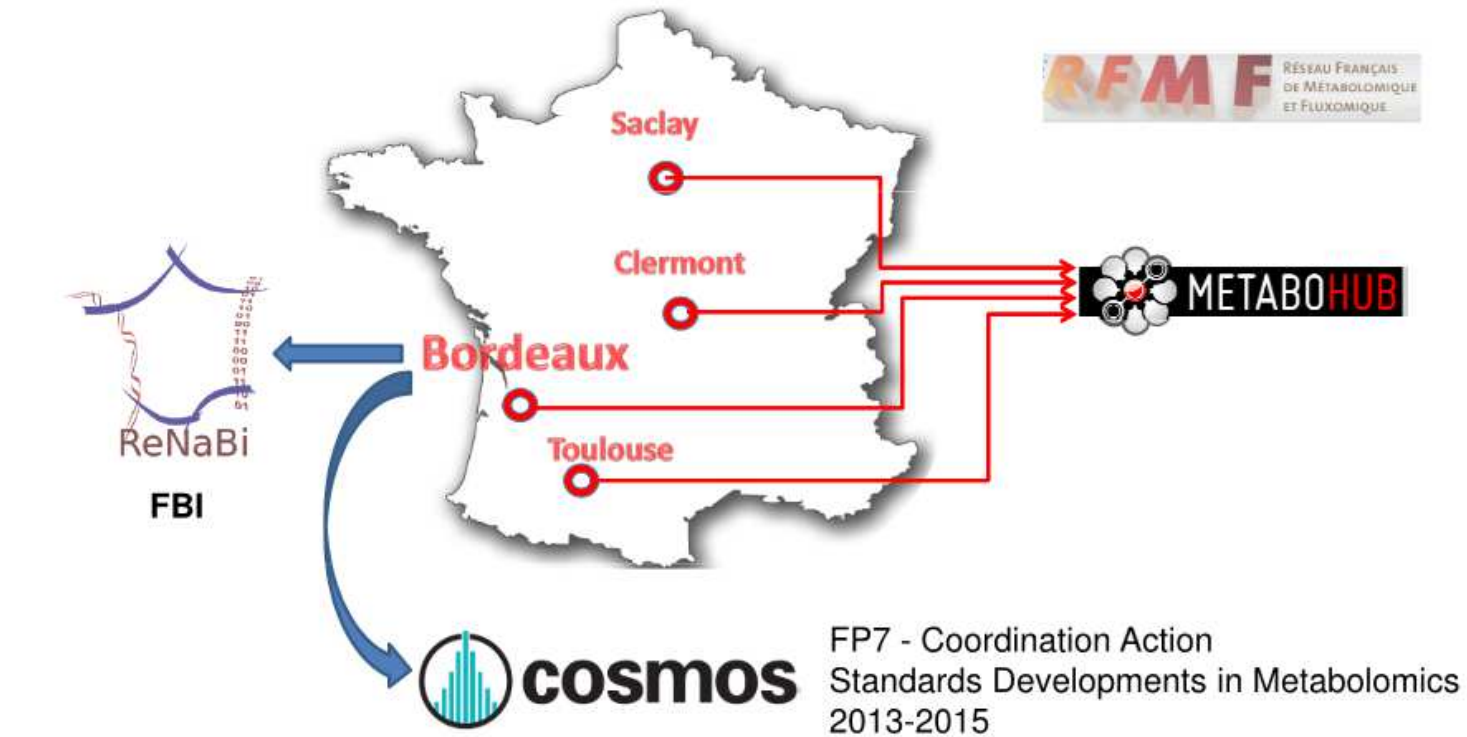

cgfb
CENTRE BORDEAUX
GÉNOMIQUE FONCTIONNELLE
cgfb
MÉTABOLOME
http://www.cgfb.u-bordeaux2.fr/fr/metabolome
La 1ère PF Métabolome labellisée IBiSA
et PF Stratégique INRA 2008-2012
Annick Moing & Catherine Deborde

Networks



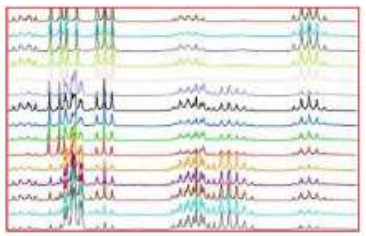
Bordeaux in the French metabolomics and bioinformatics infrastructures and networks

Objectifs et positionnement scientifique

Fédérer des outils et savoir-faire pour l'étude du métabolisme

- **Satisfaire les besoins en métabolomique non ciblée ou ciblée et phénotypage métabolique haut débit liés aux activités de recherche** de laboratoires académiques et privés
  - **services ou collaboration**
  - identification et/ou analyse de métabolites (LC, RMN et MS),
  - mesure d'enrichissements isotopiques après marquage ^{13}C
- **Ouverture** à l'ensemble de la communauté pour la mise à disposition de services, d'équipements et d'expertise
- **Formation**, Ecole Chercheur
- **Accueil** de masters, doctorants, chercheurs



Savoir-Faire

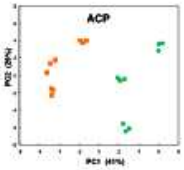
- **Métabolome – Lipidome – Profils & Phénotypage métaboliques**

0. Métadonnées échantillons

1. Extraction(s) 

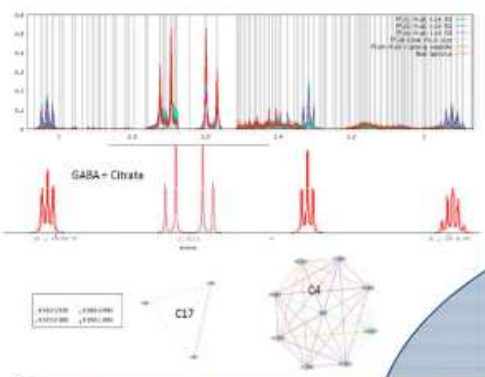
2. Analyses biochimiques ciblées ou non  

3. Pré-traitement des données 

4. Visualisation et exploration des données 

5. Intégration des données 

Bioinformatic Activities

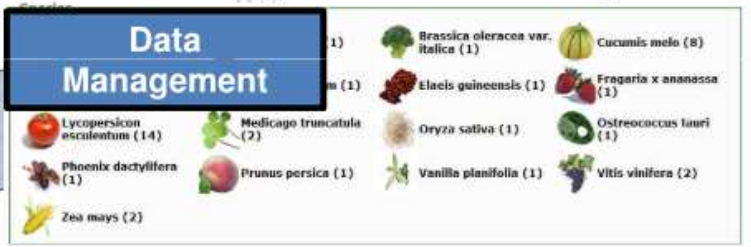


MERY B

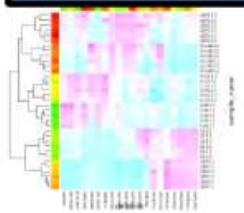
MeRy-B is a plant metabolomics knowledgebase allowing the storage and visualisation of metabolic profiles.

