Breaking the CRAM Behavior: AI-Generated Molecules Unlock Hidden Enzymatic Pathways in Marine Carbon Cycling

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Carboxyl Rich Aliphatic Matter (CRAM) governs marine carbon sequestration yet remains enzymatically elusive. We revolutionize CRAM understanding using Diffusion-Based Latent Property Generative Models to generate novel CRAM molecules, then systematically dock both AI-generated and database structures against six critical enzyme families across multiple bacterial species.

Our breakthrough methodology generates chemically diverse CRAM variants while preserving essential carboxyl characteristics. Comprehensive molecular docking analysis across Baeyer-Villiger monooxygenases, CO2-adding carboxylases, decarboxylases, reversible decarboxylases, ring-cleaving dioxygenases, and ω-oxidation enzymes reveals unprecedented insights. High-resolution crystal structures from Thermobifida fusca, Escherichia coli, Staphylococcus aureus, and marine bacteria enable precise active site mapping and binding affinity quantification.

Remarkably, AI-generated CRAM molecules exhibit superior enzymatic compatibility compared to natural variants, discovering previously inaccessible binding modes and transformation pathways. Statistical analysis reveals distinct enzyme preferences, with diffusion-generated structures showing enhanced binding diversity particularly in oxidative enzymes. Cross-enzyme docking identifies promiscuous substrates capable of multi-pathway degradation, unveiling complex transformation networks crucial for environmental persistence.