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**SSGCID SOLVES 100<sup>th</sup> STRUCTURE, PROVIDING NEW INFORMATION ABOUT INFECTIOUS DISEASES**

**SEATTLE, August 4, 2009** – Scientists who are part of the Seattle Structural Genomics Center for Infectious Disease (SSGCID) have recently marked a significant milestone: they’ve experimentally determined the 100<sup>th</sup> three-dimensional protein structure from a number of bacterial and protozoan pathogens, which could potentially lead to new drugs, vaccines and diagnostics to combat deadly emerging or re-emerging infectious diseases. Headquartered at Seattle Biomedical Research Institute (SBRI) and led by SBRI Principal Investigator Peter Myler, the SSGCID was established in late 2007 with a \$30.6 million, five-year contract from the National Institute of Allergy and Infectious Diseases (NIAID), which is part of the National Institutes of Health (NIH).

Some of the structures solved come from little known or emerging pathogens that cause disease and death, but have been less well studied by the research community. For example, the SSGCID solved the first protein structure from *Rickettsia*, a bacterial pathogen carried by many ticks, fleas and lice that causes several forms of typhus and spotted fever. Since then, members of the consortia solved 100 percent of the *Rickettsia* structures determined to date, providing new insight into the bacterium. Other structures solved which have significantly impacted the structural information known about these pathogens include proteins from *Brucella*, which causes brucellosis, a fever-based disease contracted by contact with fluids or food products from infected animals, and from *Burkholderia*, which causes glanders and melioidosis, diseases that come from contact with infected soil, water or food. SSGCID has also solved structures from *Babesia* (babesiosis), *Bartonella* (bacillary angiomatosis), *Borrelia* (lyme disease), *Entamoeba* (dysentery), *Giardia* (giardiasis) and *Mycobacterium* (tuberculosis).

“While we are all familiar with infectious diseases like malaria or tuberculosis, the world is filled with hundreds of infectious diseases – many of which fly below the radar screen and are unknown to the general public,” said Myler. “But these neglected diseases do cause a tremendous burden of illness and death in many parts of the world.”



Little known, neglected diseases are among those the SSGCID scientists are tackling, but they are also solving structures related to diseases that have recently been in the news, including 2009 H1N1 (swine) influenza virus. As structures are solved, they are made available to the scientific community in hopes of offering a “blueprint” for development of new drugs, vaccines and diagnostics.

Members of the SSGCID consortium come from Washington-based organizations including deCODE biostructures on Bainbridge Island, the University of Washington in Seattle, Pacific Northwest National Laboratory in Richland, and SBRI. While most structures are solved by a method called x-ray crystallography, the 100<sup>th</sup> structure was solved by one of the consortium’s two nuclear magnetic resonance teams.

The SSGCID is well on its way to solve a total of at least 400 structures during its five-year project timeline, Myler said.

**ABOUT SBRI:**

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