Ferry-Dumazet et al. BMC Plant Biology

Data Management

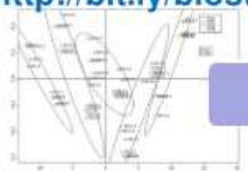


Spectra Processing & Data mining



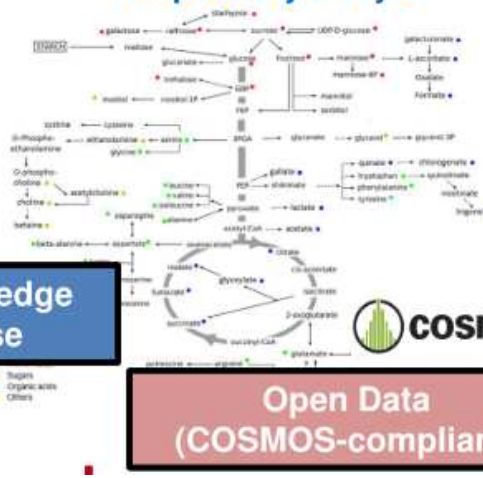
Data Analysis

http://bit.ly/biostatflow



BioStatFlow

http://bit.ly/meryb



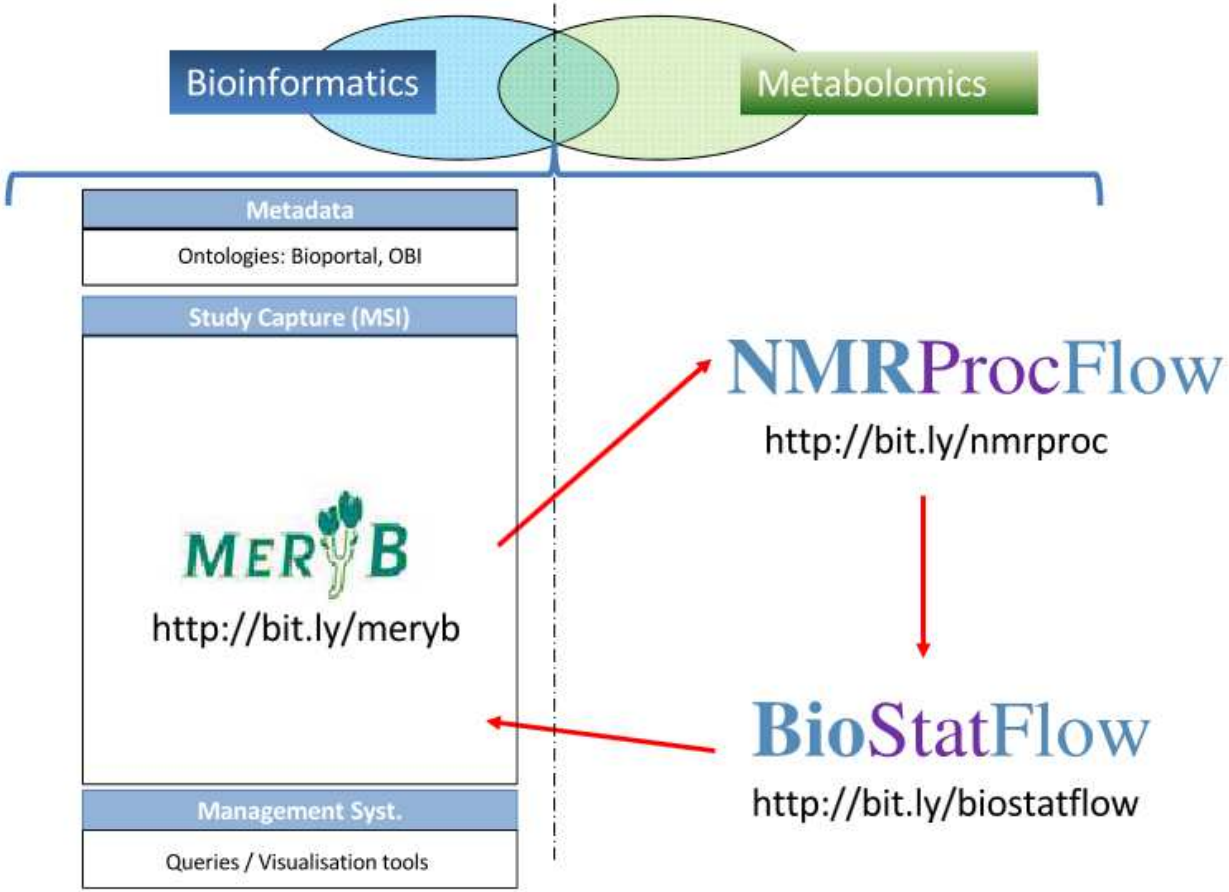
Knowledge Base

cosmos

Open Data (COSMOS-compliant)

Metabolomics & Bioinformatics

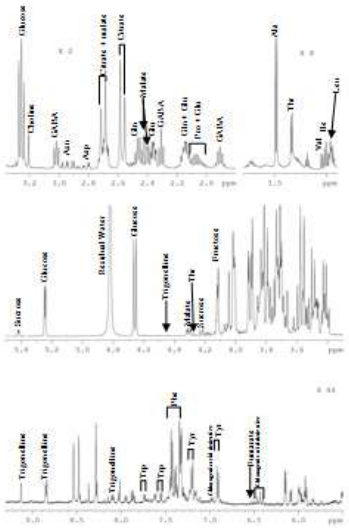
- Design and Implementation :
  - Tools for data management and data mining

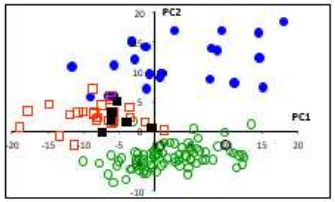


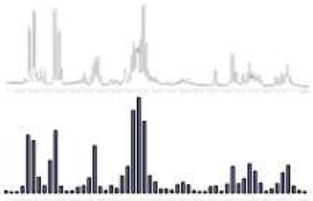
Metabolomics : several approaches

Experiment Design

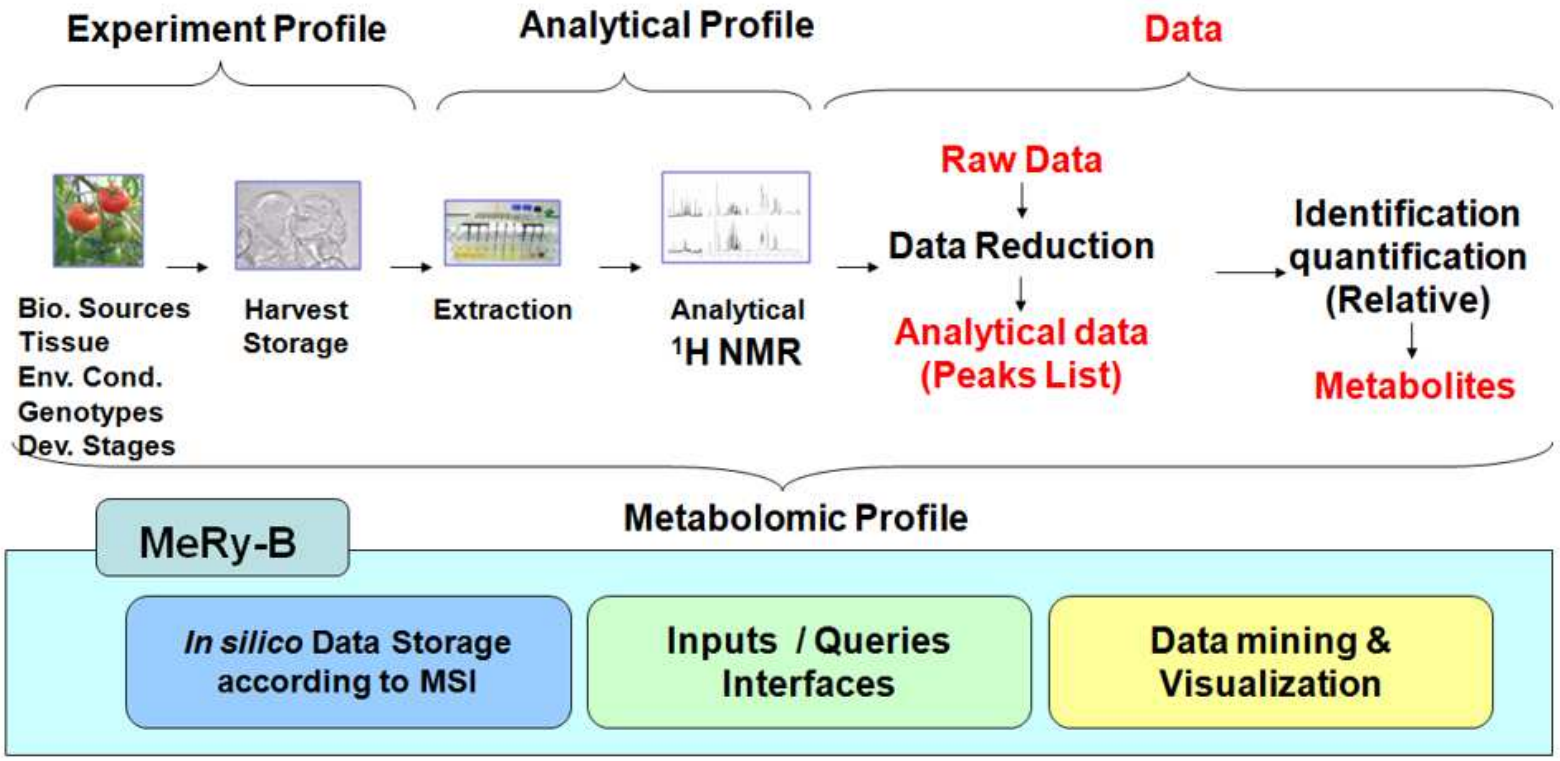
Metabolic Profiling	**Metabolic fingerprinting**
Metabolites **Identification / quantification** (ex: biological Pathways) involve to know the pattern of metabolites for the analytical technique referred	**Global approach,** without *prior knowledge* *Goal*: research of **patterns / biomarkers** Discriminant analysis, clustering (PCA,HCA)







