

www.lipidmaps.org

LIPID MAPS Lipidomics Workshop

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Lipidomic Analysis of Phosphoglycerolipids

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LIPID MAPS Phospholipid Core H Members:

Mass spectrometry

Stephen Milne

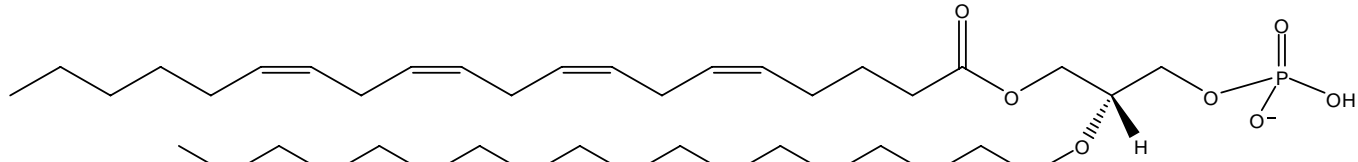
David Myers

Pavlina Ivanova

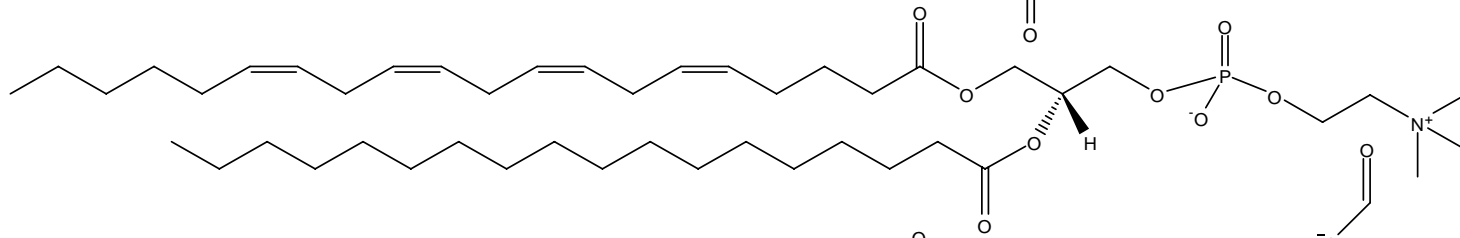
Overview

- 1) Phospholipid Classes Analyzed
- 2) Extraction Protocol
- 3) LC/MS Analysis
- 4) Internal Standards and Standard Curves
- 5) MS/MS Identification of Lipids
- 6) Online Tools for Lipid Identification
- 7) Phospholipid References

