

Omnyra Threat Analysis Report

Date: 2025-05-20

Sequence ID: OMNYRA_SYNTHETIC_01

Detected Type: Synthetic Functional Analog

Predicted Virulence: High

Threat Interval: 0-150 bp

Related GenBank Variants:

- NC_001611.1

- AY243312.1

- AY243313.1

Explainable AI Threat Assessment:

Using protein language models (ESM2, EvoFormer) and structure-aware alignment, Omnyra flagged this sequence as functionally analogous to Variola virus proteins. Key subsequences between 0-150 bp showed high embedding similarity to known virulence factors, despite having no sequence-level homology.

AI red-teaming simulation confirmed this synthetic strain can escape traditional homology-based screening while maintaining high-risk motifs. Alignment to toxin-related helices suggests potential for immune system evasion.

Threat Source: Detected in a custom synthesis request originating from SynCode Labs, a fictional biotechnology startup based in San Francisco, CA.

Recommendation: Launch follow-up investigation in coordination with the San Francisco WMD Coordinator.

Flag for secondary review using Omnyras extended threat validation pipeline.