Strategy


Experiment Profile
Analytical Profile
Data
Bio. Sources
Tissue
Env. Cond.
Genotypes
Dev. Stages
Harvest
Storage
Extraction
Analytical
¹H NMR
Raw Data
Data Reduction
Analytical data
(Peaks List)
Identification
quantification
(Relative)
Metabolites
Metabolomic Profile
MeRy-B
In silico Data Storage
according to MSI
Inputs / Queries
Interfaces
Data mining &
Visualization

http://www.cbib.u-bordeaux2.fr/MERYB/

Metabolomic Repository Bordeaux

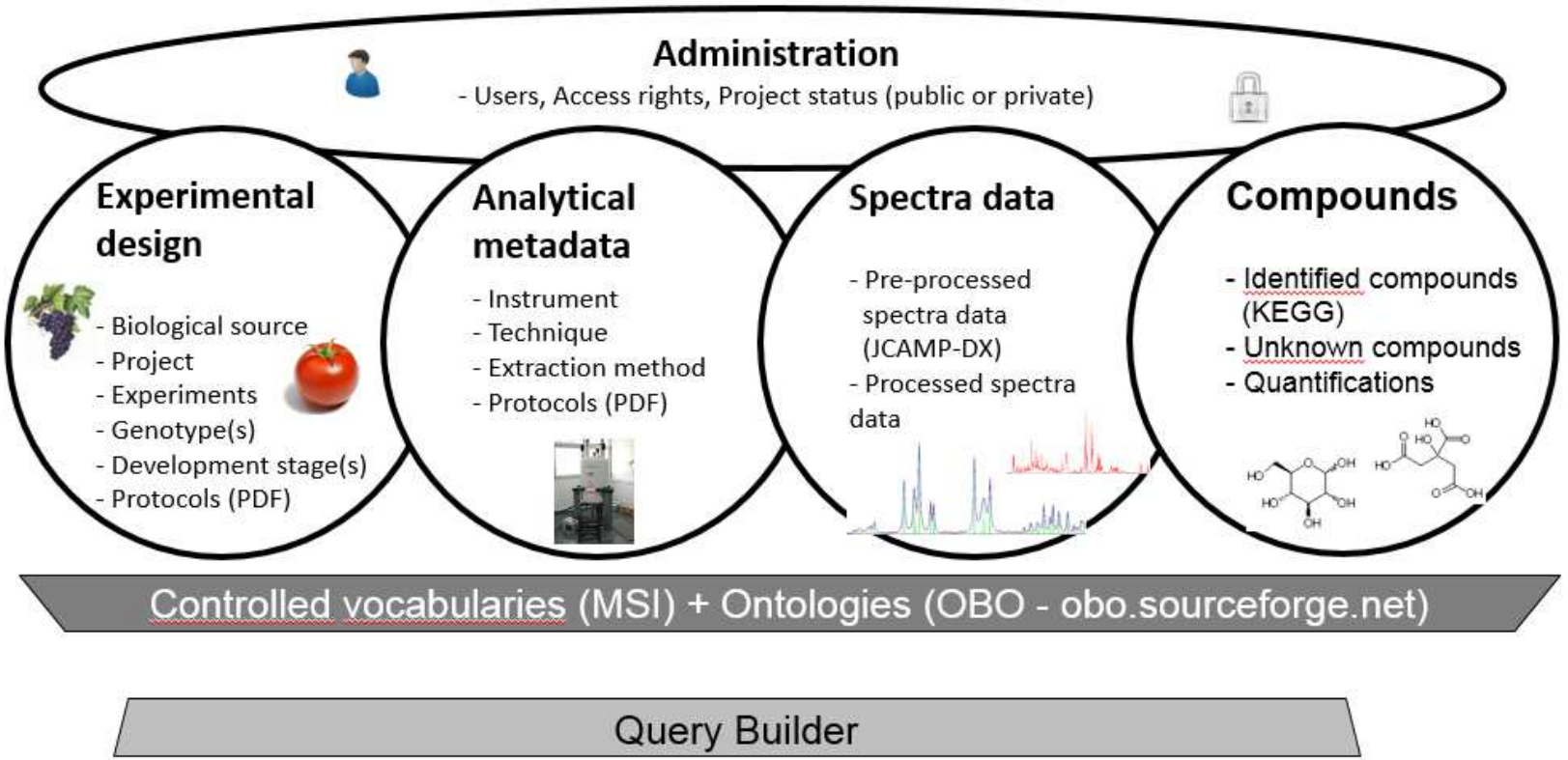
MeRy-B is a plant metabolomics knowledgebase allowing the storage and visualisation of metabolic profiles from plants ... read more

Summary (public/all)

Projects :	17 / 41	(41%)
Experiments :	42 / 107	(39%)
Plants :	199 / 464	(43%)
Spectra :	1027 / 2063	(50%)
Compounds :	138 / 180	(77%)

MSI-Compliant & OBO-Compliant

Ferry-Dumazet H., Jacob D *et al* BMC Plant Biology 2011


Administration
- Users, Access rights, Project status (public or private)
Experimental design
- Biological source
- Project
- Experiments
- Genotype(s)
- Development stage(s)
- Protocols (PDF)
Analytical metadata
- Instrument
- Technique
- Extraction method
- Protocols (PDF)
Spectra data
- Pre-processed spectra data (JCAMP-DX)
- Processed spectra data
Compounds
- Identified compounds (KEGG)
- Unknown compounds
- Quantifications
Controlled vocabularies (MSI) + Ontologies (OBO - obo.sourceforge.net)
Query Builder

Tomato- Metabolomics - 2006 (T06002) | Lycopersicon esculentum
UMR 619 Biologie du Fruit - INRA, University Bordeaux 1 and 2 - Bordeaux (France)

Description

Global approach to characterize changes in metabolic profiles in two interdependent tissues Seed and Flesh from the same tomato fruits during tomato fruit development.