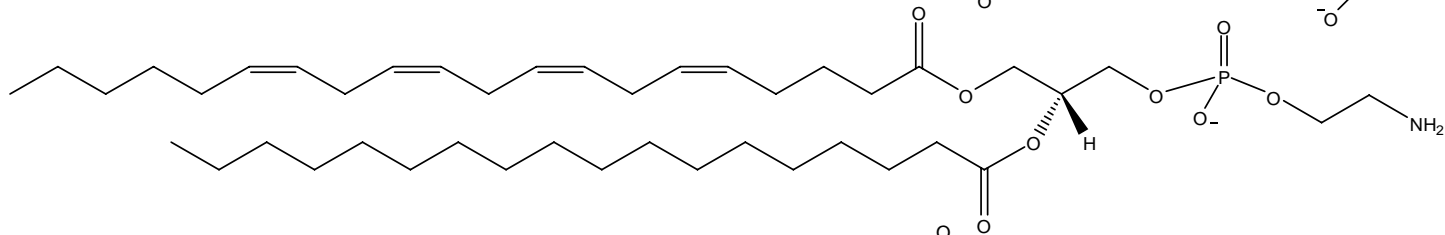
6 Major Glycerophospholipid Classes



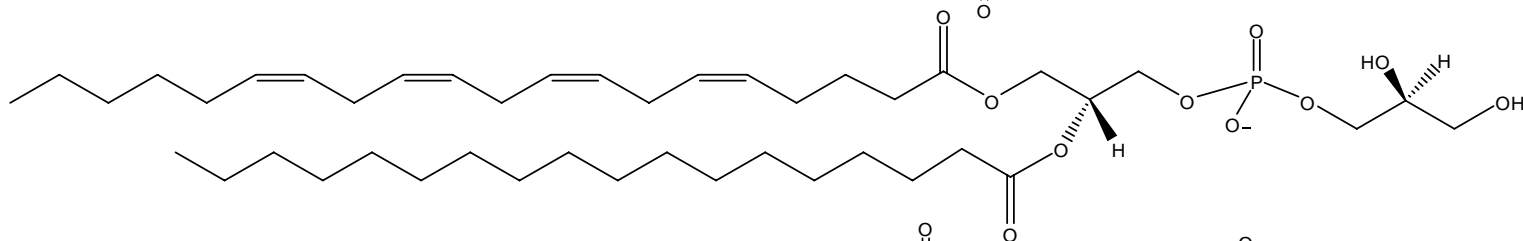
PA



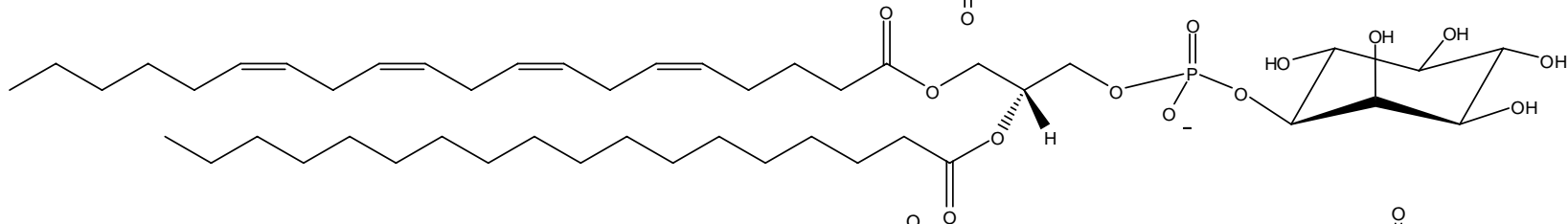
PC



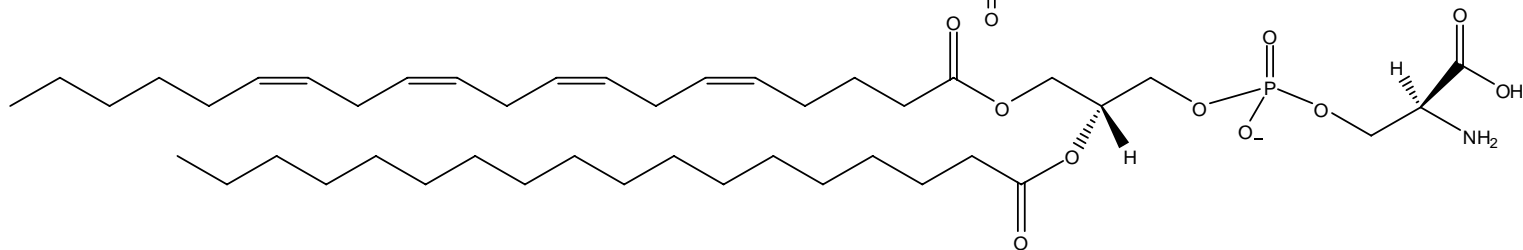
PE



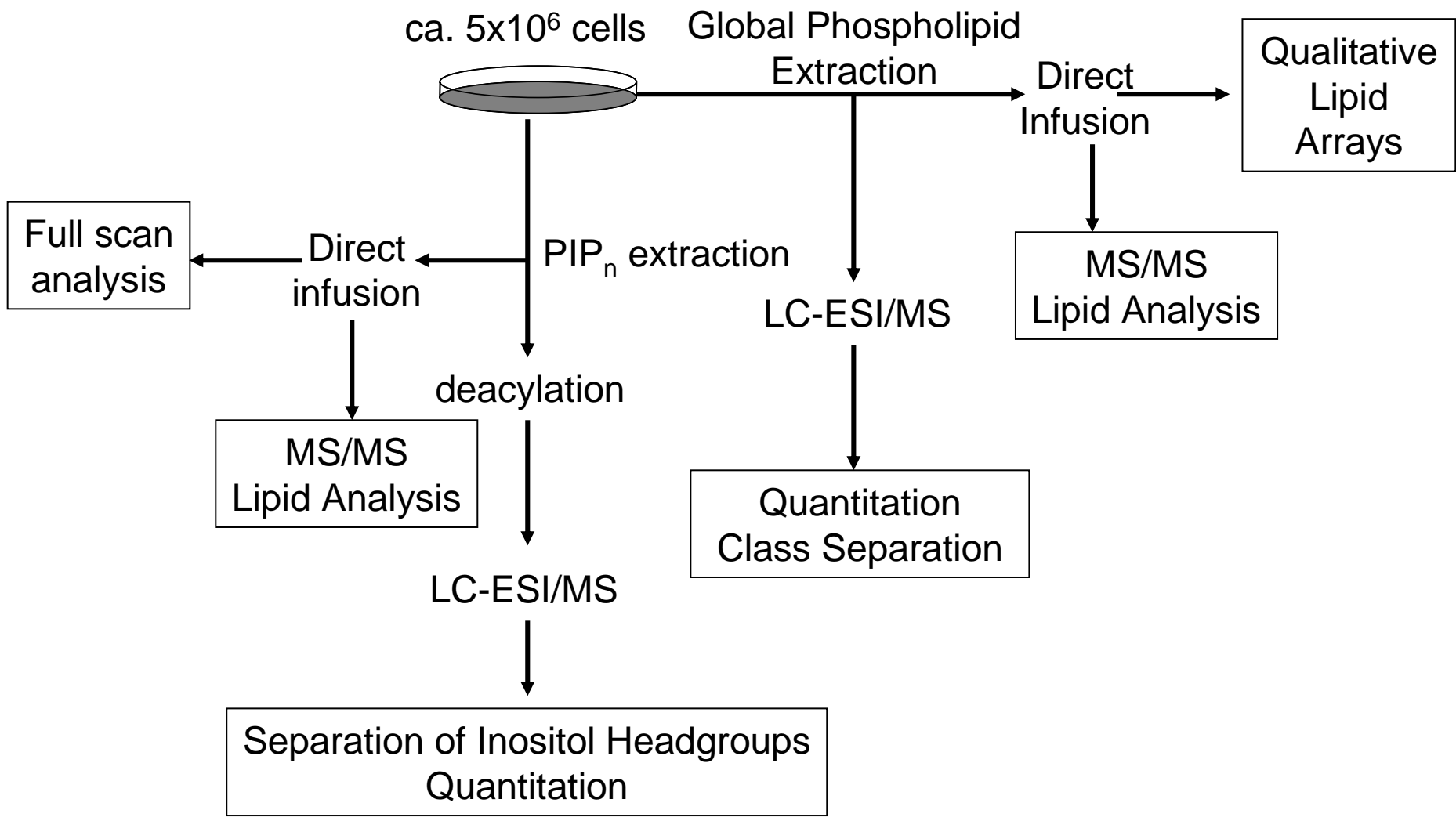
PG

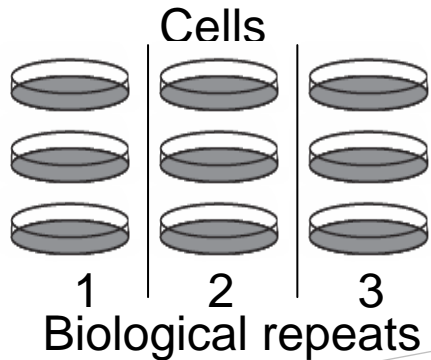


PI



PS





Extraction



Data analysis

Spectra

Direct inject pipeline



HAB lab analysis programs.
3 stds per mode (+,-)
Match peaks to ID list
Filter S/N>3
Deisotope (isotope abundance corrections)



Stat analysis
Powerful 3x3 design of reps for Anova

LC-MS pipeline



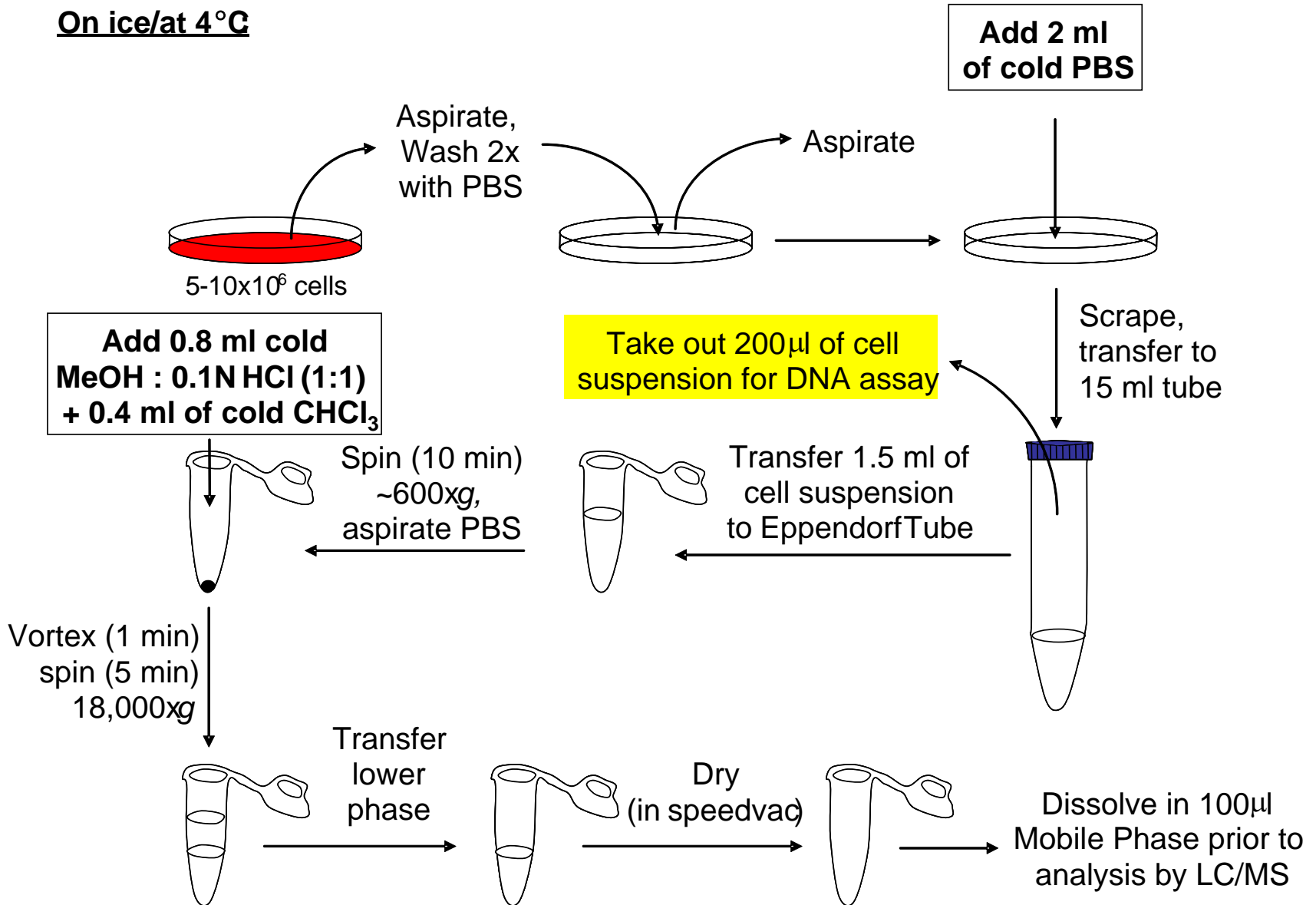
Open source converter



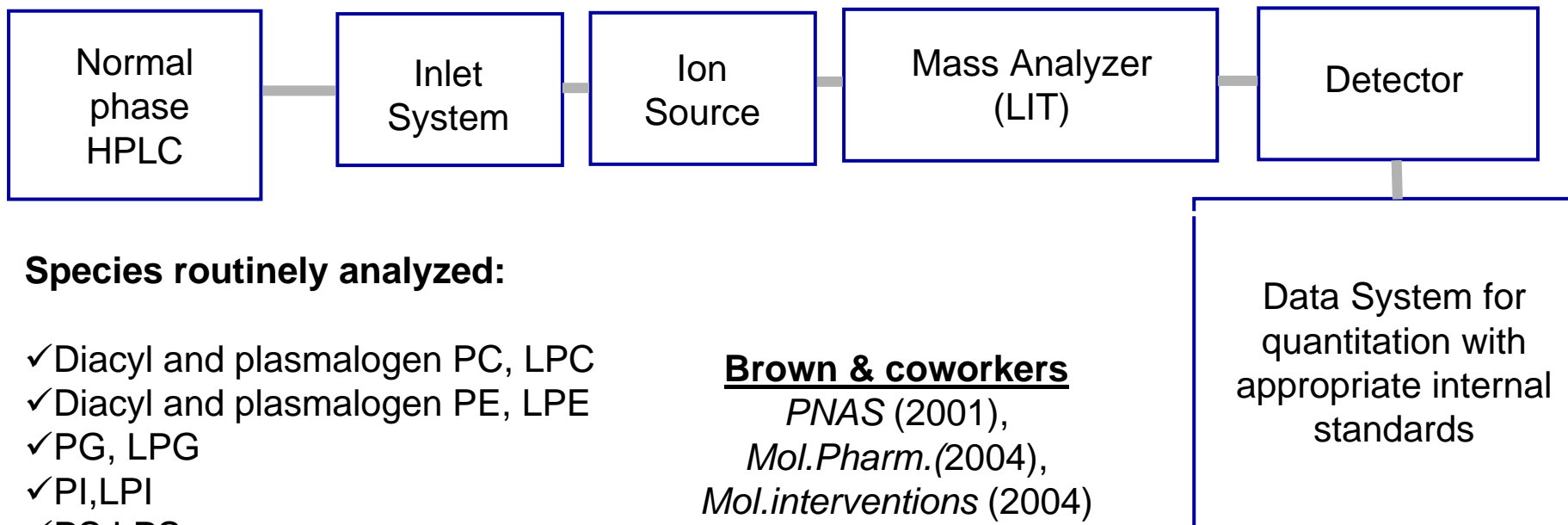
4 odd carbon standards per class.
Match peaks to ID list
Filter S/N>3
Deisotope
Apply nearest neighbor standard curve slope

