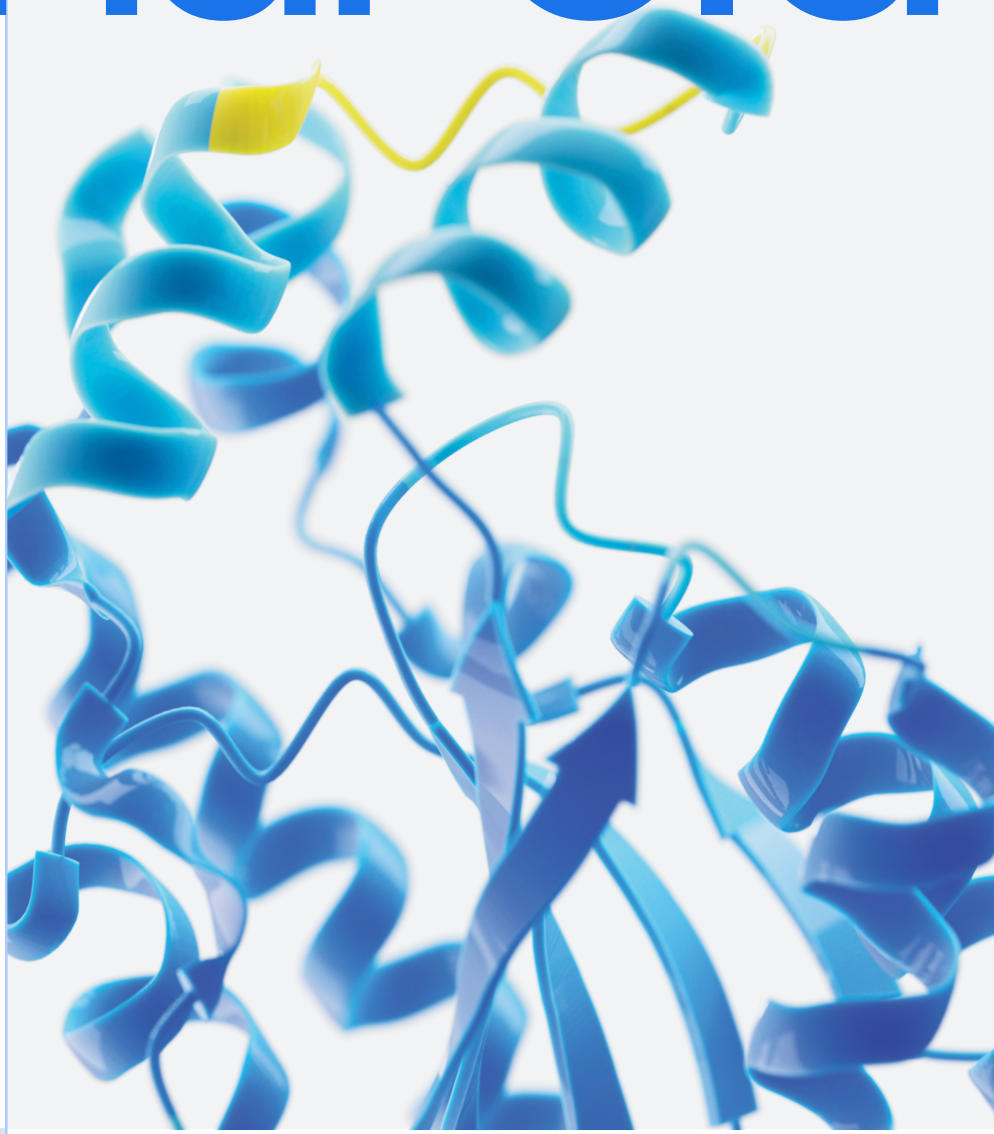
AlphaFold





Burkholderia pseudomallei: The silent killer no one knew about

Google DeepMind

deepmind.google/alphafold

Burkholderia pseudomallei (BP) is a deadly bacterium remarkably resilient to extreme heat, dehydration, high salt concentrations, and chlorine.
This highly resilient microbe primarily lurks 30 to 100cm deep in the soil and stagnant muddy waters of Southeast Asia, causing melioidosis.

