

Metabolomics Workbench and the National Metabolomics Data Repository

University of California San Diego

and

San Diego Supercomputer Center

MetStat summary tool

NIH Common Fund's National Metabolomics Data Repository

(supported by NIH grant, U2C-DK119886)

MetStat Summary Statistics for experimental datasets in NMDR

Search/Summarize by **analysis type** (e.g. GCMS ,LCMS, NMR) and/or MS ion mode (+ or -)

Search/Summarize by **disease association** (cancer, diabetes, obesity, etc.)

Search/Summarize by **species** (human, mouse, rat, etc.)

Search/Summarize by **sample source** (blood, urine, feces, muscle, bacterial cells, etc.)

Summarize by metabolite **structural class**

What metabolites are **detected** within selected criteria (and which are most commonly detected)?

Which metabolites show **significant changes** across experimental conditions in selected data?

What (human) **biochemical pathways** are these metabolites involved in?

What is the average **variance across sample replicates** for a given metabolite?

What is the **ANOVA p-value** for a given metabolite under a given experimental condition?

MetStat: Summary Statistics for experimental datasets in NMDR

View most frequently encountered metabolites in NMDR studies across all conditions

Browse and Search Studies

• Browse

- Summary of all studies
- Summary of all projects (groups of studies)
- Bubble plots of studies by disease, sample source, species, pathway and metabolite class
- MetStat: View most frequently encountered metabolites in NMDR (mapped to RefMet)**

• Search

- Experimental Projects / Studies
- MetStat: Perform meta-analysis on named metabolites across all studies:
 - Refine by analysis type, species, sample source, disease association, metabolite classification and biochemical pathway
- Select Studies by species, sample source or disease association
- Search data/metadata in experimental projects/studies
- Search Untargeted MS data by m/z, retention time, instrumentation
- REST service
 - Use the Metabolomics Workbench REST service to retrieve different types of data



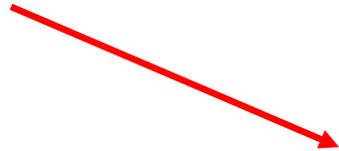
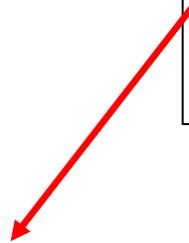
MetStat: Summary table of metabolites most frequently reported in NMDR studies

Perform detailed search (All metabolite names were mapped to RefMet nomenclature) Records to display:

Refmet Name	Studies	Super Class	Main Class	Sub Class
Glutamic acid	452	Organic acids	Amino acids and peptides	Amino acids
Tyrosine	441	Organic acids	Amino acids and peptides	Amino acids
Phenylalanine	437	Organic acids	Amino acids and peptides	Amino acids
Glutamine	435	Organic acids	Amino acids and peptides	Amino acids
Valine	428	Organic acids	Amino acids and peptides	Amino acids
Aspartic acid	423	Organic acids	Amino acids and peptides	Amino acids
Proline	413	Organic acids	Amino acids and peptides	Amino acids
Lysine	407	Organic acids	Amino acids and peptides	Amino acids
Malic acid	404	Organic acids	TCA acids	TCA acids
Tryptophan	395	Organic acids	Amino acids and peptides	Amino acids
Methionine	394	Organic acids	Amino acids and peptides	Amino acids
Isoleucine	392	Organic acids	Amino acids and peptides	Amino acids
Alanine	390	Organic acids	Amino acids and peptides	Amino acids
Serine	384	Organic acids	Amino acids and peptides	Amino acids
Citric acid	377	Organic acids	TCA acids	TCA acids
Leucine	371	Organic acids	Amino acids and peptides	Amino acids
Threonine	367	Organic acids	Amino acids and peptides	Amino acids
Lactic acid	365	Organic acids	Short-chain acids	Short-chain acids
Succinic acid	363	Organic acids	TCA acids	TCA acids
Glycine	354	Organic acids	Amino acids and peptides	Amino acids
Histidine	352	Organic acids	Amino acids and peptides	Amino acids
Ornithine	335	Organic acids	Amino acids and peptides	Amino acids
Asparagine	328	Organic acids	Amino acids and peptides	Amino acids
Fumaric acid	324	Organic acids	TCA acids	TCA acids
Stearic acid	320	Fatty Acyls	Fatty acids	Saturated FA
Oleic acid	319	Fatty Acyls	Fatty acids	Unsaturated FA
Taurine	313	Organic acids	Sulfonic acids	Sulfonic acids
Palmitic acid	310	Fatty Acyls	Fatty acids	Saturated FA
AMP	305	Nucleic acids	Purines	Purine ribonucleoside monophosphates
Arginine	295	Organic acids	Amino acids and peptides	Amino acids
Hypoxanthine	279	Nucleic acids	Purines	Hypoxanthines
Pyroglutamic acid	273	Organoheterocyclic compounds	Pyrroline carboxylic acids	Pyrroline carboxylic acids
Oxoglutaric acid	270	Organic acids	TCA acids	TCA acids
Creatinine	266	Organoheterocyclic compounds	Azolines	Imidazolines
Glucose	262	Carbohydrates	Monosaccharides	Monosaccharides
Citrulline	260	Organic acids	Amino acids and peptides	Amino acids
LPC 16:0	255	Glycerophospholipids	Glycerophosphocholines	LPC
Pyruvic acid	254	Organic acids	Short-chain acids	Short-chain acids
Myristic acid	249	Fatty Acyls	Fatty acids	Saturated FA
Pantothenic acid	248	Organic acids	Amino acids and peptides	Amino acids
Uric acid	244	Nucleic acids	Purines	Xanthines
Uridine	242	Nucleic acids	Pyrimidines	Pyrimidine ribonucleosides
Inosine	239	Nucleic acids	Purines	Purine ribonucleosides
Carnitine	238	Organic nitrogen compounds	Carnitines	Carnitines
Palmitoleic acid	238	Fatty Acyls	Fatty acids	Unsaturated FA
Linoleic acid	236	Fatty Acyls	Fatty acids	Unsaturated FA
Arachidonic acid	235	Fatty Acyls	Fatty acids	Unsaturated FA
Xanthine	232	Nucleic acids	Purines	Xanthines