Mammalian Cell Glycerophospholipid Extraction Procedure

On ice/at 4°C



Glycerophospholipid analysis by LC-MS/MS



Species routinely analyzed:

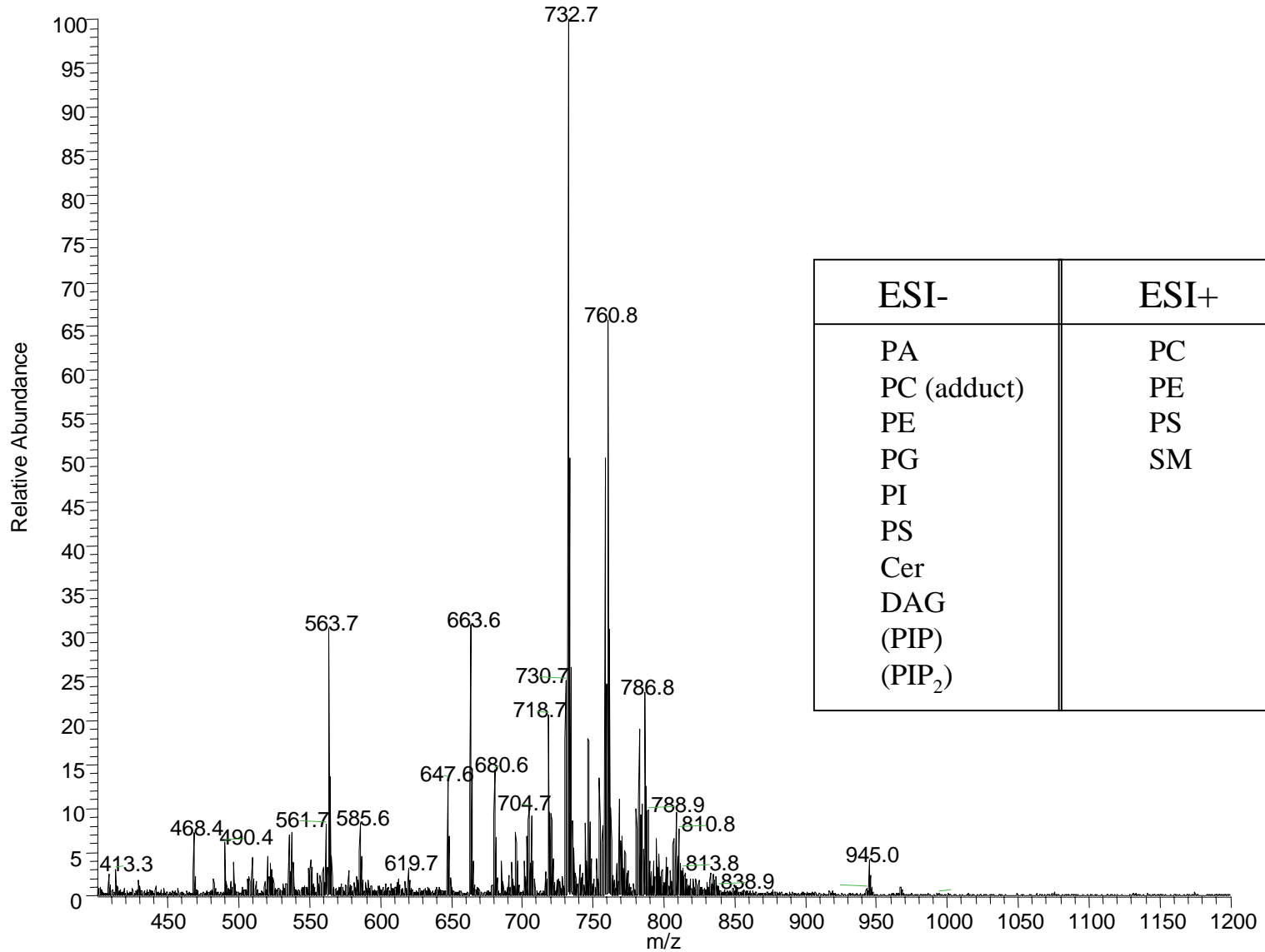
- ✓ Diacyl and plasmalogen PC, LPC
- ✓ Diacyl and plasmalogen PE, LPE
- ✓ PG, LPG
- ✓ PI, LPI
- ✓ PS, LPS
- ✓ PA, LPA
- ✓ PIP, PIP₂
- ✓ SM

Brown & coworkers
PNAS (2001),
Mol.Pharm.(2004),
Mol.interventions (2004)
JLR (2005),
Methods (2006),
Meth. Enzymol. (2008)
Nature Chem Bio (2009)

Data System for
quantitation with
appropriate internal
standards

ESI+

There are > 1000 Phospholipids in a mammalian cell



The majority fall in the 700 and 900 *m/z* range

Quantitation Via Direct Infusion MS Isn't Possible for Most Phospholipid Classes

Every m/z between 700 and 900 has either a parent or isotopic peak from two or more lipid classes. As an example, lipids from 4 classes are present between m/z 758-762 in ESI⁻ mode. When considering different fatty acid combinations, there are 28 different phospholipids present in this mass range. Quantitation in regions this complex isn't possible.

m/z	PC	PE	PG	PS
758		38:1e		34:2
759			35:2	
760				34:1
761			35:1	
762	32:1e (form)	38:6		34:0

LC/MS Analysis of Phospholipids

Instrument Used: 4000 QTrap MS

Luna Silica Column, reconstituted to 100 μ L, 20 μ L injection,
hexane, IPA, ammonium formate solvent system. 350 to 1200 m/z scan range

HPLC parameters:

Phenomenex Luna Silica column 2 x 250 mm 5 micron

Mobile phase A: IPA:Hexane: 100 mM $\text{NH}_4\text{CO}_2\text{H}_{(\text{aq})}$ 58:40:2

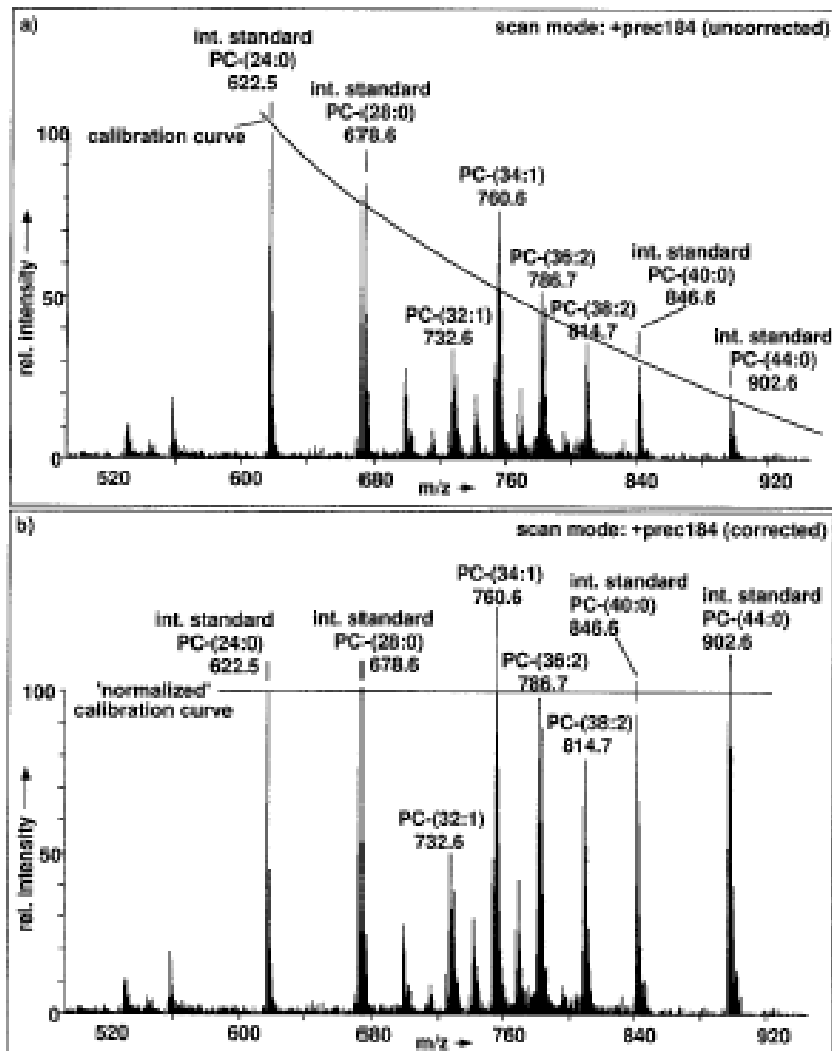
Mobile phase B: IPA:Hexane: 100 mM $\text{NH}_4\text{CO}_2\text{H}_{(\text{aq})}$ 50:40:10