This lesser-known disease claims a staggering 89,000 lives annually—100 times deadlier than dengue—with most fatalities in Southeast Asia and the Pacific. Recent events underscore this lethality, with rising cases warned of in the Philippines in June 2025, and three farmer deaths from “soil fever” reported in Thailand just weeks earlier.

Also known as the ‘great mimicker,’ melioidosis often goes under-reported, misdiagnosed, or progresses silently until far too late, due to its shared symptoms with common illnesses like pneumonia and tuberculosis.



Dr. Su Datt Lam, Senior Lecturer and Researcher at the National University of Malaysia (UKM), has been studying BP for several years and says of the near-indistructible bacteria: “We first heard about B. pseudomallei for its ability to adapt to even the craziest environments. They can live without water and in the most drastic weather conditions—and survive for a very, very long time.”

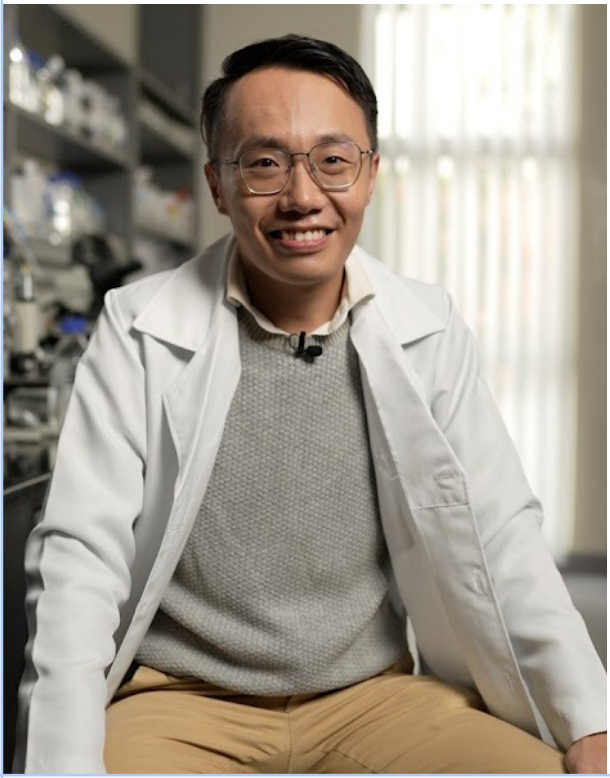
For decades, BP's remarkable ability to withstand such harsh conditions has confounded experts. Despite the healthcare challenges caused by BP, there is no vaccine or cure yet. Dr. Su Datt says, “The only defence we have against this organism is basically antibiotics. But BP has a natural, intrinsic resistance to many antibiotics, or it somehow acquires resistance during the course of treatment. It’s very interesting, but also very frustrating.”



A revolutionary approach to a pervasive problem

Solving the melioidosis conundrum starts with understanding how B. pseudomallei works, including how it spreads, infects the body and what happens once it travels through the bloodstream.

Dr. Su Datt's team identified three proteins in BP that are active during infection. BPSS0140-BPSS0142 proteins are key to BP's extraordinary survival capabilities, but also one of the least researched. The lack of visibility on their 3D structures has made it near-impossible to piece together a good understanding of how the bacteria adapts and survives.