Links to MW structure database and list of studies containing each metabolite

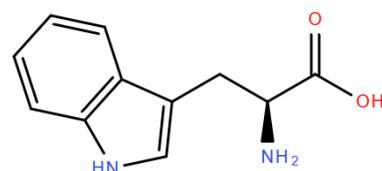
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Malic acid	404	Organic acids	TCA acids	TCA acids
Tryptophan	395	Organic acids	Amino acids and peptides	Amino acids
Methionine	394	Organic acids	Amino acids and peptides	Amino acids
Isoleucine	392	Organic acids	Amino acids and peptides	Amino acids
Alanine	390	Organic acids	Amino acids and peptides	Amino acids



Structure (MW database)

Metabolomics Structure Database

Download file MDLMOL



MW REGNO: 37505

PubChem CID: 6305

Common Name: L-Tryptophan

List of Studies

Study_id	Study_title
ST000009	Mixed meal tolerance
ST000010	Lung Cancer Cells 4
ST000011	African Metabolomics
ST000016	NPM-ALK metabolic regulation
ST000017	Rat HCR/LCR Stamina Study
ST000040	Heatshock response of C. elegans using IROA (I)
ST000041	High PUFA diet in humans
ST000042	BALF Control vs ALI by RPLC-MS
ST000043	MDA-MB-231 cells and p38 gamma knockdown

MetStat query buider: Select criteria, e.g. species, sample source, analysis type, ion mode, disease association, metabolite class.

Browse and Search Studies

- Browse
 - Summary of all studies
 - Summary of all projects (groups of studies)
 - Bubble plots of studies by disease, sample source, species, pathway and metabolite class
 - MetStat: View most frequently encountered metabolites in NMDR (mapped to RefMet)
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 - REST service
 - Use the Metabolomics Workbench REST service to retrieve different types of data

MetStat: Generate Metabolite report for studies on the Metabolomics Workbench

Tables of metabolites (identified by RefMet name) show the **number of unique studies containing that metabolite** along with the median value of the **relative standard deviation (RSD)** across all those studies. ($RSD=100 \cdot \text{Std.Deviation}/\text{mean}$). RSD is first calculated for each experimental condition within each analysis to assess the variance across sample replicates.

The RefMet metabolite names are mapped to the **MW classification system** and displayed as "Main class" and "Sub class". Rows are also color-coded based on 11 top-level classification groups: Amino acids/peptides, Glycerolipids, Fatty acyls, Terpenoids, Sugars, Phospholipids, Sterols, Sphingolipids, Nucleic acids, Flavonoids and "Others".

ANOVA p-values and FDR-corrected values are calculated for each metabolite and each distinct experimental condition in every analysis.

RefMet metabolite names are hyperlinked to the molecular structures in the MW database and to the relevant **biochemical pathways** in HMDB and KEGG (where applicable)

Analysis Type:	<input type="text"/>	MS Ion Mode:	<input type="text"/>
Chromatography Type:	<input type="text"/>		
Disease:	<input type="text"/>		
Sample source:	Blood (183)		
Species:	Human (183)	Sp. class:	<input type="text"/>
RefMet name:	Contains <input type="text"/>		(case insensitive)
Metabolite superclass:	All		
Human pathway:	<input type="text"/>		
Records to display:	200	Generate	Reset

- 1 Amino acid/peptides
- 2 Glycerolipids
- 3 Fatty acyls
- 4 Terpenoids
- 5 Sugars
- 6 Phospholipids
- 7 Sterols
- 8 Sphingolipids
- 9 Nucleic acids
- 10 Flavonoids
- 11 Others

In this example, all human studies with blood* as the sample source are selected

* "Blood" may refer to whole blood, serum or plasma-see individual study metadata for details

MetStat summary table of human metabolites detected in blood

Sorted by number of studies in which that metabolite is reported

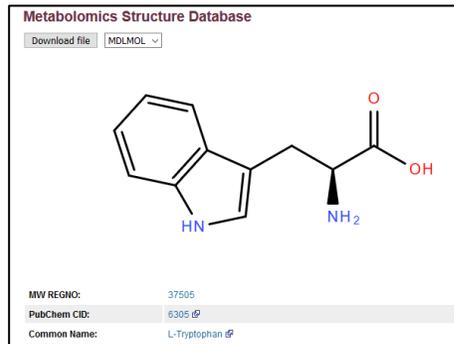
MetStat: Search parameters: Source:Blood Species:Human | Most significant ANOVA measurements