Flow rate: 300 $\mu\text{L}/\text{min}$

Initial %B 50

Gradient program:

<u>Time</u>	<u>Event</u>	
0.01	Controller	Start
5.00	Pump B	50%
30.00	Pump B	100%
40.00	Pump B	100%
41.00	Pump B	50%
50.00	Controller	Stop



Standard Curves Should be Generated for as Many Analytes as Possible. Curves for Other Lipids can be Approximated from their Nearest Neighbors. At Least 2-4 Internal Standards per Class Should be Added to Every Sample.

Proc. Natl. Acad. Sci. USA
 Vol. 94, pp. 2339-2344, March 1997
 Cell Biology

Cell Biology: Brügger *et al.*

FIG. 7. An unprocessed total lipid extract of 5000 CHO cells containing equimolar amounts of PC-(24:0), -(28:0), -(40:0), and -(44:0) was analyzed by parent ion scanning for m/z 184. (a) Uncorrected ion intensities. The signal intensities of the internal standards were used for generation of the calibration plot insert. (b) Corrected ion intensities of the PC signals so that the monoisotopic signals represent the true molar abundances of the corresponding PC molecular species.

Selection of internal standards

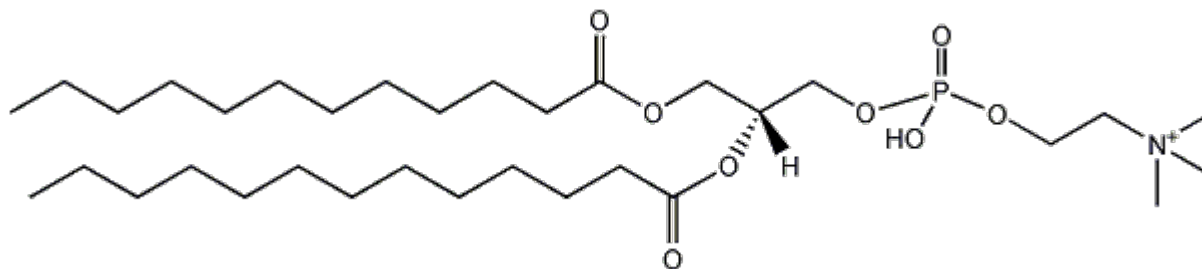
- **It is essential to use IS with similar instrument response**
- **Use several IS for each class**
 - Allows greater number of low abundance species to be detected and quantified at higher total PL concentration
 - Loosens the requirements for control the total PL concentration (low, to use fewer or 1 IS)
 - Helpful with peak assignments

LIPID MAPS internal standard cocktail

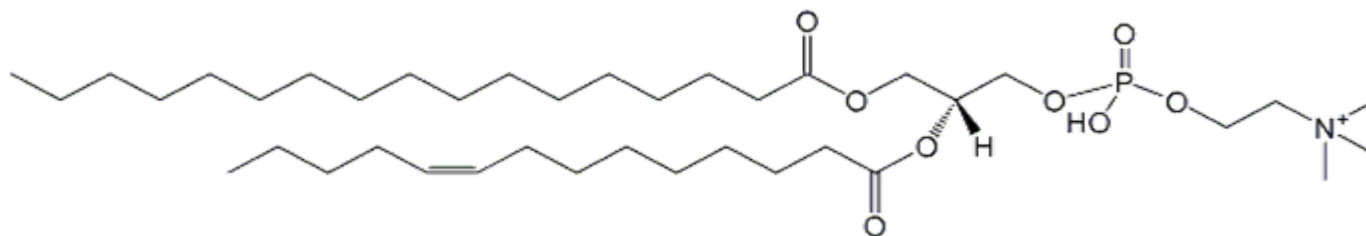
4 Odd-Carbon different length FA standards are used for each class, containing different number of double bonds (25:0,31:1,37:4 and 43:6)

LIPID MAPS MS standards (available from Avanti Polar Lipids): 28 uncommon phospholipid species that are used to spike samples prior to analysis

