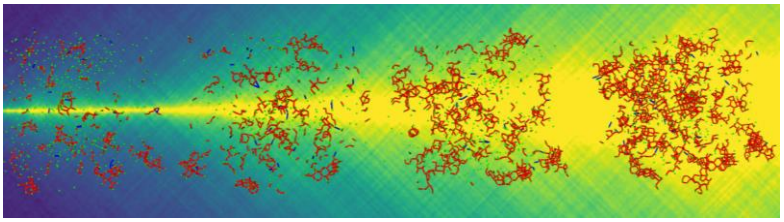
SCIENCE AT THE ADVANCED PHOTON SOURCE

AN EXCEPTIONALLY LONG EXPERIMENT REVEALS STRUCTURAL EVOLUTION IN A METALLIC GLASS

Metallic glasses (MGs) are alloys that possess an amorphous (disordered) structure instead of a crystalline lattice. This jumbled atomic arrangement often yields materials with exceptional properties, for instance very high yield strength and toughness. These exceptional features have led to the incorporation of MGs into advanced biomedical implants, superior sports equipment, energy-saving electrical devices, and many other applications.

Unfortunately, the disordered structure of MGs inevitably leads to their atoms migrating over time, which can seriously degrade their superior properties. For years scientists have investigated the complex structural rearrangements that occur within metallic glasses, but important details of this dynamic process remain obscure. In this study, researchers measured atomic-level movements in a metallic glass over the unprecedented time span of nearly 3½ days, using X-ray photon correlation spectroscopy (XPCS) performed at beamline 8-ID-E of the Advanced Photon Source. Their work appeared in the journal *Nature Communications*.

The extremely high-resolution XPCS measurements, recorded continuously over the entire experiment, provide new information about MG aging. For instance, the experiment revealed long stretches of robust structural changes punctuated by periods of minimal internal movements. This study demonstrates the feasibility of long-duration XPCS observations of metallic glasses, while also providing important new insights into their long-term internal dynamics.



B. Riechers, et. Al., "Intermittent cluster dynamics and temporal fractional diffusion in a bulk metallic glass," *Nat Commun* **15** 6595 (2024)

A computer simulation depicts the formation and migration of atomic clusters over time within the metallic glass. Clusters of atoms appear as tiny colored segments. This and similar simulations helped clarify and extend the experimental X-ray results. The illustration's background, transitioning from blue to yellow, depicts the emergence of longer decorrelation (reorganization) timescales. From left to right, the density of atomic clusters is seen to increase with time, while the pace of structural changes decreases.

The experimental results revealed a decidedly complex interplay of alternating structural changes. The results from this long-duration experiment considerably expands knowledge of how metallic glasses evolve over time. Ultimately these new insights will help materials scientists develop more stable and higher-performing MGs, which is increasingly important as the demand for these exceptional materials steadily grows.

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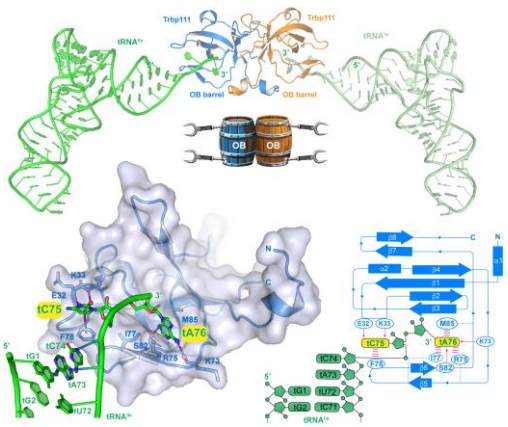
GRABBING A tRNA BY THE TAIL



A.U. Juru[1], et. Al. "Structural basis of tRNA recognition by the widespread OB fold," *Nat Commun* **15** 6385 (2,024)

The figure shows how the OB beta barrel uses its two protruding loops as "pincers" to capture the terminal CA dinucleotide of the tRNA in various representations

Transfer RNAs (tRNAs) are RNA molecules used by all forms of life, from bacteria to plants to humans, to transfer amino acids to growing protein molecules that have been coded by DNA and transcribed into messenger RNA (mRNA) for translation by ribosomes into proteins. This is one of the most basic, crucial processes of life.

However, tRNAs do more than just perform this essential function and are known to have regulatory roles in translation, transcription, stress response, and even immunity, via specific interactions with a wide array of cellular molecules. Disruption of these interactions has also been shown to be associated with some types of neurological disease and cancer, making it critical to understand how proteins in the cell recognize tRNAs.

Recent research from a team at the National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK) has provided new, previously unrecognized, insights into how a particular protein called the OB-fold recognizes the 3' tail of tRNA molecules and how these interactions impact the function of tRNAs. The research team used X-ray diffraction data collected at the South East Regional Collaborative Access Team (SER-CAT) beamline 22-ID of the Advanced Photon Source.

Data confirmed that the interactions are entirely mediated by the tail. Addition of more nucleotides or phosphate groups to the tail also abolished or diminished binding, showing that Trbp111 precisely recognizes the 3' terminus of mature tRNAs. These data provide valuable insights into how TRBD proteins interact with tRNAs to perform their essential functions. This new research provides important information for understanding basic cellular processes and for designing treatments.

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