Testimonials

USA

“As someone who has worked on O-GlcNAcylation for nearly 40-years, I regard the O-GlcNAc database (https://www.oglcnac.mcw.edu) developed by Dr. Olivier-Van Stichelen and her colleagues to be one of the most important contributions to our field. To date, more than 16,000 proteins (9,000 human proteins) from various species have been shown to be O-GlcNAcylated. Like phosphorylation, the functions of O-GlcNAc on these proteins are both site and protein specific. Since most O-GlcNAc sites mapped, appear only in the supplements of proteomic/glycomic studies, discovering the existing data on O-GlcNAc was nearly impossible prior to the development of this database. One effect of the database is to prevent duplication of effort when a researcher begins to study the O-GlcNAcylation of a protein. This database also allows, for the first time, systems and bioinformatic analyses of O-GlcNAc’s many functions in cells. It is critical that this outstanding group be allowed to keep this database up to date. Since O-GlcNAcylation is directly involved in the etiology of neurodegeneration, diabetes, heart disease and cancer, the existence of this outstanding resource will greatly accelerate progress in this important area, and it will help many researchers develop new avenues for therapeutics.” **Gerald W. Hart, Ph.D., Complex Carbohydrate Research Center, University of Georgia, USA**

“The O-GlcNAc database established by Dr. Stephanie Olivier-Van Stichelen is an invaluable resource for researchers in our field. It provides One-Stop-Shopping for identifying O-GlcNAc proteins and annotated site analysis. The database fuels discoveries in multiple diverse fields. It serves novice investigators as well as investigators such as me with 40 years of experience in O-GlcNAc biology. The importance of this database cannot be overstated!” **John Hanover, Ph.D., National Institute of Health**

"The O-GlcNAc database has quickly become the definitive source for whether or not a protein is known to be modified by O-GlcNAc and if so, at what sites. With its referencing function and links to UniProt and glygen, it has also saved me invaluable time tracking down primary information regarding particular O-GlcNAc modified proteins." **Lance Wells, Ph.D., Complex Carbohydrate Research Center, University of Georgia, USA**

“Dear Dr. Olivier-Van Stichelen, the O-GlcNAc database that your lab has developed has become an essential resource for my laboratory. The absence of a well-curated database of O-GlcNAcylated proteins was a major limitation in developing O-GlcNAc biology. As a result, your O-GlcNAc database enables us to achieve better results using fewer resources and will greatly help advance the field of O-GlcNAc biology.” **John Chatham, Ph.D., the University of Alabama at Birmingham, USA**

“Trying to ascertain what is known or unknown about a protein’s O-GlcNAcylation status from a hodge-podge of source data is difficult and presents a barrier to entry into the field. However, the O-GlcNAc database simply and conveniently collates large and dispirit datasets into one easily searchable site. The site allows my laboratory to quickly engage with other researchers who want to collaborate but are uncertain if O-GlcNAc could regulate their protein of interest.” **Chad Slawson, Ph.D., University of Kansas Medical Center, USA**

“My lab has a long-standing interest in the biological consequences of site-specific O-GlcNAc modifications on various proteins. To accomplish this goal, we use synthetic protein chemistry to prepare homogenous O-GlcNAc-modified proteins for subsequent in vitro, cellular, and in vivo experiments. A major roadblock in our approach has been identifying O-GlcNAc sites with a high

likelihood of functional effects on proteins of interest. In the past, we kept our own spreadsheet-based list of known O-GlcNAc modified proteins and their sites of modification; however, this process was incredibly time-consuming and labor-intensive. The O-GlcNAc database from Prof. Oliver-Van Stichelen has been transformative for us in this regard. In the relatively short time that the database has been online, we have already used it to identify two new proteins for our approach, resulting so far in a J Am Chem Soc paper showing that O-GlcNAc inhabits the DNA-damage repair function of the protein HMGB1. We continually revisit the database to identify more potential protein targets, and I am confident it will remain an indispensable aid to my research program for years." **Matt Pratt, Ph.D., University of Southern California**

"The O-GlcNAc database from the Olivier-Van Stichelen lab is the ***go-to resource*** for anyone interested in O-GlcNAc in the proteome. The database has made integration of O-GlcNAc across datasets and other types of modifications readily comparable, lookup the parent reference for validation facile, and is user-friendly! We use it regularly when assessing O-GlcNAc proteins and sites… including for our own datasets!" **Christina Woo, Ph.D., Harvard University, USA**

"O-GlcNAc modification is fundamentally important to cell signaling, gene regulation, metabolic physiology, and human disease. The O-GlcNAc Database is the most comprehensive, update-to-date resource that enables investigators of all levels to tackle this rapidly evolving field." **Xiaoyong Yang, Ph.D. Yale School of Medicine**

"When investigating new O-GlcNAc modified proteins in our research, the "O-GlcNAc database" is our first stop. The collation of citations and the scoring algorithm allow students to rapidly identify the correct literature and assess previous research. When presenting OMIC data identifying proteins modified by O-GlcNAc, we are often asked to determine which proteins have previously been identified as glycosylated. Before the generation of the O-GlcNAc database, such studies were performed by manual literature search." **Natasha Zachara, Ph.D., John Hopkins**

