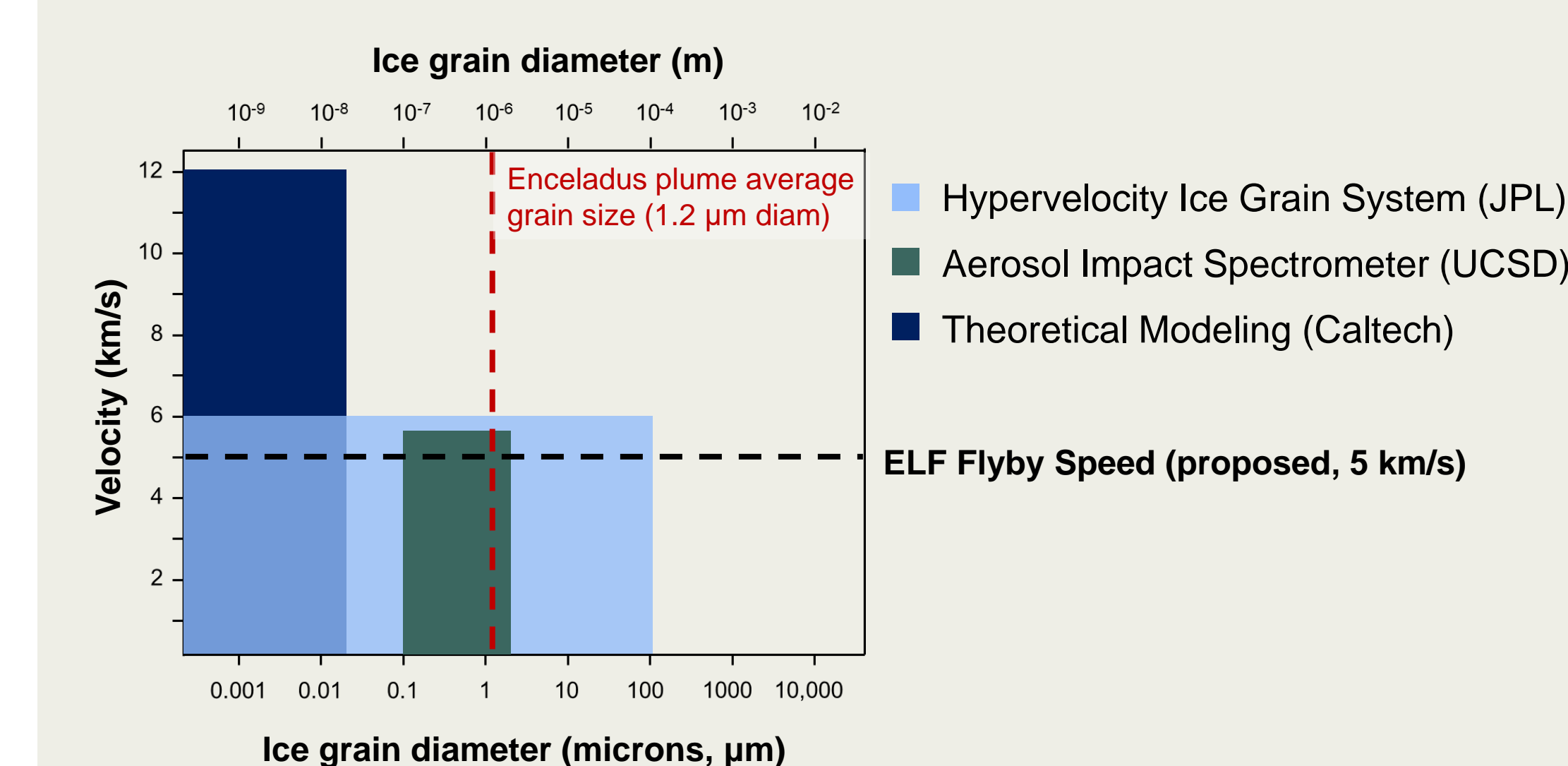