Refmet Name [Pathways]	Studies [Data Details]	RSD	Main Class	Sub Class
Proline [P]	111 [Data]	32.29	Amino acids and peptides	Amino acids
Tryptophan [P]	110 [Data]	22.04	Amino acids and peptides	Amino acids
Phenylalanine [P]	110 [Data]	21.72	Amino acids and peptides	Amino acids
Tyrosine [P]	108 [Data]	25.37	Amino acids and peptides	Amino acids
Valine [P]	108 [Data]	24.01	Amino acids and peptides	Amino acids
Glutamine [P]	105 [Data]	25.71	Amino acids and peptides	Amino acids
Histidine [P]	105 [Data]	25.80	Amino acids and peptides	Amino acids
Methionine [P]	105 [Data]	26.67	Amino acids and peptides	Amino acids
Lysine [P]	105 [Data]	26.12	Amino acids and peptides	Amino acids
Glutamic acid [P]	101 [Data]	43.28	Amino acids and peptides	Amino acids
Ornithine [P]	101 [Data]	34.02	Amino acids and peptides	Amino acids
Serine [P]	99 [Data]	26.11	Amino acids and peptides	Amino acids
Isoleucine [P]	99 [Data]	28.60	Amino acids and peptides	Amino acids
Leucine [P]	98 [Data]	27.90	Amino acids and peptides	Amino acids
Creatinine [P]	95 [Data]	29.39	Azolines	Imidazolines
Stearic acid [P]	94 [Data]	30.47	Fatty acids	Saturated FA
Alanine [P]	93 [Data]	26.38	Amino acids and peptides	Amino acids
Uric acid [P]	92 [Data]	25.65	Purines	Xanthines
Linoleic acid [P]	91 [Data]	50.53	Fatty acids	Unsaturated FA
Asparagine [P]	89 [Data]	25.38	Amino acids and peptides	Amino acids
Threonine [P]	88 [Data]	27.93	Amino acids and peptides	Amino acids
Palmitic acid [P]	88 [Data]	33.31	Fatty acids	Saturated FA
Oleic acid [P]	88 [Data]	49.22	Fatty acids	Unsaturated FA
Aspartic acid [P]	87 [Data]	39.78	Amino acids and peptides	Amino acids
Taurine [P]	84 [Data]	39.66	Sulfonic acids	Sulfonic acids
Arachidonic acid [P]	84 [Data]	42.06	Fatty acids	Unsaturated FA
Citrulline [P]	83 [Data]	29.88	Amino acids and peptides	Amino acids
Lactic acid [P]	82 [Data]	37.17	Short-chain acids	Short-chain acids
Citric acid [P]	82 [Data]	30.27	TCA acids	TCA acids
Palmitoleic acid [P]	82 [Data]	63.72	Fatty acids	Unsaturated FA
Myristic acid [P]	81 [Data]	42.07	Fatty acids	Saturated FA
Glycine [P]	81 [Data]	30.30	Amino acids and peptides	Amino acids
Arginine [P]	81 [Data]	26.07	Amino acids and peptides	Amino acids
Malic acid [P]	80 [Data]	35.52	TCA acids	TCA acids
Hypoxanthine [P]	80 [Data]	55.48	Purines	Hypoxanthines
Succinic acid [P]	80 [Data]	33.90	TCA acids	TCA acids
Cholesterol [P]	79 [Data]	24.16	Sterols	Cholesterols
Pyroglutamic acid [P]	78 [Data]	31.77	Pyroline carboxylic acids	Pyroline carboxylic acids
Kynurenine [P]	75 [Data]	30.52	Butyrophenones	Butyrophenones
LPC 16:0 [P]	74 [Data]	35.90	Glycerophosphocholines	LPC
Carnitine [P]	73 [Data]	23.34	Carnitines	Carnitines

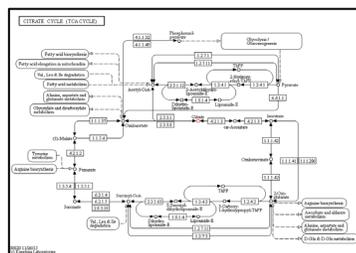
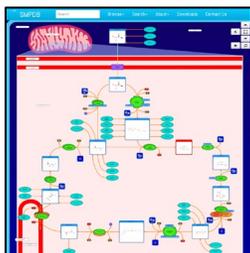
List of Studies

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ST000043	MDA-MB-231 cells and p38 gamma knockdown

Structure (MW db)



[P]:Human Pathways (SMP/KEGG)



Relative standard deviation (RSD) = $100 \times \text{Standard deviation} / \text{mean}$

The RSD is calculated separately for each experimental condition within each study.

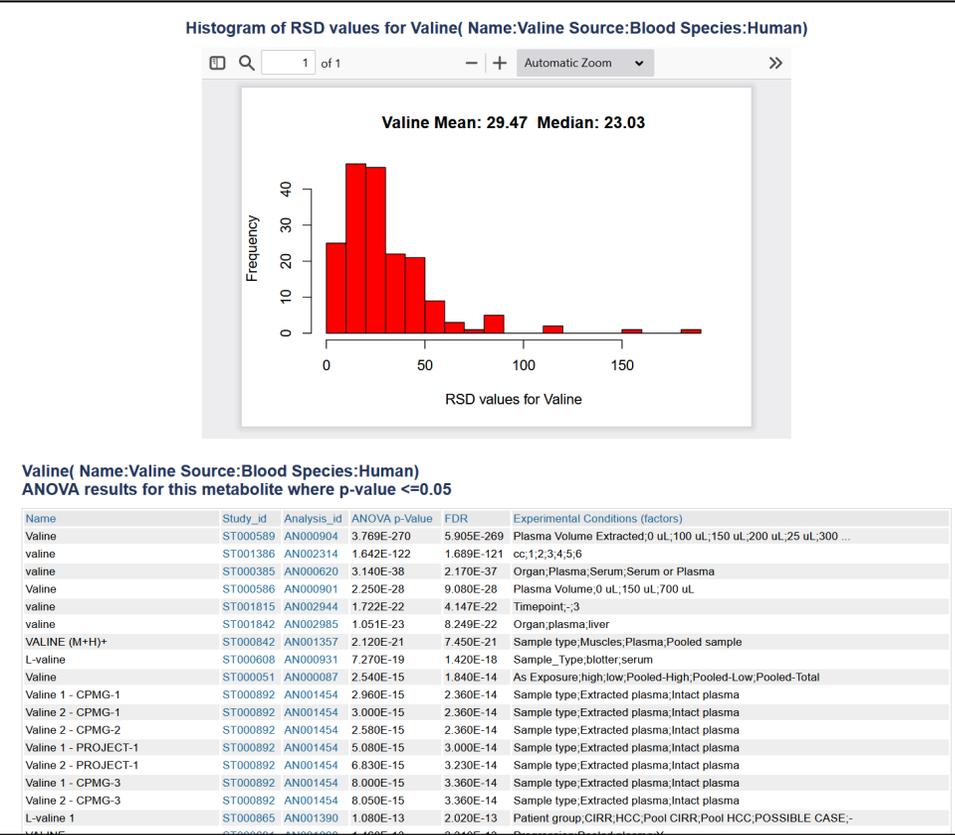
It is a measure of the variance across sample replicates