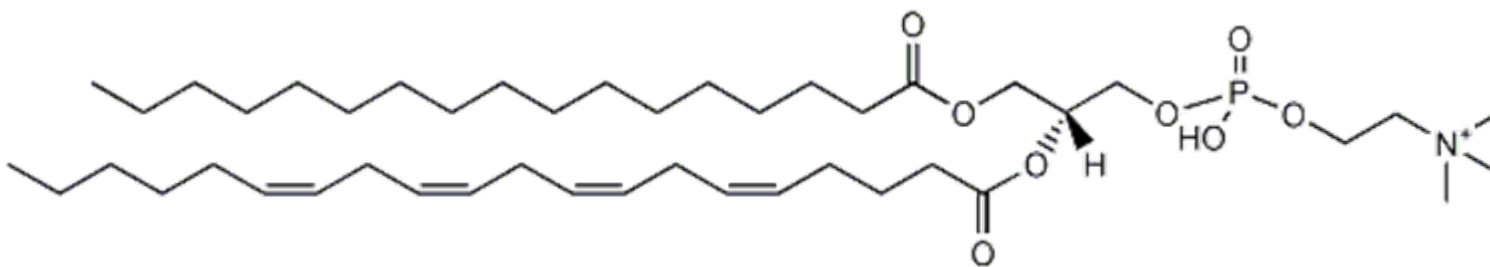
Odd-Carbon PC Internal Standards



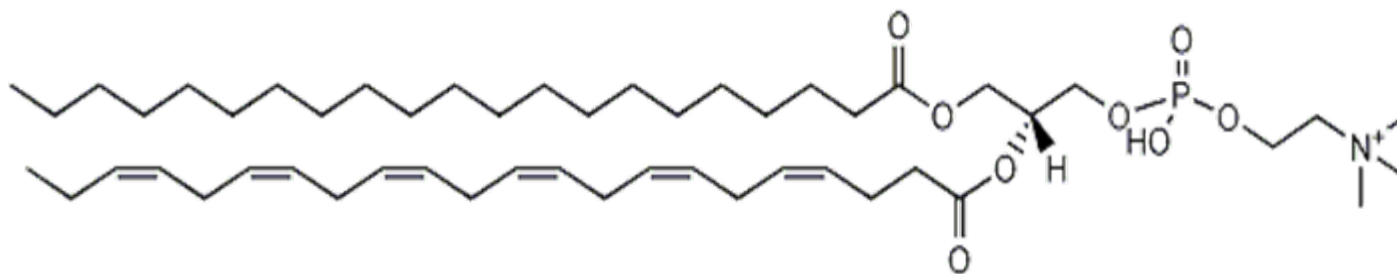
25:0 PC



31:1 PC

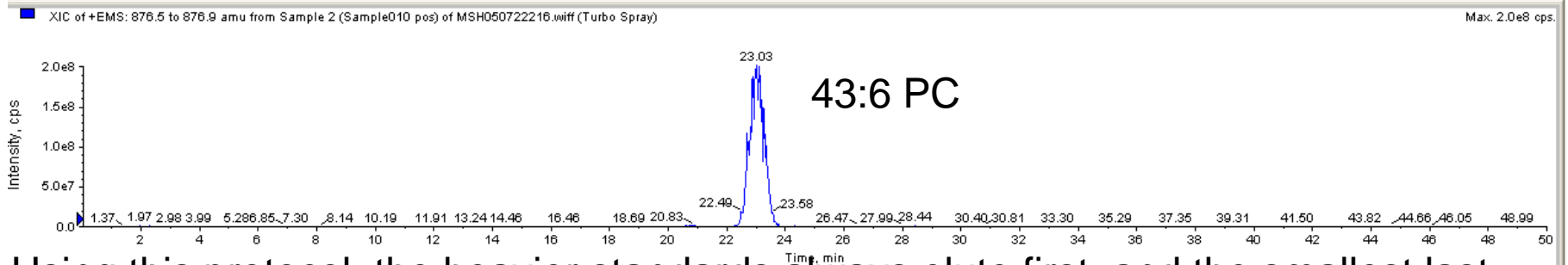
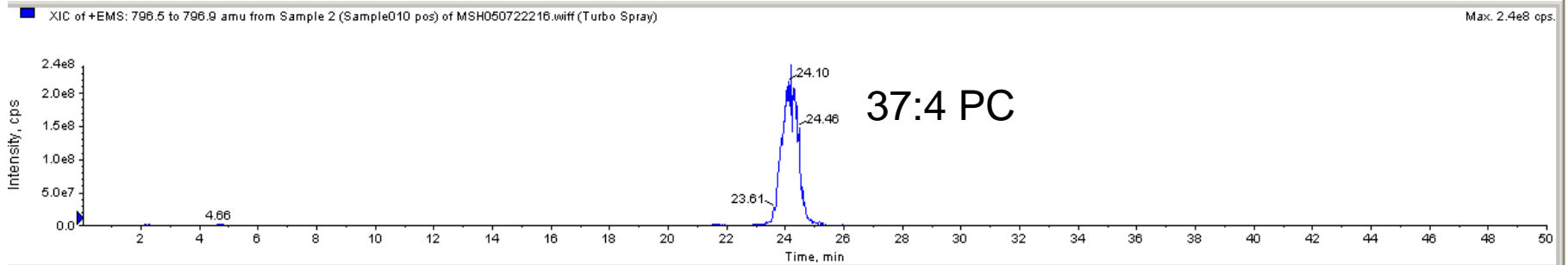
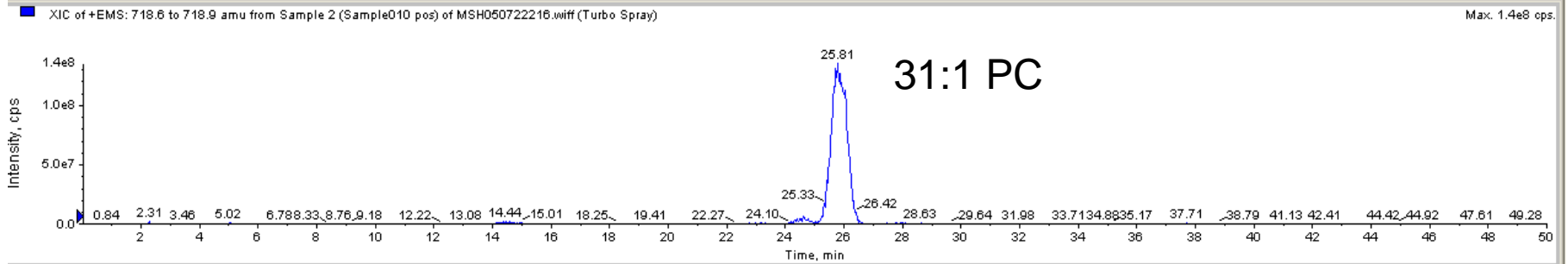
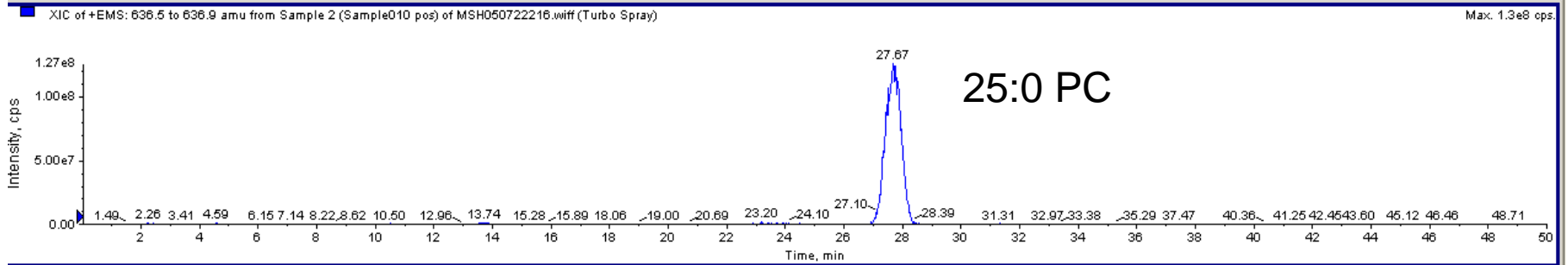