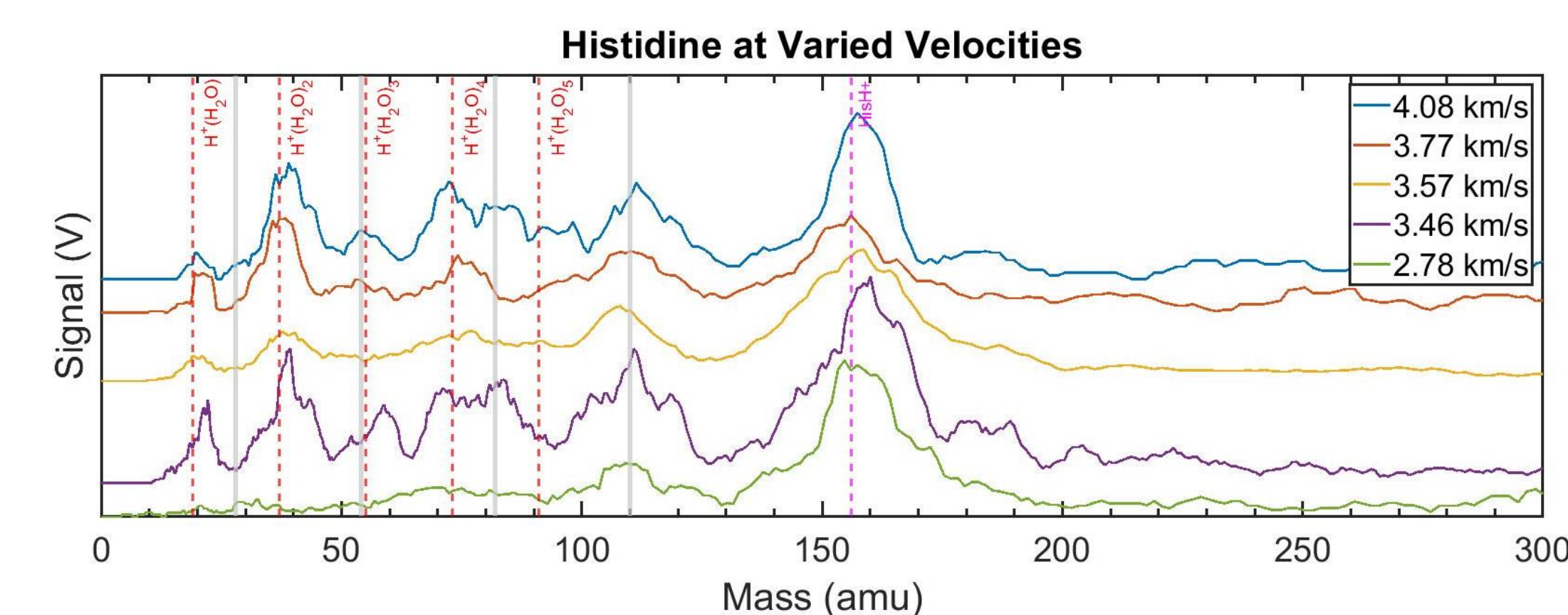
Approach and Results