MetStat “data” link displays a histogram of RSD data across all studies containing Valine

Additional data on ANOVA statistics in each study and RSD/replicate information

MetStat: Search parameters: Source:Blood Species:Human | Most significant ANOVA measurements

Refmet Name [Pathways]	Studies [Data Details]	RSD	Main Class	Sub Class
Proline [P]	111 [Data]	32.29	Amino acids and peptides	Amino acids
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Pyroglutamic acid [P]	78 [Data]	31.77	Pyroline carboxylic acids	Pyroline carboxylic acids
Kynurenine [P]	75 [Data]	30.52	Butyrophenones	Butyrophenones
LPC 16:0 [P]	74 [Data]	35.90	Glycerophosphocholines	LPC
Carnitine [P]	73 [Data]	23.34	Carnitines	Carnitines



Valine(Name:Valine Source:Blood Species:Human)
List of studies, analyses, submitted metabolite names, experimental conditions and RSD values

Replicate numbers reflect the number of replicates for each experimental condition where the measured value was not null

Name	Study_id	Analysis_id	Factors	Range(RSD)	Replicates
Valine	ST000046	AN000079	Cognitive Status:AD	23.56	30
Valine	ST000046	AN000079	Cognitive Status:CN	17.51	30
Valine	ST000046	AN000079	Cognitive Status:MCI	20.69	30
Valine	ST000051	AN000087	As Exposure:high	19.32	25
Valine	ST000051	AN000087	As Exposure:low	18.43	25
valine	ST000062	AN000100	Source:Group 1 - Score 0	19.37	48
valine	ST000062	AN000100	Source:Group 2 - Score 50	18.63	49
Val_Valine	ST000091	AN000145	Treatment:Control	16.59	9
Val_Valine	ST000091	AN000145	Treatment:Insulin Deprived	22.96	8
Val_Valine	ST000091	AN000145	Treatment:Insulin Treatment	20.16	9

Search summary showing metabolite name, median RSD and classification

Search parameters: Source:Diabetes | Most significant ANOVA measurements

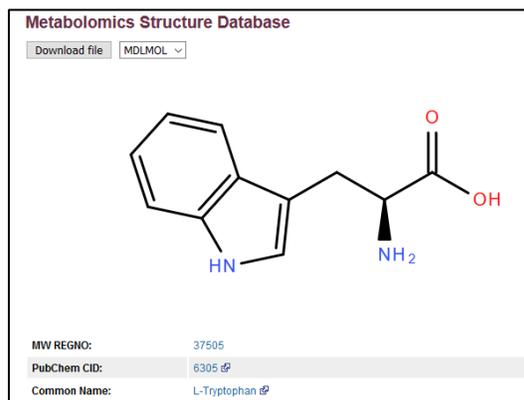
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Tyrosine [P]	26 [Data]	22.18	Amino acids and peptides	Amino acids
Glutamic acid [P]	26 [Data]	29.46	Amino acids and peptides	Amino acids
Tryptophan [P]	25 [Data]	23.41	Amino acids and peptides	Amino acids
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Lysine [P]	24 [Data]	25.48	Amino acids and peptides	Amino acids
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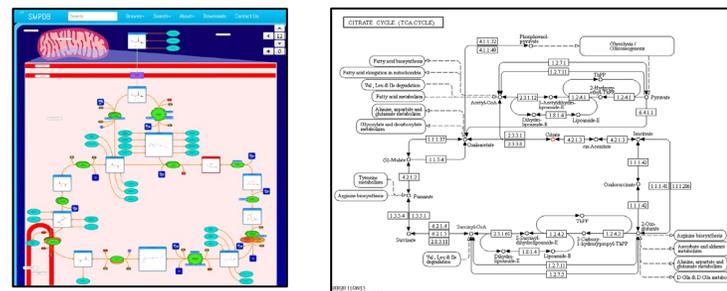
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It is a measure of the variance across sample replicates

Structure (MW db)



Human Pathways (SMP/KEGG)



List of Studies

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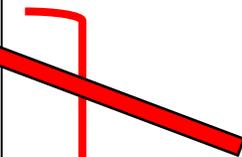
List of human studies on blood that report Proline

List of Studies (Metabolite:Proline Source:Blood Species:Human)

Study_id	Analysis_id	Study_title	Source	Species	Disease	Institute	Units(range)
ST001037	AN001698	High Resolution GC-MS and FID Metabolomics of Human Serum	Blood	Human		Wake Forest Baptist Medical Center	Abundance
ST000450	AN000705	Metabolic features of chronic fatigue syndrome	Blood	Human	Chronic fatigue syndrome	University of California, San Diego	Area under curve
ST000617	AN000947	Validation of the application of targeted metabolomic approach in the diagnosis of CFS	Blood	Human	Chronic fatigue syndrome	University of California, San Diego	Area under curve
ST000041	AN000062	High PUFA diet in humans	Blood	Human		University of Michigan	Counts
ST000041	AN000063	High PUFA diet in humans	Blood	Human		University of Michigan	Counts
ST000105	AN000173	SCOR Metabolomics	Blood	Human		University of Chicago	Counts
ST000105	AN000174	SCOR Metabolomics	Blood	Human		University of Chicago	Counts
ST000106	AN000175	IWMS Study 1:Weight comparison of obese and lean patients	Blood	Human	Obesity	University of Michigan	Counts
ST000106	AN000176	IWMS Study 1:Weight comparison of obese and lean patients	Blood	Human	Obesity	University of Michigan	Counts
ST000368	AN000602	Investigation of metabolomic blood biomarkers for detection of adenocarcinoma lung cancer	Blood	Human	Cancer	University of California, Davis	Counts

...