37:4 PC



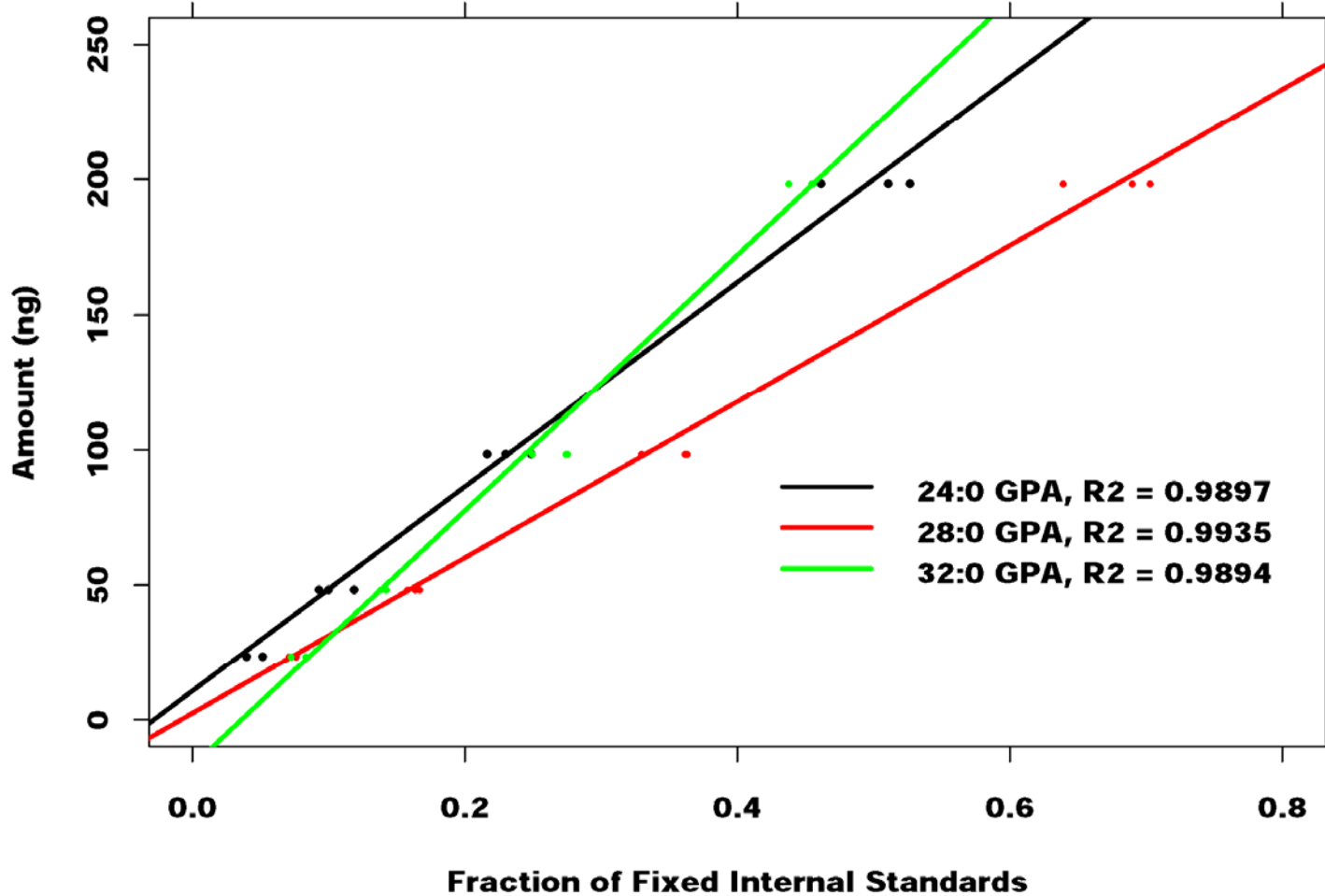
43:6 PC

HPLC Elution Pattern for PC Standards



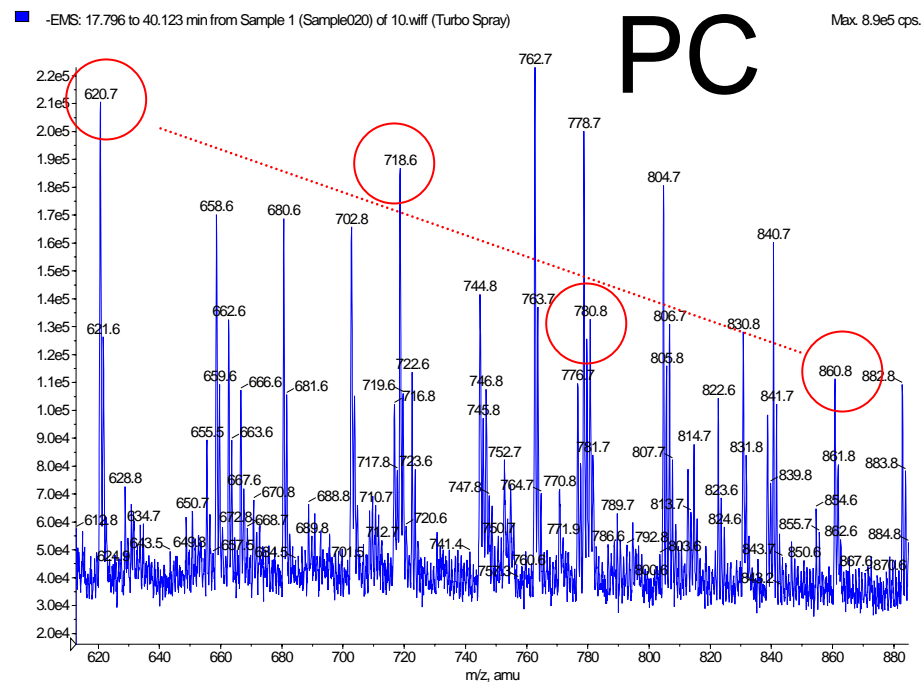
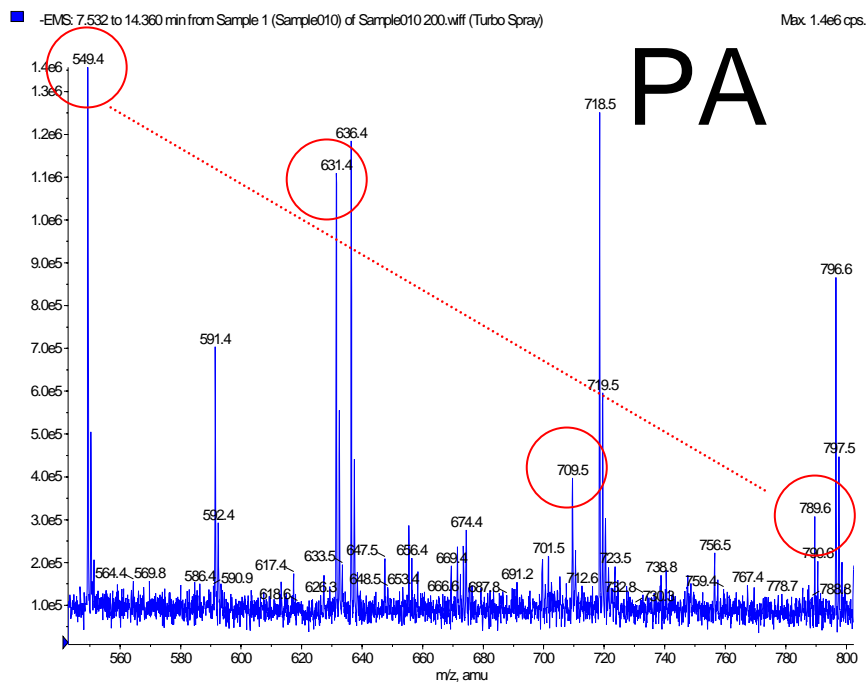
Using this protocol, the heavier standards always elute first, and the smallest last. Carbon number has greater impact on RT than does degree of unsaturation.

Example of 3 Saturated PA Standard Curves



The above curves were generated using even carbon PA standards and fixed amounts of 4 odd-carbon PA internal standards.

Use multiple odd internal standards per class (25:0, 31:1, 37:4, 43:6) covers the diversity of heterogenous, chemically defined space



LC/MS analysis

- **Elution Order of Phospholipid Classes:
PG<PE<PI<PA<PS<<PC**
- **Least Polar< Most Polar**
- **Lyso Lipids Elute a Few Minutes After
Diacyl Variants.**

Identification of Phospholipids by MS/MS Fragmentation

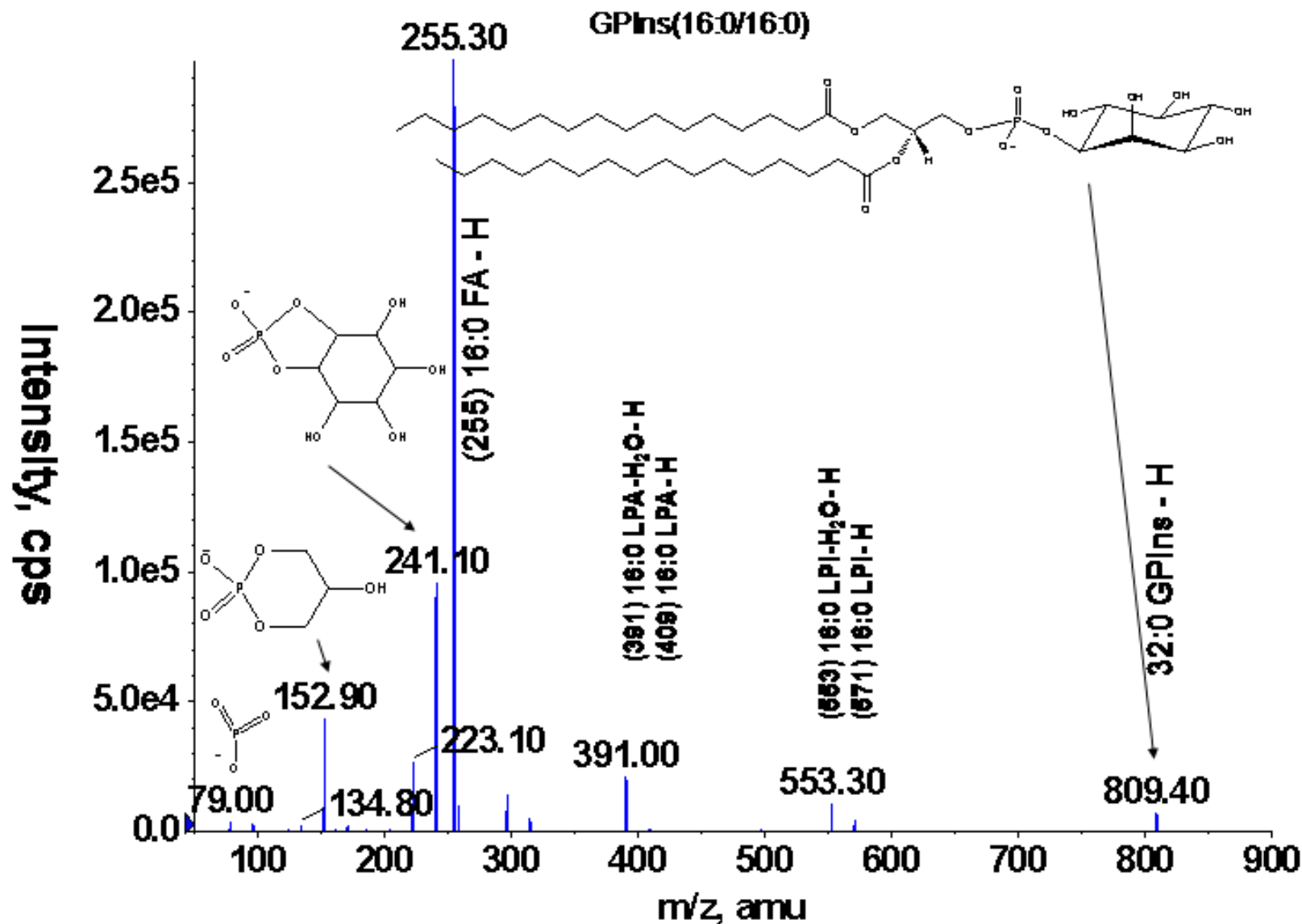
- 1) All six classes can be analyzed in ESI negative mode.
- 2) ESI negative mode is best for gathering structural information.
- 3) *sn*-1 and *sn*-2 fatty acid positions in mixtures of lipids can not be determined.
- 4) Each lipid class (except PA) has characteristic headgroup MS/MS fragments.