"The O-GlcNAcome database by Olivier-Van Stichelen et al is an ESSENTIAL resource for our O-GlcNAc studies. We regularly compare our experimental datasets against the *O*-GlcNAcome for validation. In developing our "GlycoID" tool (ACS Chem Biology, 2022) we used the *O*-GlcNAcome as the key benchmark to validate our datasets to measure the selectivity of our novel tool vs. the known O-GlcNAc glycoproteome. In recent unpublished work, we are using the *O*-GlcNAcome to validate proteomic hits from in vivo tissue samples and verify their disease relevance. Having this regularly curated collection of all reported O-GlcNAc glycoproteins and sites enables us to advance our scientific directions at both "big data" as well as "specific protein" levels of analysis." **Charlie Fehl, Ph.D., Wayne State University, USA**

"Professor Olivier-Van Stichelen's O-GlcNAc database has been a tremendous boon to the work in my lab and to many others in the field. My lab studies the role of O-GlcNAc in a variety of cell biological processes, including several that are dysregulated in such human diseases as cancer, diabetes and neurodegeneration. Identifying the proteins and specific sites modified by O-GlcNAc is critical for understanding its role in health and disease and yet is notoriously difficult from a technical perspective. The O-GlcNAc database has curated a wealth of these crucial data and made them accessible to a wide range of biologists, specialists, and non-specialists alike. For example, my group regularly uses the O-GlcNAc database to find modification sites on proteins of interest from humans and rodents and to query whether a particular protein of interest might be O-GlcNAc-modified. This resource allows us to generate and test hypotheses in a fraction of the time they used to require. Indeed, the database is so comprehensive and user-friendly that it completes searches in minutes that might take days for a Ph.D. student or postdoc to execute without the resource. In this way, the O-GlcNAc database has greatly empowered research on this essential yet incompletely understood aspect of biology, enabling experiments and discoveries that were previously impossible." **Mike Boyce, Ph.D., Duke University**

CANADA

"The O-GlcNAc database is a precious resource for our team. It provides a one-stop location with curated data where we go to analyze our proteomics data. The ability to carry out these analyses provides a route to the logical generation of testable hypotheses." **David Vocadlo, Ph.D., Simon Fraser University, Vancouver, Canada**

"The O-GlcNAc database, developed by Stephanie Olivier's group, is the to-go database for exploring the curated O-GlcNAcylation data that is buried in thousands of research articles. Until now, there was no comprehensive resource that would make O-GlcNAc data available to the research community in an easy and intuitive way without having to explore other resources or manually extract and interpret the information from the papers. The development O-GlcNAc database plugs the gap by providing highly curated O-GlcNAc data, extracted, integrated and harmonized from over 2400 GlcNAc research papers using machine learning methods. The database displays the data in a simple and user-friendly way that even novice researchers can use it confidently and expand their knowledge of the O-GlcNAc domain. The database also has a download option, APIs and other programmatic tools for advanced exploration. In addition, the database provides the reference PMIDs from where the data was curated and links to other resources such as GlyGen and UniProt for further research enabling high confidence in data and facilitating data sharing. Our resource, GlyGen, a glycoinformatics resource, has integrated data for human, mouse, rat and drosophila through collaboration and made it available to users with linkbacks to The O-GlcNAc database. With the integration of O-GlcNAc data, GlyGen now provides an extensive list of glycosylated proteins and sites. Without The O-GlcNAc database's effort, it would have been difficult to extract and curate the data from papers and further understand the interplay of O-GlcNAcylation and phosphorylation and cellular functions such as protein localization, interactions and stability, cell signaling, transcription, immune response, etc. The O-GlcNAc database is accelerating research and discovery in the glycoscience field and providing fascinating insights about health and diseases." **Jeet Vora, Ph.D., GlyGen Team**

FRANCE

The O-GlcNAc database is an outstanding tool for glycobiologists and especially scientists working in O-GlcNAcylation. For us, the O-GlcNAc database was particularly helpful in studying fatty acid synthase, a massive protein of 2,511 amino acids hard to work with. Thanks to the database we were able to collect the previously described O-GlcNAcylated sites and start site-directed mutagenesis which would have been difficult to achieve by questioning servers such as PubMed by keywords. Without the database, we would have had also to spend a lot of time exploring proteomic data files because often the identification of amino-acid sites where PTMs such as O-GlcNAcylation reside are buried in tables of several thousand rows. The O-GlcNAc database is a powerful and valuable tool that should boost research dedicated to studying O-GlcNAcylation." **Tony Lefebvre, Ph.D., University of Lille, France**

DENMARK

"The O-GlcNAc database from the Olivier-van Stichelen group is an essential tool for research in this (and neighboring) fields. Understanding how this unique modification is linked to cellular functions and a range of diseases (diabetes, cancers, and neurological disorders) is one of the big challenges and can be compared to finding a needle in a haystack. What the O-GlcNAc database uniquely provides is a **curated** haystack. Every site is linked to all the underpinning evidence and given a confidence score, and the database is fully searchable using several

advanced query possibilities. My group is interested in finding links between a new type of intellectual disability caused by mutations in the O-GlcNAc transferase. The O-GlcNAc database is helping us focus on candidate O-GlcNAc proteins." **Daan Van Aalten, Ph.D., Aarhus University, Denmark**

GERMANY

"The O-GlcNAc database helped us to reference our chemical proteomics approach for identification of O-GlcNAc proteins. It provides all critical information about this important protein post-translational modification and thus ensures the integrity of the research outcomes. I am convinced that further database development will advance the knowledge by integrating and sorting the data mined by various methods." **Pavel Kielkowski, Ph.D., LMU München, Germany**

UK

As it is an emerging research focus, the O-GlcNAc database has helped our team uncover vital information to help with our work investigating the molecular basis of how metabolic disease impacts outcomes for patients undergoing coronary artery bypass graft." **Israel Olapeju Bolanle** and **Tim Palmer, Ph.D., University of Hull, UK**