ST001515	AN002511	A Metabolomic Signature of Glucagon Action in Healthy Individuals with Overweight/Obesity Humans	Blood	Human	Obesity	Translational Research Institute-AdventHealth Orlando	scaled units
ST000091	AN000145	Quantitative Metabolomics by 1H-NMR and LC-MS/MS Confirms Altered Metabolic Pathways in Diabetes	Blood	Human	Diabetes	Mayo Clinic	uM
ST000137	AN000219	Metabolomics in sarcoidosis	Blood	Human	Sarcoidosis	Wayne State University	uM
ST000168	AN000262	Effect of Insulin Sensitizer Therapy on Amino Acids and Their Metabolites	Blood	Human	Diabetes	Mayo Clinic	uM
ST000435	AN000685	Quantitative measurements of amino acids in T1D poor control, good control, and controls.	Blood	Human	Diabetes	Mayo Clinic	uM
ST000483	AN000749	Amino Acid Quantification of obese patients on a 16 week caloric restriction from Plasma	Blood	Human	Obesity	Mayo Clinic	uM
ST000491	AN000757	Sleep apnea and cardiovascular samples amino acid metabolites	Blood	Human	Sleep apnea	Mayo Clinic	uM
ST000524	AN000802	Effects of Curcumin Supplementation on the Amino Acid Concentration of Older Adults: Relation to Vascular Function	Blood	Human	Heart disease	Mayo Clinic	uM
ST000605	AN000926	Whole blood reveals more metabolic detail of the human metabolome than serum as measured by 1H-NMR spectroscopy: Implications for sepsis metabolomics	Blood	Human		University of Michigan	uM
ST000641	AN000973	Targeted Amino Acids in American Indian Adolescents (part II)	Blood	Human	Diabetes	Mayo Clinic	uM
ST000783	AN001239	Absolute Quantification of 180 metabolites in serum from african american and european american in prostate cancer and case control samples	Blood	Human	Cancer	Baylor College of Medicine	uM
ST000785	AN001244	Pharmacometabolomics of L-Carnitine Treatment Response Phenotypes in Patients with Septic Shock	Blood	Human	Sepsis	University of Michigan	uM
ST000825	AN001311	CHEAR Christiani Biocrates	Blood	Human		RTI International	uM
ST000826	AN001414	CHEAR Christiani NMR	Blood	Human		RTI International	uM
ST000876	AN001413	Human serum for a patient with neuropathy being treated with L-serine.	Blood	Human	Neuropathy	University of Helsinki	uM
ST000944	AN001549	Amino Acids, Acylcarnitine, & Insulin for P20 Participants	Blood	Human		University of Michigan	uM
ST000995	AN001624	Amino Acid Concentrations of Primary Sclerosing Cholangitis (part I)	Blood	Human		Mayo Clinic	uM
ST001012	AN001654	Amino Acid Concentrations in Serum for Muscle Wasting in Cancer Cachexia (part-VII)	Blood	Human	Cachexia	Mayo Clinic	uM
ST001097	AN001785	Metabolomics of Metabolic Risk in Patients Taking Atypical Antipsychotics	Blood	Human	Schizophrenia	University of Michigan	uM
ST001176	AN001952	Metabolite changes in human plasma before and after YF17D vaccination in symptomatic and asymptomatic subjects	Blood	Human	Yellow fever	Duke-NUS Medical School	uM
ST001295	AN002156	Estimating Platelet Mitochondrial Function in Patients with Sepsis - WB NMRs (part-II)	Blood	Human	Sepsis	University of Michigan, University of Mississippi, University of Minnesota	uM
ST001319	AN002195	Pre-treatment L-Carnitine Pharmacometabolomics in Sepsis (CaPS) Patients	Blood	Human	Sepsis	University of Michigan	uM
ST001354	AN002253	48 hours post-treatment L-Carnitine Pharmacometabolomics in Sepsis (CaPS) Patients	Blood	Human	Sepsis	University of Michigan	uM
ST001521	AN002533	Plasma metabolites of known identity profiled using hybrid nontargeted methods (part-III)	Blood	Human		Broad Institute of MIT and Harvard	unitless peak areas



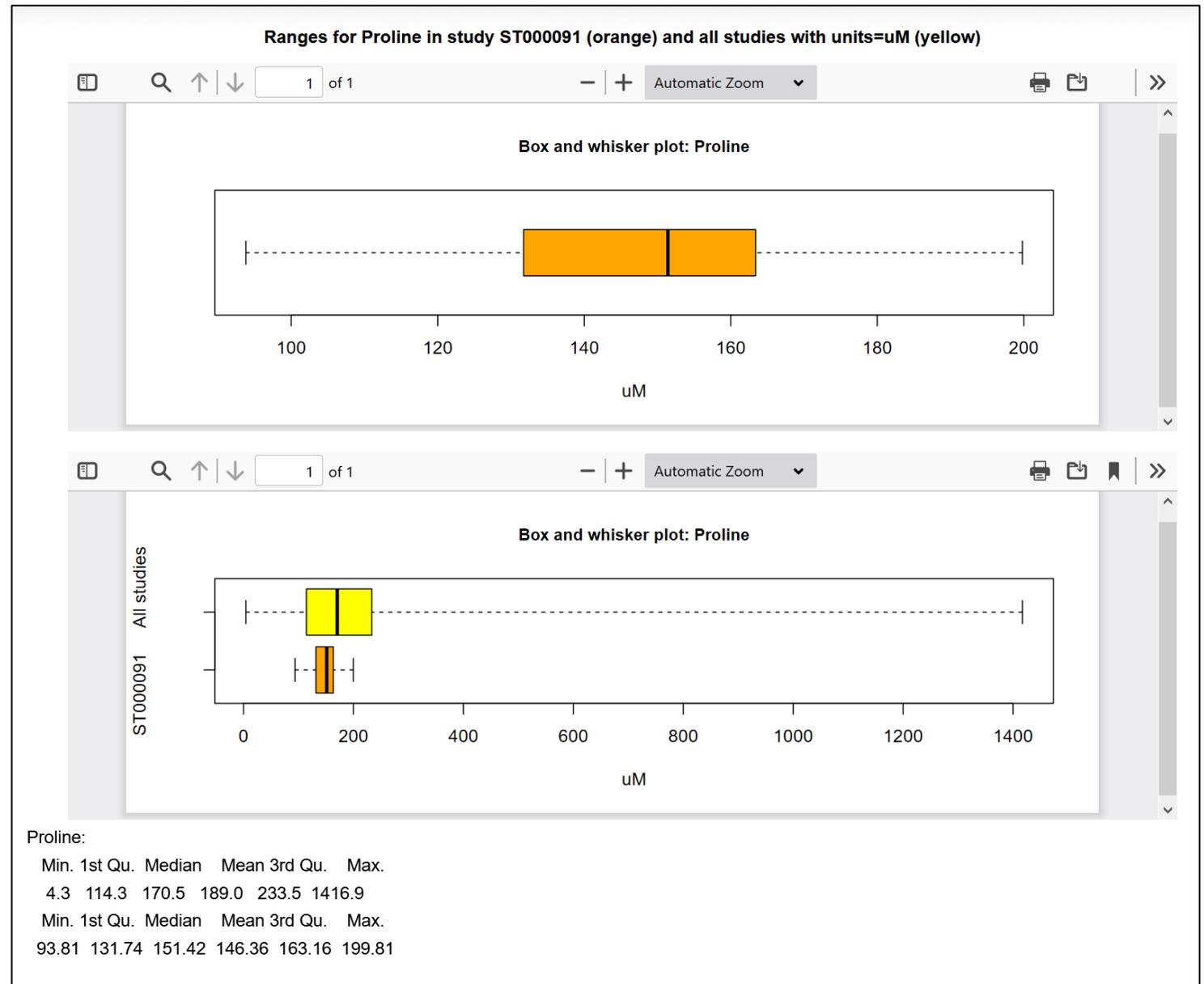
Click on a study link in the "Units(range) column