	Best Method for Detection	Characteristic Headgroup Fragments	
		ESI (-)	ESI (+)
PA	ESI (-)	no unique fragments	
PC	ESI (+)	224 (PC detected as adduct with anion)	184
PE	ESI (-)	196	NL 141
PG	ESI (-)	227	
PI	ESI (-)	223, 241, 259, 297, 315	
PS	ESI (-)	NL 87	NL 185

Fragmentation of a PI(16:0/16:0) standard

■ -MS2 (809.00) CE (-60) 0.034 to 0.972 min from Sample 1 (809PI) of 809PI.wiff (Turbo Spray)

Max. 3.0e5 cps.



Number of species quantified from a typical LC/MS scan

<u>PA</u>	<u>PC(p)</u>	<u>PE(p)</u>	<u>PG</u>	<u>PI</u>	<u>PS</u>	<u>PThr</u>
18	51(15)	37(13)	18	16	31	3

(e.g., total = 174 from this sample).

To date we have identified > 1200 species of GPL in macrophages (spectra and fragmentation available at

<http://www.lipidmaps.org/> and publications available at <http://www.alexbrownlab.org>).

lipidmaps.org

Standards for over 200
glycerophospholipids

LIPID MAPS -- LIPID Metabolites And Pathways Strategy - Windows Internet Explorer

http://lipidmaps.org/data/standards/standards.php?lipidclass=LMGP

LIPID MAPS -- LIPID Metabolites And Pathways Strategy

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LIPID MAPS

LIPID Metabolites And Pathways Strategy

About Lipid Classification Standards Experimental Data Databases Pathways Tools Protocols Home

Lipid Standards

Library of Glycerophospholipids Standards

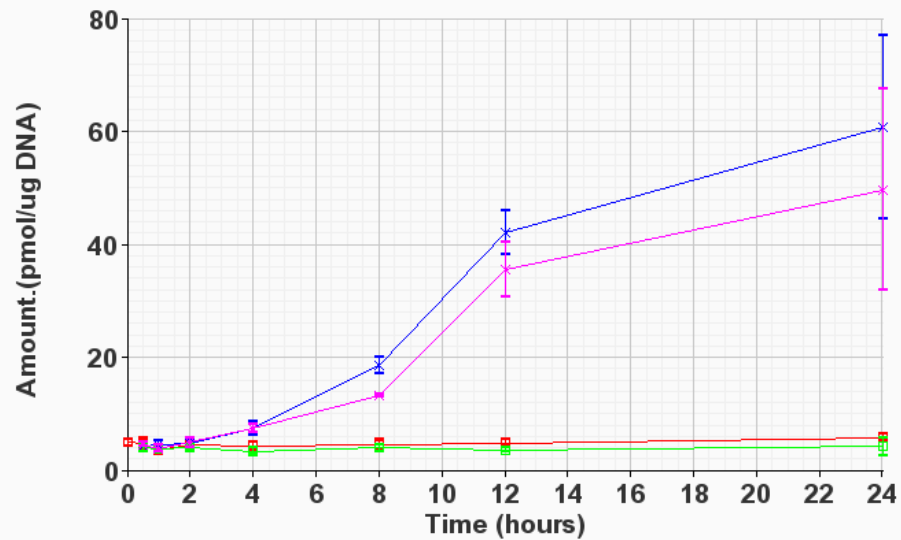
Clicking on a LM_ID displays the structure in GIF (or Chemdraw) format.
Clicking on a MS/MS value (nominal mass of precursor ion) displays the fragmentation spectrum, including structures of principal product ions.
Clicking on a Ref value displays a literature reference(s) pertaining to identification of fragment structures.
[View LC/MS/MS protocols and retention-time data](#)

Lipid Search: Name: e.g. P₁(12:0/12:0)

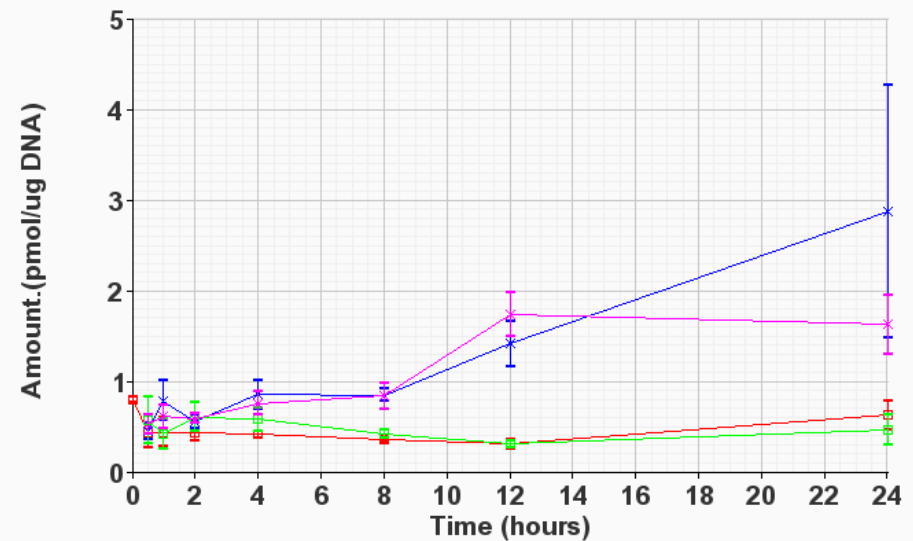
LM_ID	Name	Systematic_Name	MS/MS	Ion	Conditions
LMGP01010407	PC(11:0/11:0)	1,2-diundecanoyl-sn-glycero-3-phosphocholine	594([M+H] ⁺)	[M+H] ⁺	Details
LMGP01010407	PC(11:0/11:0)	1,2-diundecanoyl-sn-glycero-3-phosphocholine	628([M.Cl] ⁻)	[M.Cl] ⁻	Details
LMGP01010429	PC(12:0/12:0)	1,2-didodecanoyl-sn-glycero-3-phosphocholine	622([M+H] ⁺)	[M+H] ⁺	Details
LMGP01010429	PC(12:0/12:0)	1,2-didodecanoyl-sn-glycero-3-phosphocholine	656([M.Cl] ⁻)	[M.Cl] ⁻	Details
LMGP01010001	PC(12:0/13:0)	1-dodecanoyl-2-tridecanoyl-sn-glycero-3-phosphocholine	636([M+H] ⁺)	[M+H] ⁺	Details
LMGP01010001	PC(12:0/13:0)	1-dodecanoyl-2-tridecanoyl-sn-glycero-3-phosphocholine	670([M.Cl] ⁻)	[M.Cl] ⁻	Details
LMGP01010477	PC(14:0/14:0)	1,2-ditetradecanoyl-sn-glycero-3-phosphocholine	678([M+H] ⁺)	[M+H] ⁺	Details
LMGP01010477	PC(14:0/14:0)	1,2-ditetradecanoyl-sn-glycero-3-phosphocholine	712([M.Cl] ⁻)	[M.Cl] ⁻	Details
LMGP01010523	PC(14:1(9Z)/14:1(9Z))	1,2-di-(9Z-tetradecenoyl)-sn-glycero-3-phosphocholine	674([M+H] ⁺)	[M+H] ⁺	Details
LMGP01010523	PC(14:1(9Z)/14:1(9Z))	1,2-di-(9Z-tetradecenoyl)-sn-glycero-3-phosphocholine	708([M.Cl] ⁻)	[M.Cl] ⁻	Details
LMGP01010002	PC(16:0/15:1(14))	1-hexadecanoyl-2-(14-pentadecenoyl)-sn-glycero-3-phosphocholine	718([M+H] ⁺)	[M+H] ⁺	Details
LMGP01010002	PC(16:0/15:1(14))	1-hexadecanoyl-2-(14-pentadecenoyl)-sn-glycero-3-phosphocholine	752([M.Cl] ⁻)	[M.Cl] ⁻	Details
LMGP01010564	PC(16:0/16:0)	1,2-dihexadecanoyl-sn-glycero-3-phosphocholine	762([M+H] ⁺)	[M+H] ⁺	Details
LMGP01010564	PC(16:0/16:0)	1,2-dihexadecanoyl-sn-glycero-3-phosphocholine	796([M.Cl] ⁻)	[M.Cl] ⁻	Details
LMGP01010005	PC(16:0/18:1(9Z))	1-hexadecanoyl-2-(9Z-octadecenoyl)-sn-glycero-3-phosphocholine	760([M+H] ⁺)	[M+H] ⁺	Details
LMGP01010005	PC(16:0/18:1(9Z))	1-hexadecanoyl-2-(9Z-octadecenoyl)-sn-glycero-3-phosphocholine	794([M.Cl] ⁻)	[M.Cl] ⁻	Details
LMGP01010007	PC(16:0/20:4(5Z,8Z,11Z,14Z))	1-hexadecanoyl-2-(5Z,8Z,11Z,14Z-eicosatetraenoyl)-sn-glycero-3-phosphocholine	766([M-CH3] ⁻)	[M-CH3] ⁻	Details
LMGP01010007	PC(16:0/20:4(5Z,8Z,11Z,14Z))	1-hexadecanoyl-2-(5Z,8Z,11Z,14Z-eicosatetraenoyl)-sn-glycero-3-phosphocholine	782([M+H] ⁺)	[M+H] ⁺	Details
LMGP01010008	PC(17:0/14:1(9Z))	1-heptadecanoyl-2-(9Z-tetradecenoyl)-sn-glycero-3-phosphocholine	718([M+H] ⁺)	[M+H] ⁺	Details
LMGP01010008	PC(17:0/14:1(9Z))	1-heptadecanoyl-2-(9Z-tetradecenoyl)-sn-glycero-3-phosphocholine	752([M.Cl] ⁻)	[M.Cl] ⁻	Details