Reference: DOI:10.1007/s11306-007-0059-1

Fabien Mounet, Martine Lemaire-Chamley, Mickaël Maucourt, Cécile Cabasson, Jean-Luc Giraudel, Catherine Deborde, René Lessire, Philippe Gallusci, Anne Bertrand, Monique Gaudillère, Christophe Rothan, Dominique Rolin and Annick Moing. Quantitative metabolic profiles of tomato flesh and seeds during fruit development: complementary analysis with ANN and PCA. Metabolomics, 2007, 3:273-288

select

Select: -- all experiments ---

Experiment Name	Tissue/Organ	Env. Conditions	BS	GT	I	Dev. Stage	Tech	SD
Tomato-Seed	seed	Normal	WT	Ailsa Craig	1	FF.01 fruit size 30% (8) FF.02 fruit size 50% (12) FF.03 fruit size 70% (20) FF.04 final fruit size (35) FR.04 fruit ripening complete (45)	1H NMR	25
Tomato-Flesh	fruit	Normal	WT	Ailsa Craig	1	FF.01 fruit size 30% (8) FF.02 fruit size 50% (12) FF.03 fruit size 70% (20) FF.04 final fruit size (35) FR.04 fruit ripening complete (45)	1H NMR	29

Legend:

Env. Conditions	Environmental Conditions	Dev. Stage	Development Stage
BS	Background	Tech	Analytical technique
GT	Genotype	SD	Number of Spectral Data
I	Number of individuals		

Tissue/Organ	Environmental Conditions	Study Type
seed	Normal	growth chamber study

Growth Protocol	Harvest Protocol	Storage Protocol
PG- Tomato - Metabolomics - 2006	PH- Tomato - Metabolomics - 2006	PS-Tomato-UMR619-1

Background	Genotype : Ind Code	FF.01 fruit size 30%	FF.02 fruit size 50%	FF.03 fruit size 70%	FF.04 final fruit size	FR.04 fruit ripening complete
WT	Ailsa Craig : Seed	S8.1.1 - 1H NMR S8.2.1 - 1H NMR S8.3.1 - 1H NMR S8.123.2 - 1H NMR	S12.1.1 - 1H NMR S12.1.2 - 1H NMR S12.2.1 - 1H NMR S12.2.2. - 1H NMR S12.3.1 - 1H NMR S12.3.2 - 1H NMR	S20.1.1 - 1H NMR S20.1.2 - 1H NMR S20.2.1 - 1H NMR S20.2.2 - 1H NMR S20.3.1 - 1H NMR S20.3.2 - 1H NMR	S35.1.1 - 1H NMR S35.1.2 - 1H NMR S35.2.1 - 1H NMR S35.2.2 - 1H NMR S35.3.1 - 1H NMR S35.3.2 - 1H NMR	S45.1.2 - 1H NMR S45.2.2 - 1H NMR S45.3.2 - 1H NMR

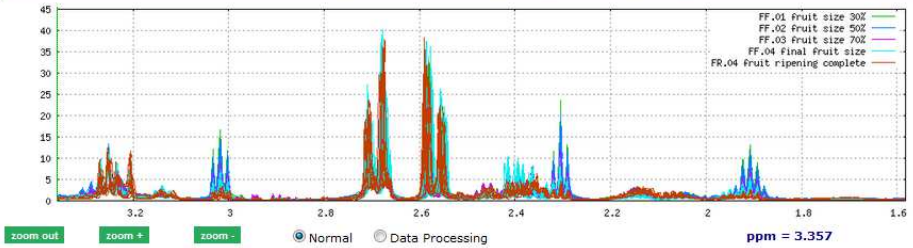
Lycopersicon esculentum

Tomato- Metabolomics - 2006

Global approach to characterize changes in metabolic profiles in two interdependent tissues Seed and Flesh from the same tomato fruits during tomato fruit development.

select

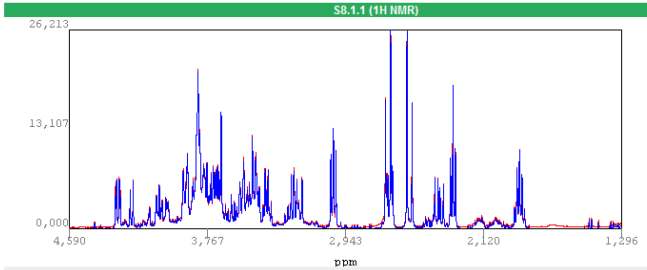
Select: 1H NMR | Tomato -Metabolomics - 2006 | -- all experiments --- | Dev. Stage



zoom out | zoom + | zoom - | Normal | Data Processing | ppm = 3.357

Information | Viewer | Compounds | Edit | Log

S8.1.1 (1H NMR)



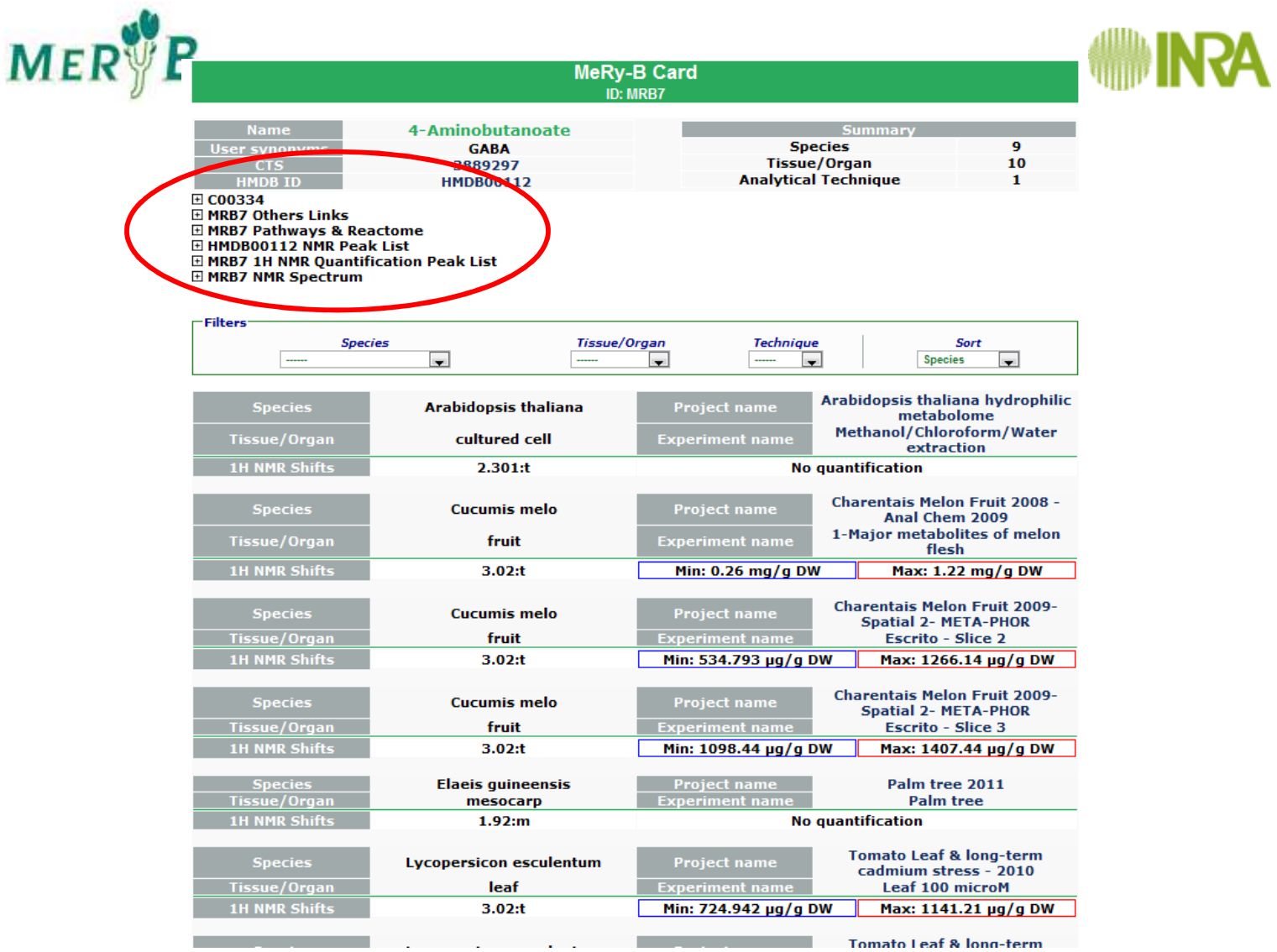
ppm=4.5902, I=20.2902 | model | peaks | both | none

