NIH Public Access
Author Manuscript
J Chem Educ. Author manuscript; available in PMC 2014 April 22.

Published in final edited form as:
J Chem Educ. 2012 January 10; 89(2): 291–292. doi:10.1021/ed200088u.

LIPID MAPS-Nature Lipidomics Gateway: An Online Resource for Students and Educators Interested in Lipids

Manish Sud[1], **Eoin Fahy**[1], **Dawn Cotter**[1], **Edward A. Dennis**[2], and **Shankar Subramaniam**[1,3,*]

[1]San Diego Supercomputer Center, University of California, San Diego, La Jolla, California 92093 United States

[2]Department of Chemistry and Biochemistry, and Department of Pharmacology, University of California, San Diego, La Jolla, California 92093 United States

[3]Departments of Bioengineering, Chemistry and Biochemistry, University of California, San Diego, La Jolla, California 92093 United States

Abstract

The LIPID MAPS-Nature Lipidomics Gateway is a free, comprehensive online resource providing tutorials and instructional material, experimental data for lipids and genes along with protocols and standards, databases of lipid structures and lipid-associated genes or proteins, and a variety of lipidomics tools.

Keywords

Graduate Education/Research; Upper-Division Undergraduate; Biochemistry; Interdisciplinary/Multidisciplinary; Computer-Based Learning; Internet/Web-Based Learning; Lipids; Mass Spectrometry

The LIPID Metabolites and Pathways Strategy (LIPID MAPS) consortium ([i]) has developed a set of comprehensive online resources available at the LIPID MAPS-Nature Gateway ([ii]) Web site for students, educators, and researchers interested in lipids. These resources include tutorials and instructional material, experimental data for lipids and genes along with protocols and standards, databases of lipid structures and lipid-associated genes or proteins, tools for structure drawing and mass spectrometry analysis, and pathways with integrated lipid and gene expression data. An overview of these resources is provided in this report.

The Gateway Web site provides various tutorials on lipids chemistry and lipid metabolomics as PowerPoint slides that may be used by students to learn about lipids or incorporated by educators into their instruction material. The tutorials or lectures are available on the following topics: (a) lipid chemistry and classification; (b) fatty acid biosynthesis; (c) fatty acid oxidation; (d) ketone bodies and essential fatty acids; (e) prostaglandins and other eicosanoids; (f) glycerolipids and glycerophospholipids; (g) sphingolipids; (h) cholesterol

*Corresponding Author, shankar@ucsd.edu.

NIH-PA Author Manuscript
NIH-PA Author Manuscript
NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

and other sterols; (i) lipoproteins; and (j) fat-soluble vitamins. These tutorials make extensive use of a comprehensive lipids classification system ([iii],[iv]) developed by the consortium.

The complete lipidomic and gene expression experimental data sets generated by the consortium laboratories across murine macrophage RAW 264.7 ([v]) cell line and primary macrophage cells under various stimulatory conditions are available on the Gateway Web site. Integrated lipid, gene, and pathway maps have also been created using these lipidomic and gene array data sets. Educators may incorporate these experimental data sets, along with integrated pathway maps, into course material for analysis and hypothesis generation leading students to explore on line material for further details.

The following two new databases are available on the Gateway Web site: the LIPID MAPS Structure Database (LMSD) ([vi]) and LIPID MAPS Proteome Database (LMPD) ([vii]). The LMSD contains over 30,000 lipid structures along with their physicochemical properties; the LMPD has over 1,200 lipid-related proteins for each of human and mouse species. These databases provide a comprehensive source of information for lipid structures and lipid-associated genes or proteins for students, educators, and researchers interested in lipids.

The Gateway Web site provides a suite of online mass spectrometry (MS) prediction and structure drawing tools ([viii]). These tools allow users to perform MS analysis and generate complicated lipid structures in a relatively straightforward manner. Researchers may use the MS tools to identify a variety of lipid molecular ions from mass spectral data. Students and educators may apply the structure drawing tools to generate consistent lipid structure representations for reports, presentations, and publications.

Continuous development of online tools, databases, and other resources will continue based on the feedback received from the LIPID MAPS consortium members and the community at large. Additional lipids will be added from non-mammalian sources such as plants, bacteria, algae, and marine organisms to the LMSD over the next couple of years. In addition to existing online structure generation tools for *Mycobacterium tuberculosis* lipidome, development of structure drawing tools for other species-specific lipidomes is envisioned. The consortium members plan to perform additional experiments using primary macrophage cells under various stimulatory and inhibitory conditions and make all the experimental data available on the Gateway Web site. Pedagogic material associated with lipid biochemistry and biology will also be augmented on the Gateway Web site.

Acknowledgments

We thank our LIPID MAPS colleagues, including H. Alex Brown, Christopher Glass, Alfred Merrill, Jr., Robert C. Murphy, Christian R. H. Raetz, David Russell, Walter Shaw, Michael VanNieuwenhze, Stephen H. White, and Joseph Witztum, and their laboratories for their contributions to this work. This work was supported by National Institutes of Health (NIH) and National Institute of General Medical Sciences (NIGMS) Glue Grant NIH/NIGMS Grant U54 GM69338. Funding to pay the Open Access publication charged was also provided by Glue Grant NIH/NIGMS Grant U54 GM69338.

NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

References

i. Schmelzer K, Fahy E, Subramaniam S, Dennis EA. Methods in Enzymology, Academic Press. 2007; 432:169–181. Nov 2011).

iii. Fahy E, Subramaniam S, Brown HA, Glass CK, Merrill AH Jr. Murphy RC, Raetz CRH, Russell DW, Seyama Y, Shaw W, Shimizu T, Spener F, van Meer G, VanNieuwenhze MS, White SH, Witztum JL, Dennis EA. J. Lipid Res. 2005; 46:839–862. [PubMed: 15722563]

iv. Fahy E, Subramaniam S, Murphy RC, Nishijima M, Raetz CR, Shimizu T, Spener F, van Meer G, Wakelam MJ, Dennis EA. J. Lipid Res. 2009; 50:S9–S14. [PubMed: 19098281]

v. Dennis E, Deems R, Harkewicz R, Quehenberger O, Brown A, Milne S, Glass C, Hardiman G, Reichart D, Merrill Al, Sullards MC, Wang E, Murphy R, Raetz C, Garrett T, Guan Z, Ryan A, Russell D, McDonald J, Thompson B, Shaw W, Sud M, Fahy E, Subramaniam S. J. Bio. Chem. 2010; 285:39976–39985. [PubMed: 20923771]

vi. Sud M, Fahy E, Cotter D, Brown A, Dennis EA, Glass CK, Merrill AH Jr. Murphy RC, Raetz CR, Russell DW, Subramaniam S. Nucleic Acids Res. 2007; 35:D527–D532. [PubMed: 17098933]

vii. Cotter D, Maer A, Guda C, Saunders B, Subramaniam S. Nucleic Acids Res. 2006; 34:D507–D510. [PubMed: 16381922]

viii. Fahy E, Sud M, Cotter D, Subramaniam S. Nucleic Acids Res. 2007; 35:W606–W612. [PubMed: 17584797]