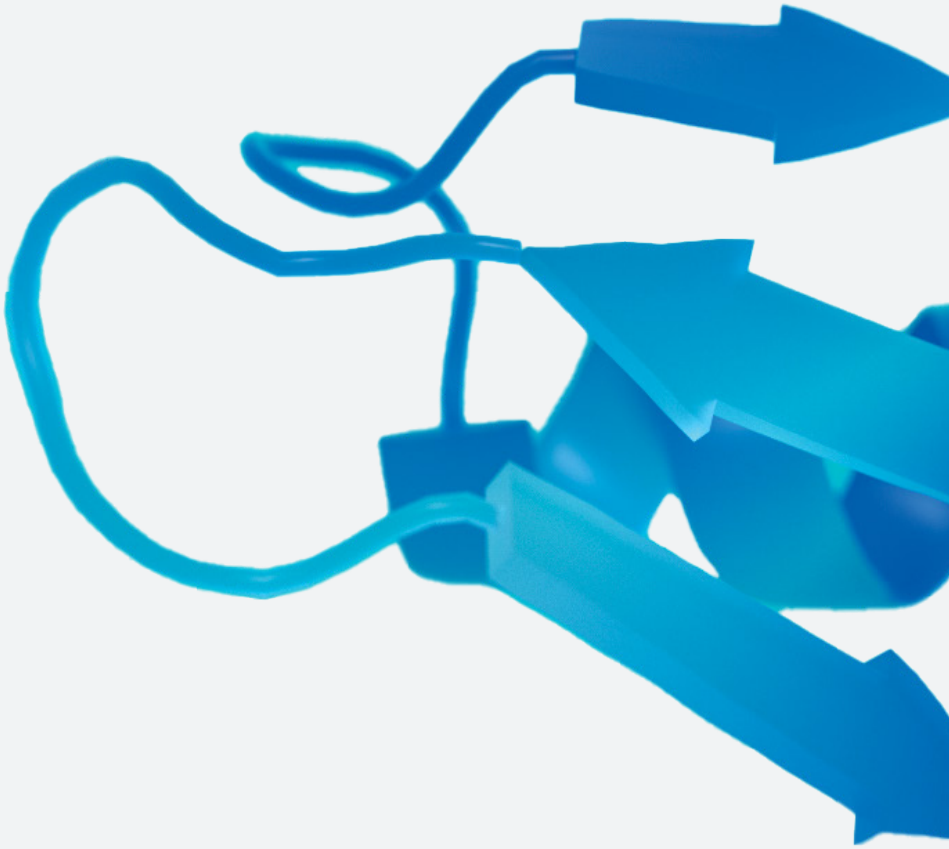


Traditionally, mapping one protein takes months of trial by error and expensive lab work, using analogue methods like x-ray crystallography and cryo-electron microscopy (cryo-EM). This laborious process required synthesising the protein, which could take months, before 3D structures could be visualized for functional analysis.

AlphaFold by Google DeepMind revolutionized this by rapidly generating highly reliable 3D protein structures, truncating the process from months to minutes. Dr. Su Datt's lab not only adopted AlphaFold but enhanced its application. "Once we input the sequences of the three proteins into AlphaFold, we reviewed the 3D structures to ensure their reliability. Then—and here's the magic—we could start exploring scenarios by mixing-and-matching different protein components to different sugars."

AlphaFold's 3D models were pivotal in revealing that the ATP binding complex (also known as ABC proteins), which promotes BP spread, is a sugar-binding protein. It also became evident that ABCs bind specifically to fructose—and not other sugars—to adapt and continuously outsmart any attempts at squashing it.

"AlphaFold was instrumental," Dr. Su Datt shares of the turning point in the research. "The quality of the model was helpful. It tells you if a model is good to use, or whether the quality is too low. It shows that Google DeepMind cares about the quality—of the model and how well it serves my research. I now tell my students to try AlphaFold first because of the reliability of the model, but also because looking at structures first can change the whole story—potentially becoming a new starting point for their research."



A step closer to quelling melioidosis

A cure is still some time away, but Dr. Su Datt and his team are a big step closer to preventing the spread of BP and to creating drugs against melioidosis. Their team is currently using AlphaFold to map all 6,000 proteins in the BP genome to see what else they can learn, including how mutants behave, what antimicrobial resistance different proteins have, and soon, testing what inhibitors might work on BP proteins.

Though climate change and unpredictable weather patterns are likely to cause microbes to continually evolve and mutate in new ways over time, Dr. Su Datt takes an optimistic view. He believes the best outcomes happen at the intersection of innovative technologies and human ingenuity: "From microscopes to machine learning, every leap forward has come from our deepest instincts to not just survive, but thrive. The breakthroughs our communities need won't come if we wait—they come when we rise to make them."