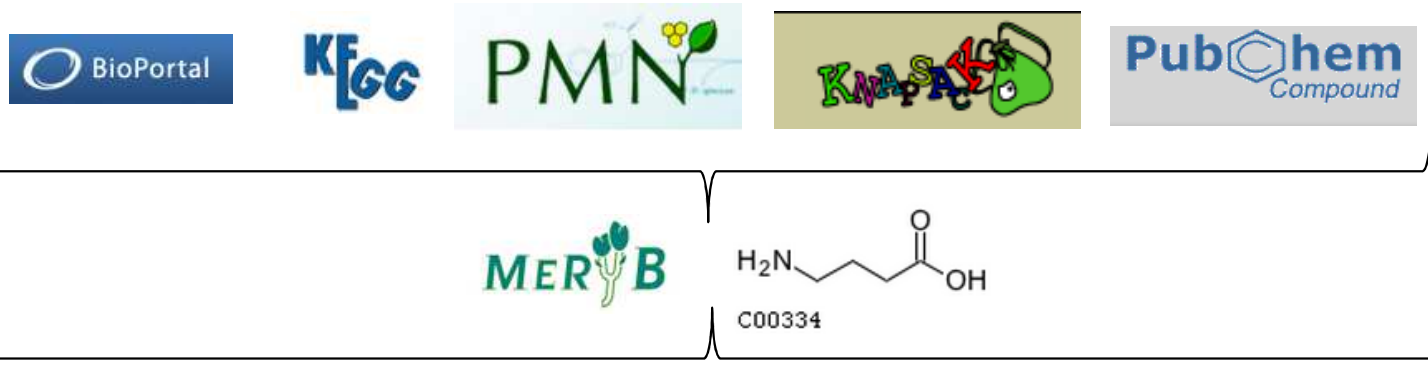
Window: | Imax: | < | 0.01 | Zoom : | - | All

S8.1.1 (1H NMR)

Nb	Name	User synonym	Shift/Multiplicity	Comment	Quantification	Links
1	4-Aminobutanoate	GABA	1.92 | m 2.3 | t 3.01 | t	C3H2 C2H2 C4H2	- - 33925.2 µg/g DW	MRB7
2	5-Oxoproline	pyroglutamic acid	4.18 | dd	C2H	-	MRB21
3	Acetylcholine	Acetylcholine	3.22 | s	N-(C(5)H3)3	-	MRB5
4	Alanine	Alanine	1.48 | d	C(3)H3	497.819 µg/g DW	MRB63
5	Asparagine	Asparagine	2.92 | m	C(3)H2	1810.78 µg/g DW	MRB85
6	Aspartate	Aspartate	2.81 | m	1/2(C(3)H2)	1098.79 µg/g DW	MRB86
7	Chlorogenate	chlorogenic acid	6.4 | d 6.96 | d 7.13 | d 7.21 | d 7.68 | d	Caffeoyl-C8H Caffeoyl-C7H	- - - - 7195.01 µg/g DW	MRB11
8	Choline	Choline	3.2 | s	N-(C(3)H3)3	1262.99 µg/g DW	MRB6
9	Citrate	Citrate	2.63 | dd	C(2)H2+ C(4)H2	38088.1 µg/g DW	MRB12
10	D-Galactose	galactose	4.6 | d	ß C(1)H	-	MRB79
11	D-Mannose	Mannose	5.2 | d	C(1)H	41.9992 µg/g DW	MRB44
12	Formate	Formate	8.47 | s	C(1)H	-	MRB13
13	Fructose	Fructose	4.12 | m	alphaC(3)H+ C(5)H+alphaC(5)H	17603.1 µg/g DW	MRB14
14	Fumarate	fumaric acid	6.53 | s	C(2)H+ C(3)H	87.7298 µg/g DW	MRB15
15	Glucose	Glucose	4.66 | d 5.25 | d	ß-C1H alpha-C1H	- 48123.6 µg/g DW	MRB45
16	Glutamate	Glutamate	2.07 | m	C(3)H2	16784.7 µg/g DW	MRB17
17	Glutamine	Glutamine	2.45 | m	C(4)H2	3842.45 µg/g DW	MRB18
18	Isoleucine	Isoleucine	1.01 | d	C(6)H3	90.6444 µg/g DW	MRB89
19	L-Threonine	Threonine	1.33 | d	C(4)H3	124.392 µg/g DW	MRB90
20	Leucine	Leucine	0.96 | t	C(5)H3+ C(6)H3	419.67 µg/g DW	MRB100
21	Malate	Malate	4.3 | dd	C(2)H	23451.4 µg/g DW	MRB19
22	N-Methylnicotinate	Trigonelline	4.44 | s 8.08 | t 8.83 | m 9.13 | s	- - - C(3)H	- - - 311.49 µg/g DW	MRB23
23	Phenylalanine	Phenylalanine	7.4 | m	C(5)H+ C(6)H+ C(7)H	638.754 µg/g DW	MRB20
24	Sucrose	Sucrose	5.41 | d	Glucopyranosyl-C(1)H	30806.9 µg/g DW	MRB22
25	Tyrosine	Tyrosine	6.91 | d	C(6)H2	212.941 µg/g DW	MRB25
26	UDP-glucose	UDPG	5.98 | m		410.142 µg/g DW	MRB102
27	Valine	Valine	1.04 | d	C(5)H3	305.852 µg/g DW	MRB92
28	unkD5.1	UnknownD5.1	5.1 | d		-	MRB159
29	unkD6.2	Adenosine-like	6.2 | d	C1H of ribose	200.558 µg/g DW	MRB101
30	unkD7.55	UnknownD7.55	7.55 | d	Caffeoyl-CxH	-	MRB160
31	unkS5.4	UnknownS5.4	5.4 | s		86.1868 µg/g DW	MRB104
32	unkS5.55	UnknownS5.55	5.55 | s		66.0024 µg/g DW	MRB161
33	unkS8.5	UnknownS8.5	8.5 | s		131.229 µg/g DW	MRB106