Focus on the targeted assays that report quantitative results (untargeted assays that report peak intensity, area, etc. are no good)

Boxplot for Proline in human blood

Study ST000091

Comparison with all studies (yellow) that report proline in human blood. Notice the outlier(s) since many different studies are involved. However, the median is not significantly affected.



MetStat query buider: Select criteria, e.g. species, sample source, analysis type, ion mode, disease association, metabolite class.

Analysis Type: LCMS **MS Ion Mode:** NEGATIVE
Chromatography Type: HILIC
Species: **Sp. class:**
Disease:
Sample source: Blood (32)
RefMet name: Contains (case insensitive)
Metabolite superclass: All
Human pathway:
Records to display: All **Generate** **Reset**

- 1 Amino acid/peptides
- 2 Glycerolipids
- 3 Fatty acyls
- 4 Terpenoids
- 5 Sugars

MetStat: Search parameters: Source:Blood Analysis Type:LCMS Ion mode:NEGATIVE Chromatography type:HILIC | Most significant ANOVA measurements

ANOVA results for all metabolites where p-value <=0.05 (Source:Blood Analysis Type:LCMS Ion mode:NEGATIVE Chromatography type:HILIC)

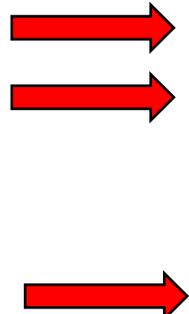
Refmet Name	Study_id	Analysis_id	ANOVA p-Value	FDR	Experimental Conditions (factors)
Glutathione	ST000121	AN000203	8.370E-169	1.070E-166	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
FAO	ST000121	AN000203	6.330E-163	4.050E-161	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
ADP-glucose	ST000121	AN000203	2.470E-155	1.050E-153	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
ITP	ST000121	AN000203	2.540E-151	5.420E-150	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
ATP	ST000121	AN000203	6.460E-147	1.180E-145	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
NAD+	ST000121	AN000203	2.830E-146	4.530E-145	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
FMN	ST000121	AN000203	4.560E-145	6.490E-144	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
GDP	ST000121	AN000203	1.930E-131	1.900E-130	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
Geranyl pyrophosphate	ST000121	AN000203	8.430E-131	7.190E-130	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
4-Hydroxybenzoic acid	ST000121	AN000203	5.670E-128	4.270E-127	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
6-Phosphogluconic acid	ST000121	AN000203	2.170E-127	1.550E-126	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
NADP+	ST000121	AN000203	4.900E-125	3.140E-124	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
NADPH	ST000121	AN000203	8.170E-125	4.880E-124	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
oAMP	ST000121	AN000203	1.200E-123	6.990E-123	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
Creatine	ST000121	AN000203	2.430E-123	1.350E-122	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
Propionyl-CoA	ST000121	AN000203	1.070E-120	5.700E-120	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
UDP-glucose	ST000121	AN000203	6.130E-120	3.140E-119	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
UDP-N-acetylglucosamine	ST000121	AN000203	2.620E-118	1.290E-117	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
Taurine	ST000121	AN000203	3.650E-115	1.730E-114	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
N-acetyl-D-glucosamine-1-phosphate	ST000121	AN000203	7.400E-115	3.390E-114	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
Phosphocreatine	ST000121	AN000203	6.970E-109	3.660E-108	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
Glutamic acid	ST000121	AN000203	9.910E-108	4.230E-107	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
Citrulline	ST000121	AN000203	2.180E-104	9.000E-104	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
Creatinine	ST000121	AN000203	1.060E-101	4.130E-101	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
Homocysteic acid	ST000121	AN000203	1.130E-101	4.250E-101	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
Acetoacetic acid	ST000121	AN000203	2.680E-101	9.810E-101	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
Ornithine	ST000121	AN000203	1.720E-100	5.940E-100	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
Tryptophan	ST000121	AN000203	5.110E-100	1.720E-99	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
Proline	ST000121	AN000203	1.020E-99	3.250E-99	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...
Serine	ST000121	AN000203	1.000E-99	1.250E-99	Tissue:Epидidymal white adipose (fat),Gastrocnemius (skeleta...