C:\Documents and Se... Internet 100%

Compactin/KDO2 Timecourse: PA(32:0)

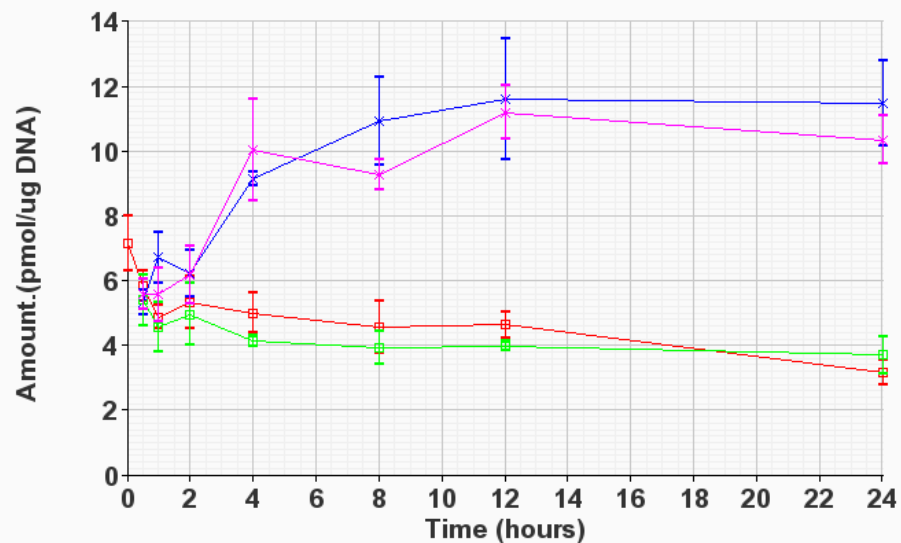


Compactin/KDO2 Timecourse: PG(32:0)

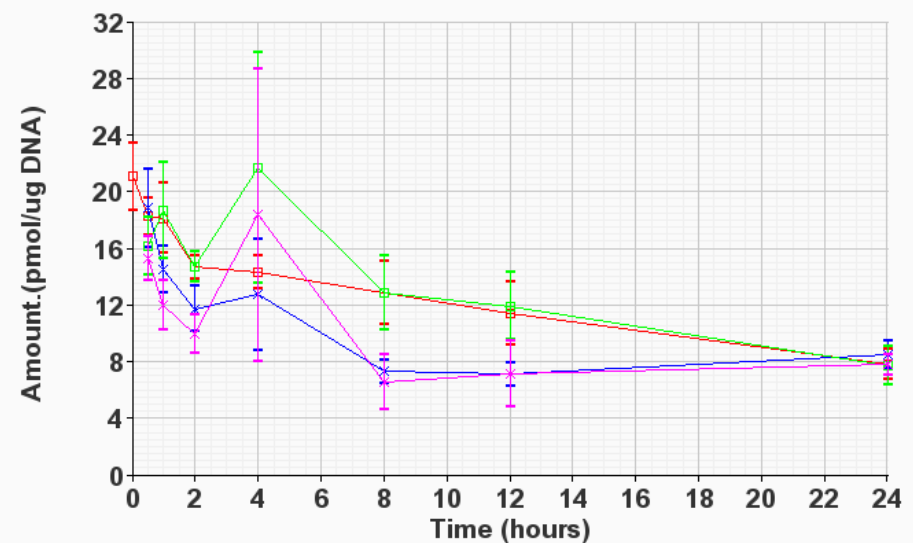


KDO/Compactin experiments in RAW cells (ctrl kdo compactin kdo+compactin)

Compactin/KDO2 Timecourse: PI(34:1)

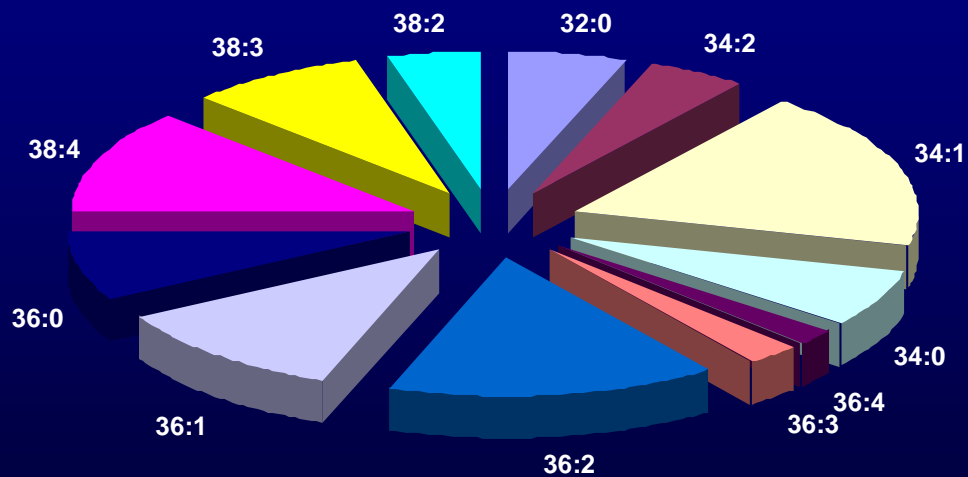


Compactin/KDO2 Timecourse: PI(38:4)



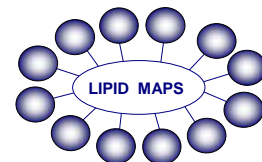
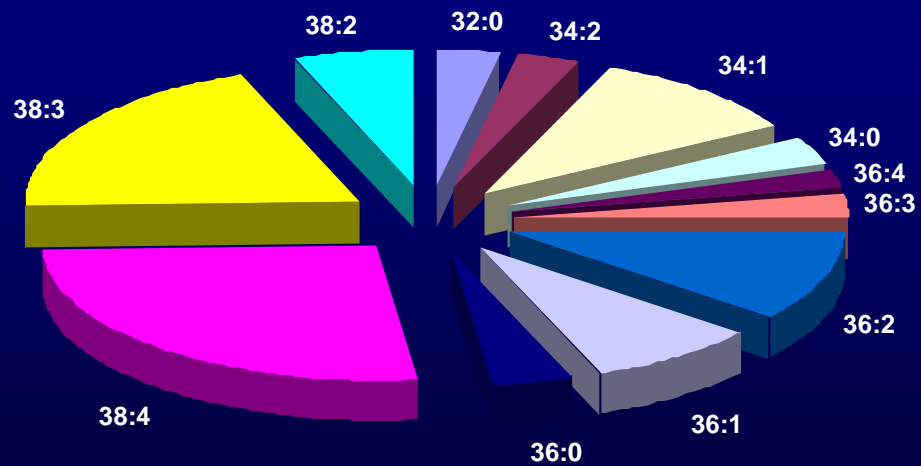
GPA Profile

20 minutes control



GPA Profile

20 minutes UDP



“Challenges and opportunities”

- Novel and Atypical lipids (e.g., ether PI) discovery.
- New MS based assay for PLD activity (PtdBuOH measurements by deuterated BuOH transesterification).
- Define lipome of cells & organisms (e.g., viruses, bacteria, macrophages, tumors).
- Substrate-product relationships (signaling and metabolic networks).