S8.1.1 (1H NMR)						
Nb	Name	User synonym	Shift/Multiplicity	Comment	Quantification	Links
1	4-Aminobutanoate	GABA	1.92 | m 2.3 | t 3.01 | t	C3H2 C2H2 C4H2	- - 33925.2 µg/g DW	MRB7
2	5-Oxoproline	pyroglutamic acid	4.18 | dd	C2H	-	MRB21
3	Acetylcholine	Acetylcholine	3.22 | s	N-(C(5)H3)3	-	MRB5
4	Alanine	Alanine	1.48 | d	C(3)H3	497.819 µg/g DW	MRB63
5	Asparagine	Asparagine	2.92 | m	C(3)H2	1810.78 µg/g DW	MRB85
6	Aspartate	Aspartate	2.81 | m	1/2(C(3)H2)	1098.79 µg/g DW	MRB86
7	Chlorogenate	chlorogenic acid	6.4 | d 6.96 | d 7.13 | d 7.21 | d 7.68 | d	Caffeoyl-C8H Caffeoyl-C7H	- - - - 7195.01 µg/g DW	MRB11
8	Choline	Choline	3.2 | s	N-(C(3)H3)3	1262.99 µg/g DW	MRB6
9	Citrate	Citrate	2.63 | dd	C(2)H2+ C(4)H2	38088.1 µg/g DW	MRB12
10	D-Galactose	galactose	4.6 | d	ß C(1)H	-	MRB79
11	D-Mannose	Mannose	5.2 | d	C(1)H	41.9992 µg/g DW	MRB44
12	Formate	Formate	8.47 | s	C(1)H	-	MRB13
13	Fructose	Fructose	4.12 | m	alphaC(3)H+ C(5)H+alphaC(5)H	17603.1 µg/g DW	MRB14
14	Fumarate	fumaric acid	6.53 | s	C(2)H+ C(3)H	87.7298 µg/g DW	MRB15
15	Glucose	Glucose	4.66 | d 5.25 | d	ß-C1H alpha-C1H	- 48123.6 µg/g DW	MRB45
16	Glutamate	Glutamate	2.07 | m	C(3)H2	16784.7 µg/g DW	MRB17
17	Glutamine	Glutamine	2.45 | m	C(4)H2	3842.45 µg/g DW	MRB18
18	Isoleucine	Isoleucine	1.01 | d	C(6)H3	90.6444 µg/g DW	MRB89
19	L-Threonine	Threonine	1.33 | d	C(4)H3	124.392 µg/g DW	MRB90
20	Leucine	Leucine	0.96 | t	C(5)H3+ C(6)H3	419.67 µg/g DW	MRB100
21	Malate	Malate	4.3 | dd	C(2)H	23451.4 µg/g DW	MRB19
22	N-Methylnicotinate	Trigonelline	4.44 | s 8.08 | t 8.83 | m 9.13 | s	 C(3)H	- - - 311.49 µg/g DW	MRB23
23	Phenylalanine	Phenylalanine	7.4 | m	C(5)H+ C(6)H+ C(7)H	638.754 µg/g DW	MRB20
24	Sucrose	Sucrose	5.41 | d	Glucopyranosyl-C(1)H	30806.9 µg/g DW	MRB22
25	Tyrosine	Tyrosine	6.91 | d	C(6)H2	212.941 µg/g DW	MRB25
26	UDP-glucose	UDPG	5.98 | m		410.142 µg/g DW	MRB102
27	Valine	Valine	1.04 | d	C(5)H3	305.852 µg/g DW	MRB92
28	unkD5.1	UnknownD5.1	5.1 | d		-	MRB159
29	unkD6.2	Adenosine-like	6.2 | d	C1H of ribose	200.558 µg/g DW	MRB101
30	unkD7.55	UnknownD7.55	7.55 | d	Caffeoyl-CxH	-	MRB160
31	unkS5.4	UnknownS5.4	5.4 | s		86.1868 µg/g DW	MRB104
32	unkS5.55	UnknownS5.55	5.55 | s		66.0024 µg/g DW	MRB161
33	unkS8.5	UnknownS8.5	8.5 | s		131.229 µg/g DW	MRB106


MeRy-B Card
ID: MRB7
Name
4-Aminobutanoate
User synonyms
GABA
CTS
3889297
HMDB ID
HMDB00112
Summary
Species 9
Tissue/Organ 10
Analytical Technique 1
C00334
MRB7 Others Links
MRB7 Pathways & Reactome
HMDB00112 NMR Peak List
MRB7 1H NMR Quantification Peak List
MRB7 NMR Spectrum
Filters
Species
Tissue/Organ
Technique
Sort
Species
Arabidopsis thaliana
cultured cell
Project name
Arabidopsis thaliana hydrophilic metabolome
Experiment name
Methanol/Chloroform/Water extraction
1H NMR Shifts
2.301:t
No quantification
Species
Cucumis melo
fruit
Project name
Charentais Melon Fruit 2008 - Anal Chem 2009
Experiment name
1-Major metabolites of melon flesh
1H NMR Shifts
3.02:t
Min: 0.26 mg/g DW
Max: 1.22 mg/g DW
Species
Cucumis melo
fruit
Project name
Charentais Melon Fruit 2009-Spatial 2- META-PHOR
Experiment name
Escrito - Slice 2
1H NMR Shifts
3.02:t
Min: 534.793 µg/g DW
Max: 1266.14 µg/g DW
Species
Cucumis melo
fruit
Project name
Charentais Melon Fruit 2009-Spatial 2- META-PHOR
Experiment name
Escrito - Slice 3
1H NMR Shifts
3.02:t
Min: 1098.44 µg/g DW
Max: 1407.44 µg/g DW
Species
Elaeis guineensis
Tissue/Organ
mesocarp
Project name
Palm tree 2011
Experiment name
Palm tree
1H NMR Shifts
1.92:m
No quantification
Species
Lycopersicon esculentum
Tissue/Organ
leaf
Project name
Tomato Leaf & long-term cadmium stress - 2010
Experiment name
Leaf 100 microM
1H NMR Shifts
3.02:t
Min: 724.942 µg/g DW
Max: 1141.21 µg/g DW
Tomato Leaf & long-term

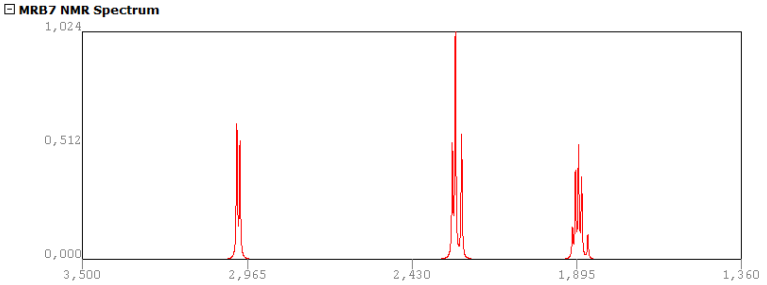


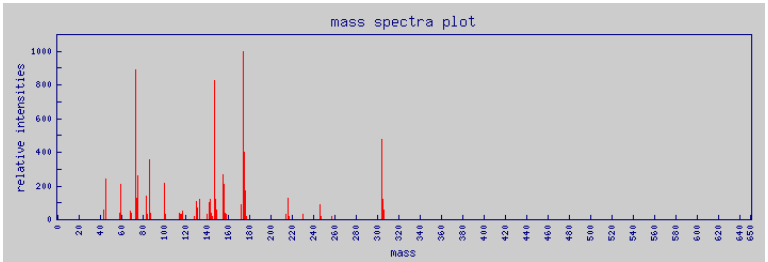
Chemical entities of biological interest

- amino acid
- biphenylyl carboxylic acid
- carbohydrate acid
- cefalotin
- cefditoren
- cefpiramide
- cefpodoxime
- cefpodoxime proxetil
- chlorocarboxylic acid
- cinalukast
- clofibric acid
- dicarboxylic acid
- gibberellin
- hexacarboxylic acid
- hydroxy carboxylic acid
- indolyl carboxylic acid
- monocarboxylic acid
- naptalam
- octacarboxylic acid
- oxo carboxylic acid
- penicillanic acids
- penillic acid
- pentacarboxylic acid
- phosphonoformic acid
- poly(methacrylic acid) macromolecule
- steroid acid
- sulfur-containing carboxylic acid
- tetracarboxylic acid
- treprostinil
- tricarboxylic acid
- ureidocarboxylic acid
- verteporfin

Biological Pathways

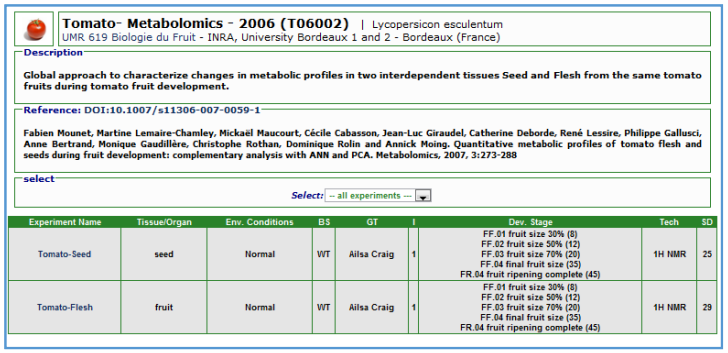
- 4-aminobutyrate degradation IV
- IAA biosynthesis I
- IAA biosynthesis II
- alanine biosynthesis II
- alanine biosynthesis III
- alanine degradation II (to D-lactate)
- alanine degradation III
- beta-alanine biosynthesis II
- biotin biosynthesis II
- gamma-coniciene and coniine biosynthesis
- glutamate degradation IV
- hypoglycin biosynthesis
- indole-3-acetyl-amino acid biosynthesis
- lupanine biosynthesis
- molybdenum cofactor biosynthesis
- phenylalanine degradation III
- serinol biosynthesis
- tRNA charging pathway