MetStat: Search parameters: Source:Blood Analysis Type:LCMS Ion mode:NEGATIVE Chromatography type:HILIC | Most significant ANOVA measurements

Refmet Name [Pathways]	Studies [Data Details]	RSD	Main Class	Sub Class
Lactic acid [P]	23 [Data]	34.01	Short-chain acids	Short-chain acids
Succinic acid [P]	21 [Data]	36.45	TCA acids	TCA acids
Glucose [P]	17 [Data]	22.87	Monosaccharides	Hexoses
Uracil [P]	17 [Data]	38.66	Pyrimidines	Pyrimidines
Taurine [P]	17 [Data]	26.77	Sulfonic acids	Sulfonic acids
Pyruvic acid [P]	17 [Data]	35.50	Short-chain acids	Short-chain acids
Malic acid [P]	17 [Data]	23.72	TCA acids	TCA acids
Fumaric acid [P]	17 [Data]	31.66	TCA acids	TCA acids
Aspartic acid [P]	17 [Data]	26.48	Amino acids and peptides	Amino acids
Orotic acid [P]	15 [Data]	46.14	Pyrimidines	Pyrimidine carboxylic acids
Oxoglutaric acid [P]	15 [Data]	34.52	TCA acids	TCA acids
Gluconic acid [P]	15 [Data]	32.80	Monosaccharides	Sugar acids
Hypoxanthine [P]	15 [Data]	53.18	Purines	Hypoxanthines
Xanthine [P]	15 [Data]	52.44	Purines	Xanthines
Allantoin [P]	15 [Data]	43.41	Ureas	Ureides
Uridine [P]	14 [Data]	26.52	Pyrimidines	Pyrimidine ribonucleosides
Myo-inositol [P]	14 [Data]	30.02	Alcohols and polyols	Inositols
Citric acid [P]	14 [Data]	37.70	TCA acids	TCA acids
Stearic acid [P]	13 [Data]	29.41	Fatty acids	Saturated FA
Uric acid [P]	13 [Data]	31.45	Purines	Xanthines
ADP [P]	12 [Data]	39.99	Purines	Purine rNDP
sn-Glycero-3-phosphate [P]	12 [Data]	26.41	Organic phosphoric acids	Organic phosphoric acids
Glyceric acid [P]	12 [Data]	19.46	Monosaccharides	Sugar acids
Benzoic acid [P]	12 [Data]	37.94	Benzoic acids	Benzoic acids
Pantothenic acid [P]	12 [Data]	42.07	Amino acids and peptides	Amino acids
Pyroglutamic acid [P]	11 [Data]	38.63	Pyrraline carboxylic acids	Pyrraline carboxylic acids
Oleic acid [P]	11 [Data]	41.57	Fatty acids	Unsaturated FA
Indoxyl sulfate [P]	11 [Data]	46.04	Indoles	Indoles
Quinic acid [P]	10 [Data]	55.68	Alcohols and polyols	Quinic acids
Hippuric acid [P]	10 [Data]	78.29	Benzamides	Hippuric acids
Sorbitol [P]	10 [Data]	54.40	Monosaccharides	Sugar alcohols
Phosphoenolpyruvic acid [P]	10 [Data]	39.18	Short-chain acids	Short-chain acids
2-Hydroxyglutaric acid [P]	10 [Data]	28.59	Fatty acids	Hydroxy FA
Fructose [P]	10 [Data]	30.19	Monosaccharides	Hexoses
Ribose 5-phosphate [P]	10 [Data]	15.89	Monosaccharides	Monosaccharide phosphates
Pseudouridine [P]	9 [Data]	20.17	Pyrimidines	Pyrimidine ribonucleosides

In this example, all studies with blood as the sample source using LCMS and HILIC chromatography in negative ion mode are selected

MetStat query buider: Select criteria, e.g. species, sample source, analysis type, ion mode, disease association, metabolite class.



Analysis Type:	LCMS ▾	MS Ion Mode:	NEGATIVE ▾	<ul style="list-style-type: none"> 1 Amino acid/peptides 2 Glycerolipids 3 Fatty acyls 4 Terpenoids 5 Sugars 6 Phospholipids 7 Sterols 8 Sphingolipids 9 Nucleic acids 10 Flavonoids 11 Others
Chromatography Type:	▾			
Species:	Human (227) ▾	Sp. class:	▾	
Disease:	▾			
Sample source:	▾			
RefMet name:	Contains ▾		(case insensitive)	
Metabolite superclass:	All ▾			
Human pathway:	Citric Acid Cycle ▾			
Records to display:	All ▾			

MetStat: Search parameters: Analysis Type:LCMS Ion mode:NEGATIVE Species:Human Pathway ID:SMP00057 | [Most significant ANOVA measurements](#)

Refmet Name [Pathways]	Studies [Data Details]	RSD	Main Class	Sub Class
Malic acid [P]	107 [Data]	32.79	TCA acids	TCA acids
Citric acid [P]	84 [Data]	30.89	TCA acids	TCA acids
Succinic acid [P]	79 [Data]	32.84	TCA acids	TCA acids
ADP [P]	62 [Data]	35.86	Purines	Purine rNDP
Fumaric acid [P]	61 [Data]	35.13	TCA acids	TCA acids
Pyruvic acid [P]	60 [Data]	37.81	Short-chain acids	Short-chain acids
Oxoglutaric acid [P]	60 [Data]	49.35	TCA acids	TCA acids
ATP [P]	52 [Data]	41.12	Purines	Purine rNTP
NAD+ [P]	40 [Data]	34.97	Nicotinamides	Nicotinamide dinucleotides
FAD [P]	35 [Data]	31.58	Flavins	Flavin nucleotides
NADH [P]	34 [Data]	36.65	Nicotinamides	Nicotinamide dinucleotides
cis-Aconitic acid [P]	30 [Data]	39.01	TCA acids	TCA acids
Oxaloacetic acid [P]	26 [Data]	25.02	TCA acids	TCA acids
GDP [P]	25 [Data]	40.99	Purines	Purine rNDP
Acetyl-CoA [P]	22 [Data]	37.03	Fatty esters	Acyl CoAs
GTP [P]	17 [Data]	29.44	Purines	Purine rNTP
Biotin [P]	11 [Data]	20.08	Heterocyclic compounds	Biotin
Coenzyme A [P]	5 [Data]	30.56	Purines	Coenzyme A
Lipoamide [P]	3 [Data]	69.53	Fatty amides	Primary amides
Thiamine diphosphate [P]	3 [Data]	80.85	Pyrimidines	Thiamine phosphates