Aerosol Impact Spectrometer (AIS)

AIS generates ice grains using electrospray ionization, and traps a single grain in an electrostatic trap. It characterizes the grain's size and charge, and then fires it at velocities up to 4.1 km/s. The advantage of this system is we can perform focused studies of how organic molecules (amino acids and fatty acids) trapped in ice grains fragment upon impact, as a function of ice grain size, charge and velocity.



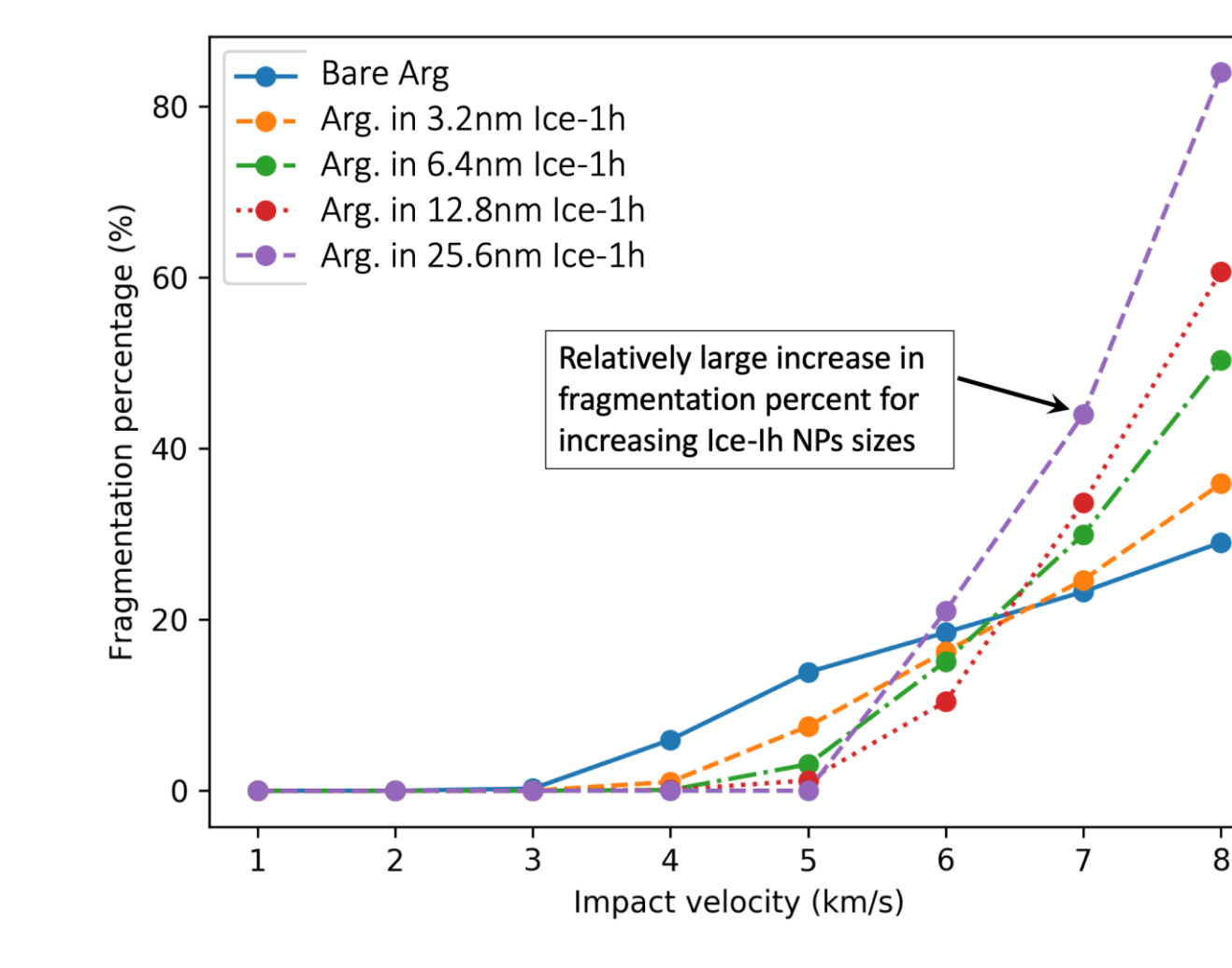
Above: Schematic of AIS and time-of-flight mass spectrometer (TOFMS) assembly. Below: Mass spectra for histidine at several impact velocities. This amino acid remains intact (as evidenced by the molecular ion being present) up to 4.1 km/s. Gray lines are literature (NIST) reported fragments of histidine, red dotted lines indicate the mass of the water cluster ion series, and the magenta dotted line marks the mass of the histidine molecular ion.



PI/Task Mgr Contact
Email: Morgan.L.Cable@jpl.nasa.gov

Theoretical Modeling

We use reactive molecular dynamics simulations to understand the effect of ice grain diameter and salt concentration in the fragmentation thresholds of biomolecules embedded in ice grains (6.4-25.6 nm in diameter), over the range of 3-10 km/s. In general, we find that larger diameter ice grains and lower salt concentrations lead to higher fragmentation velocity thresholds.