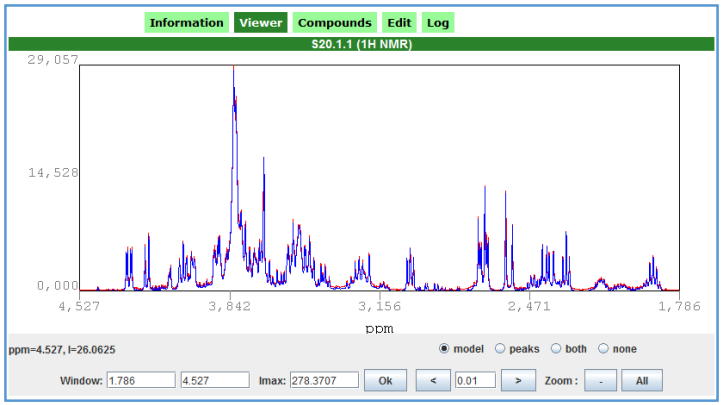


Resource-based approach

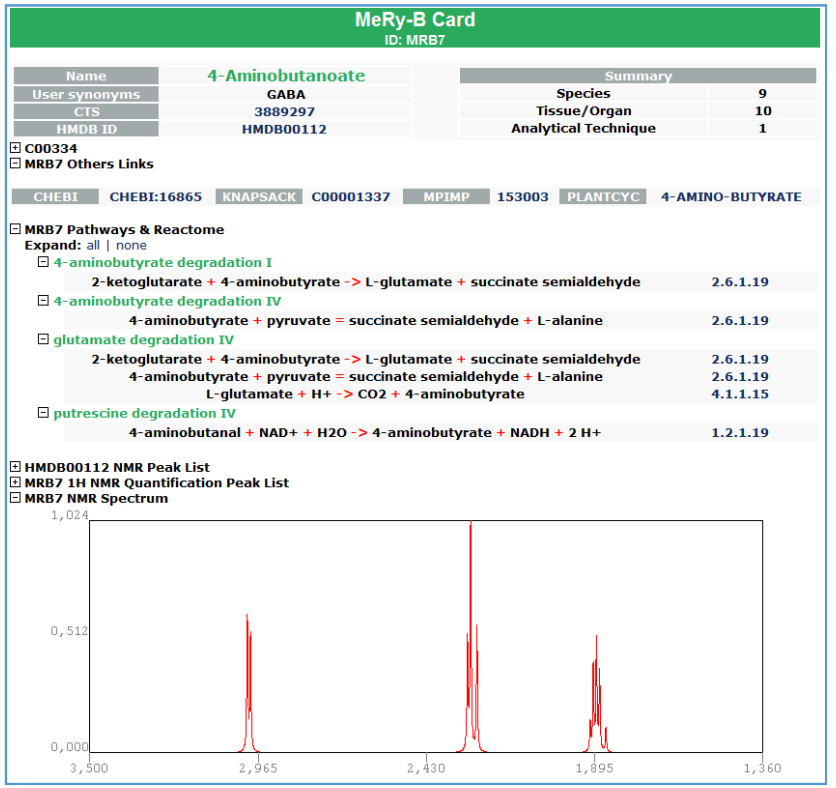
- **Access to resources separately and directly => URL nomenclature**
- URLs : http://www.cbib.u-bordeaux2.fr/MERYB/res/<resource>/<ID>/<option>
- URI scheme : meryb:resource:identifier



http://www.cbib.u-bordeaux2.fr/MERYB/res/project/T06002



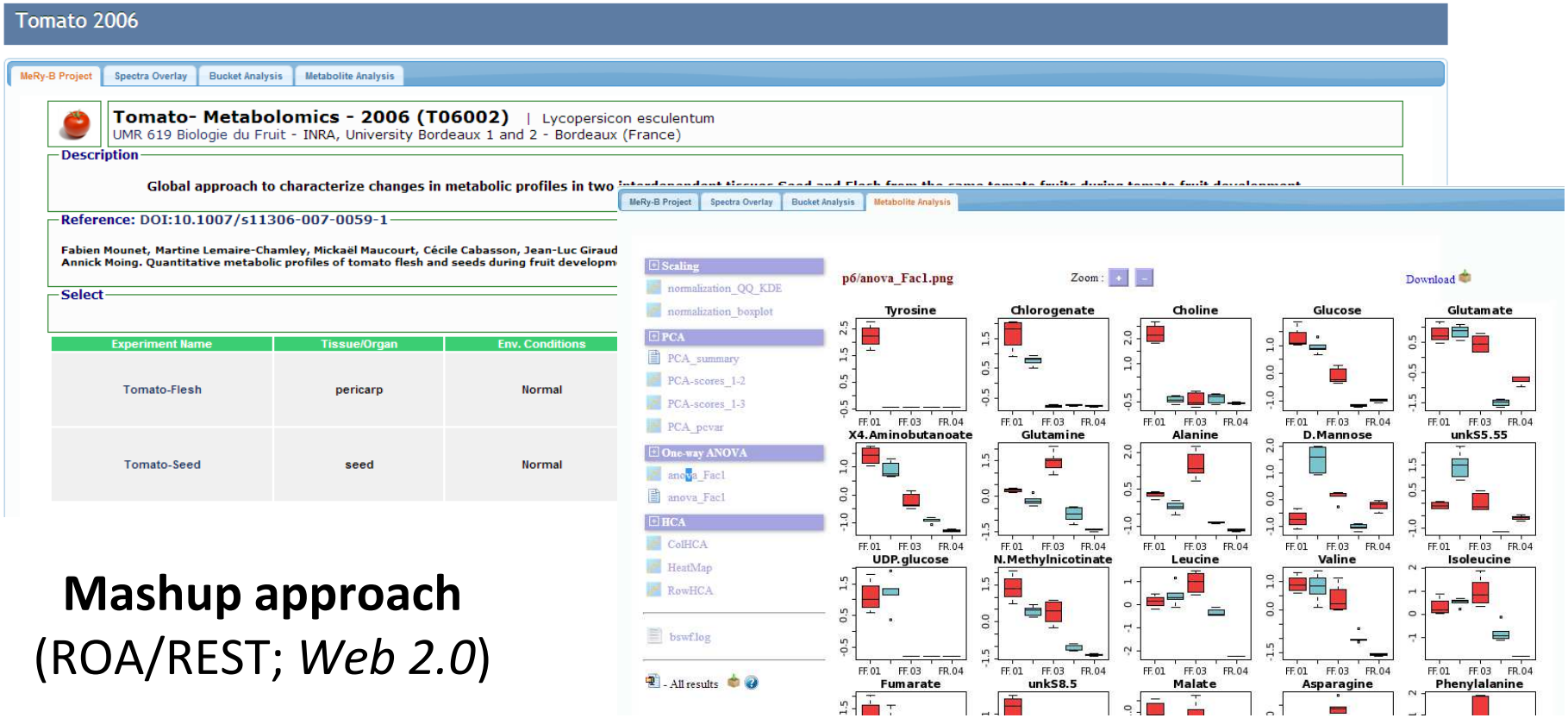
http://www.cbib.u-bordeaux2.fr/MERYB/res/spectra/S20.1.1



http://www.cbib.u-bordeaux2.fr/MERYB/res/compound/MRB7

Resource-based approach

- **Access to resources separately and directly => URL nomenclature**
- URLs : http://www.cbib.u-bordeaux2.fr/MERYB/res/<resource>/<ID>/<option>
- URI scheme : meryb:resource:identifier