In this example, human studies using LCMS in negative ion mode for Citric acid cycle metabolites are selected

MetStat query buider: Select criteria, e.g. species, sample source, analysis type, ion mode, disease association, metabolite class.

The screenshot shows the MetStat query builder interface. On the left, there are three red arrows pointing to the search criteria fields. The search parameters are as follows:

- Analysis Type: LCMS
- MS Ion Mode: NEGATIVE
- Chromatography Type: (empty)
- Species: Human (227)
- Sp. class: (empty)
- Disease: (empty)
- Sample source: (empty)
- RefMet name: Contains (case insensitive)
- Metabolite superclass: Phospholipids
- Human pathway: (empty)
- Records to display: All

Buttons for 'Generate' and 'Reset' are visible at the bottom of the search criteria section. A pink box highlights '1 Amino acid/peptides' in the search results.

The search results are displayed in a table titled 'MetStat: Search parameters: Analysis Type:LCMS Ion mode:NEGATIVE Species:Human | Most significant ANOVA measurements'. The table has the following columns: Refmet Name [Pathways], Studies [Data Details], RSD, Main Class, and Sub Class.

Refmet Name [Pathways]	Studies [Data Details]	RSD	Main Class	Sub Class
LPE 18.0 [P]	63 [Data]	40.01	Glycerophosphoethanolamines	LPE
PI 38.4 [P]	49 [Data]	34.81	Glycerophosphoinositols	PI
PI 36.2 [P]	48 [Data]	37.79	Glycerophosphoinositols	PI
PI 38.5 [P]	43 [Data]	36.94	Glycerophosphoinositols	PI
PE 36.2 [P]	42 [Data]	40.28	Glycerophosphoethanolamines	PE
PI 36.4 [P]	42 [Data]	36.92	Glycerophosphoinositols	PI
PC 34.2 [P]	40 [Data]	30.16	Glycerophosphocholines	PC
PG 36.2 [P]	40 [Data]	40.47	Glycerophosphoglycerols	PG
LPE 18.1 [P]	40 [Data]	48.15	Glycerophosphoethanolamines	LPE
PE 36.3 [P]	39 [Data]	46.77	Glycerophosphoethanolamines	PE
LPE 20.4 [P]	39 [Data]	40.00	Glycerophosphoethanolamines	LPE
PE 34.1 [P]	39 [Data]	42.35	Glycerophosphoethanolamines	PE
PI 38.3 [P]	38 [Data]	37.90	Glycerophosphoinositols	PI
PC 32.2 [P]	38 [Data]	35.95	Glycerophosphocholines	PC
LPE 16.0 [P]	38 [Data]	43.83	Glycerophosphoethanolamines	LPE
PI 34.2 [P]	38 [Data]	38.63	Glycerophosphoinositols	PI
PC 32.1 [P]	38 [Data]	38.07	Glycerophosphocholines	PC
PE 36.1 [P]	38 [Data]	39.51	Glycerophosphoethanolamines	PE
PC 36.3 [P]	37 [Data]	25.61	Glycerophosphocholines	PC
PC 32.0 [P]	37 [Data]	23.45	Glycerophosphocholines	PC
PE 38.4 [P]	37 [Data]	42.16	Glycerophosphoethanolamines	PE
PC 38.4 [P]	37 [Data]	31.52	Glycerophosphocholines	PC
PC 38.5 [P]	37 [Data]	27.02	Glycerophosphocholines	PC
PE 34.2 [P]	36 [Data]	45.35	Glycerophosphoethanolamines	PE
PC 36.1 [P]	36 [Data]	25.44	Glycerophosphocholines	PC
PC 36.2 [P]	36 [Data]	28.93	Glycerophosphocholines	PC
PE 38.6 [P]	36 [Data]	47.87	Glycerophosphoethanolamines	PE
PC 38.2 [P]	35 [Data]	25.95	Glycerophosphocholines	PC
PC 38.3 [P]	35 [Data]	31.71	Glycerophosphocholines	PC
PC 33.1 [P]	35 [Data]	31.10	Glycerophosphocholines	PC
LPE 18.2 [P]	35 [Data]	39.54	Glycerophosphoethanolamines	LPE
PC 34.3 [P]	35 [Data]	30.71	Glycerophosphocholines	PC
PI 40.5 [P]	35 [Data]	42.30	Glycerophosphoinositols	PI
PI 34.1 [P]	35 [Data]	40.51	Glycerophosphoinositols	PI
PI 36.1 [P]	35 [Data]	35.54	Glycerophosphoinositols	PI
LPE 22.6 [P]	34 [Data]	44.92	Glycerophosphoethanolamines	LPE
PC 40.6 [P]	34 [Data]	33.55	Glycerophosphocholines	PC
PC 34.1 [P]	34 [Data]	27.20	Glycerophosphocholines	PC
PC 40.5 [P]	34 [Data]	32.55	Glycerophosphocholines	PC
PC 36.4 [P]	34 [Data]	31.47	Glycerophosphocholines	PC
PS 38.4 [P]	34 [Data]	51.02	Glycerophosphoserines	PS
PE 32.1 [P]	34 [Data]	62.88	Glycerophosphoethanolamines	PE

In this example, human studies using LCMS in negative ion mode containing Phospholipids are selected