

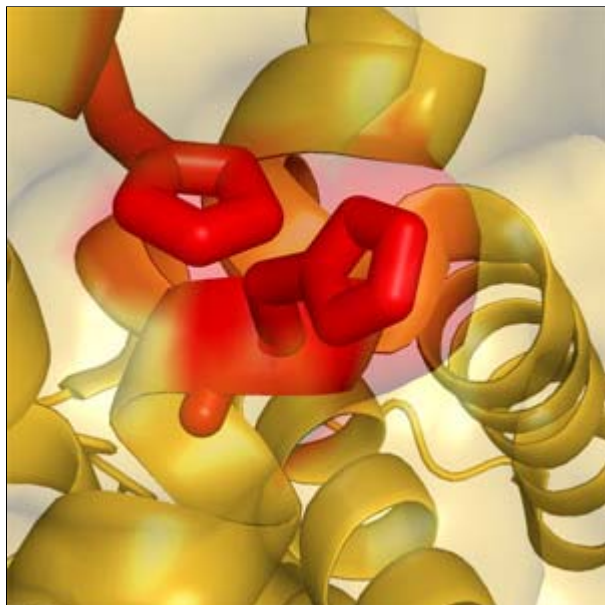
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Environmental Factor, July 2009, National Institute of Environmental Health Sciences

NIEHS-Funded Imaging Tool Logs 100,000th Job

By Eddy Ball
July 2009






"Structure of the Native and Inactive LicT PRD from *B. Subtilis*" Two histidine residues shown in red undergo phosphorylation that induces dramatic conformational change and regulates the dimerization of LicT regulatory domain — LicT-PRD, PDB id 1tlv. (Image courtesy of Jarek Meller)



From left to right, POLYVIEW-3D developers Medvedovic, Porollo, who is a CEG Next-Generation Biomedical Investigator, and Meller pose with a computer showing images generated by their tool. (Photo courtesy of UC)

The NIEHS-funded University of Cincinnati (UC) Center for Environmental Genetics (CEG) announced that its Bioinformatics Core recorded its 100,000th job submission on June 11 for its popular POLYVIEW-3D imaging tool. POLYVIEW-3D is a Web-based macromolecular-structure visualization and analysis tool developed by UC professors as


part of a series of expanded, user-friendly Web-based software applications and servers that scientists and students can use, free of charge, to extract and extrapolate structural and functional genomic data for various research projects.


POLYVIEW-3D (<http://polyview.cchmc.org/polyview3d.html>)  developers Alexey Porollo, Ph.D., the primary architect of the product, Jarek Meller, Ph.D., and Mario Medvedovic, Ph.D., are professors in the Division of Epidemiology and Biostatistics (<http://www.eh.uc.edu/epibio/>)  in the UC Department of Environmental Health. In an August 2007 article (<http://www.biomedcentral.com/1471-2105/8/316>)  published in the open access journal *BMC Bioinformatics*, Porollo and Meller announced the availability and terms of use for POLYVIEW-3D.

"We're making them [existing bioinformatics tools] better and developing new methods for analyzing the data," Porollo explained. "A growing base of users, and cross-linking by major proteomic resources such as the Protein Data Bank and various prediction meta-servers, are evidences of the competitiveness of our tools."

One of the nation's leading structural biologists, NIEHS Principal Investigator Samuel Wilson, M.D., is one of many scientists who agree with Porollo. "POLYVIEW-3D is an important tool in making the incredible excitement of structural biology more accessible for scientists, students and the public at large," he said.

By integrating the Web technology with state-of-the-art software for macromolecular visualization, POLYVIEW-3D enables versatile structural and functional annotations of proteins and their complexes, coupled with publication-quality structure rendering. In addition to static pictures, high quality animated images for electronic resources such as PowerPoint or Websites can be easily generated. In particular, POLYVIEW-3D server features the PyMol program for image rendering, providing detailed and high quality slide and animated presentations of macromolecular structures, with an easy to use Web-based interface.

POLYVIEW-3D was voted one of the top five protein structure visualization/annotation resources by MolviZ.org (<http://www.umass.edu/microbio/chime/top5.htm>) , where it is described as "easy enough for student reports or homework assignments!" There is no need for users to know any command language to use the free service — just a user-friendly form to fill out online. According to Porollo, the tool has been used by researchers in over 80 countries this year alone, and several universities include the server as part of the curriculum in practical courses on macromolecular visualization.

Citation: Porollo A, Meller J. (<http://www.biomedcentral.com/1471-2105/8/316>)  2007. Versatile annotation and publication quality visualization of protein complexes using POLYVIEW-3D *BMC Bioinformatics* 8:316. doi:10.1186/1471-2105-8-316.

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Last reviewed: 01 July 2009.