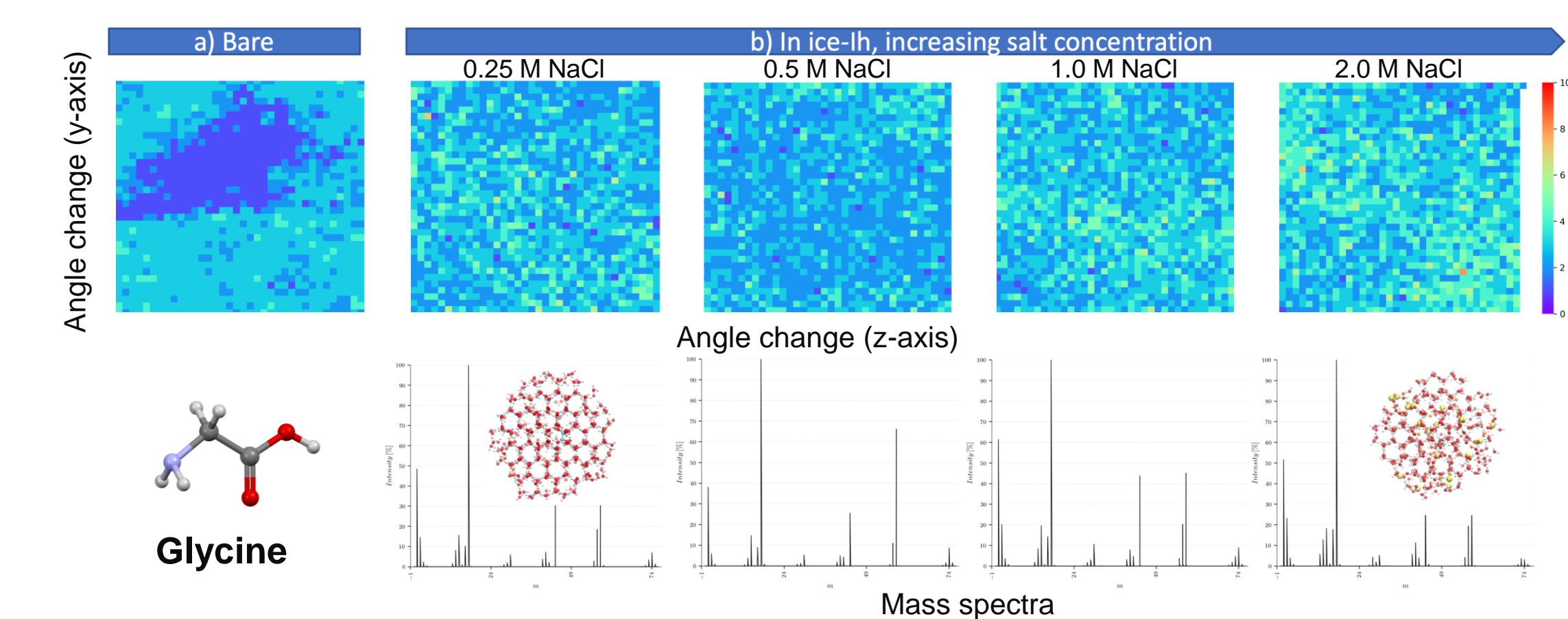
Amino acids

Molecule	v_f (km/s)
Alanine	4
Arginine	3
Aspartic acid	3
Citrulline	3
Glycine	3
Lysine	4
Ornithine	4
Serine	3
Threonine	3
Tyrosine	4

Fatty acids

Molecule	Lipid Number	v_f (km/s)
Palmitic acid	C16:0	3
Stearic acid	C18:0	4
Arachidic acid	C20:0	4
Cerotic acid	C26:0	3
Oleic acid	C18:1 cis-9	4

Velocity fragmentation threshold (v_f) is established from any single covalent dissociative event (of 1296 trajectories) induced by a collision trajectory lasting more than 3 ps.



By the Numbers – Accomplishments Over 3 Years

Fastest ice grain speed reached (HIGS)	6.3 km/s
Total impact trajectories simulated <i>in silico</i>	1,327,104
Max number of GPU cores run concurrently	458,752
New collaborations/partnerships	6
Peer-reviewed publications	7 (5 in prep)
Conference proceedings	18

Clearance Number: CL#21-4514
RPC/JPL Task Number: R19003