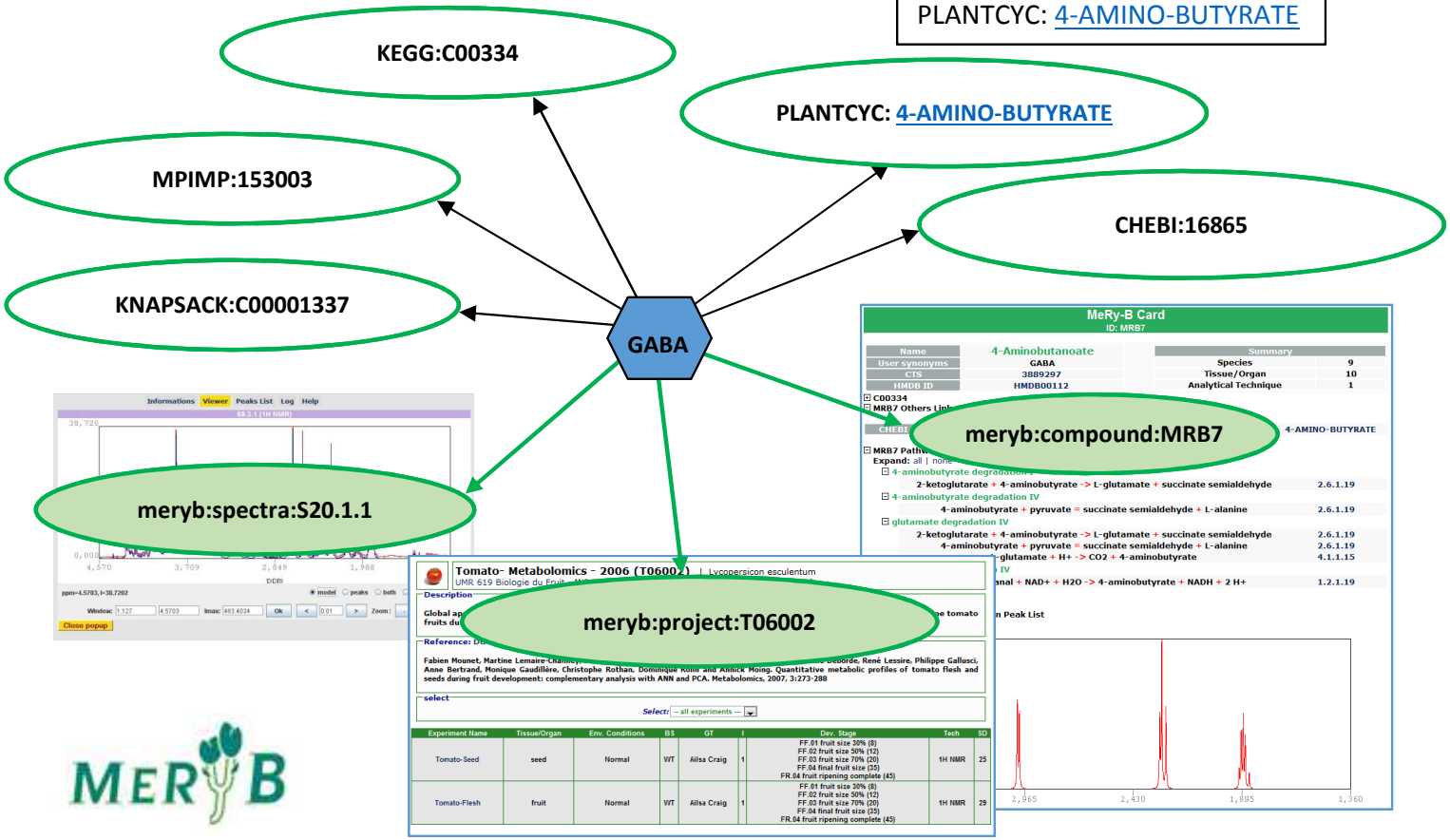
Mashup approach

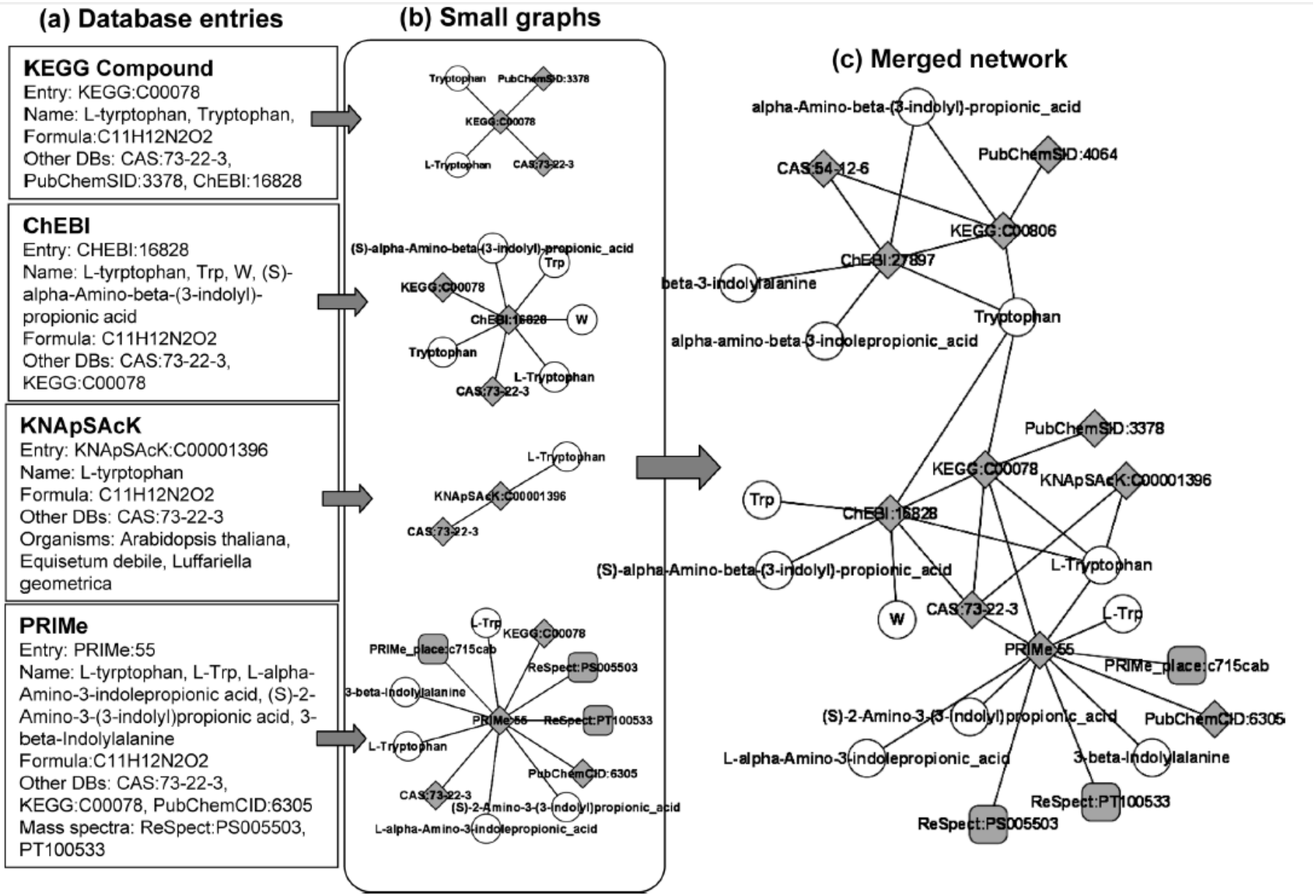
(ROA/REST; *Web 2.0*)

Resource-based approach

MERYB Compound
Name : GABA
KEGG: C00334
CHEBI : 16865
KNAPSACK: C00001337
MPIMP: 153003
PLANTCYC: 4-AMINO-BUTYRATE

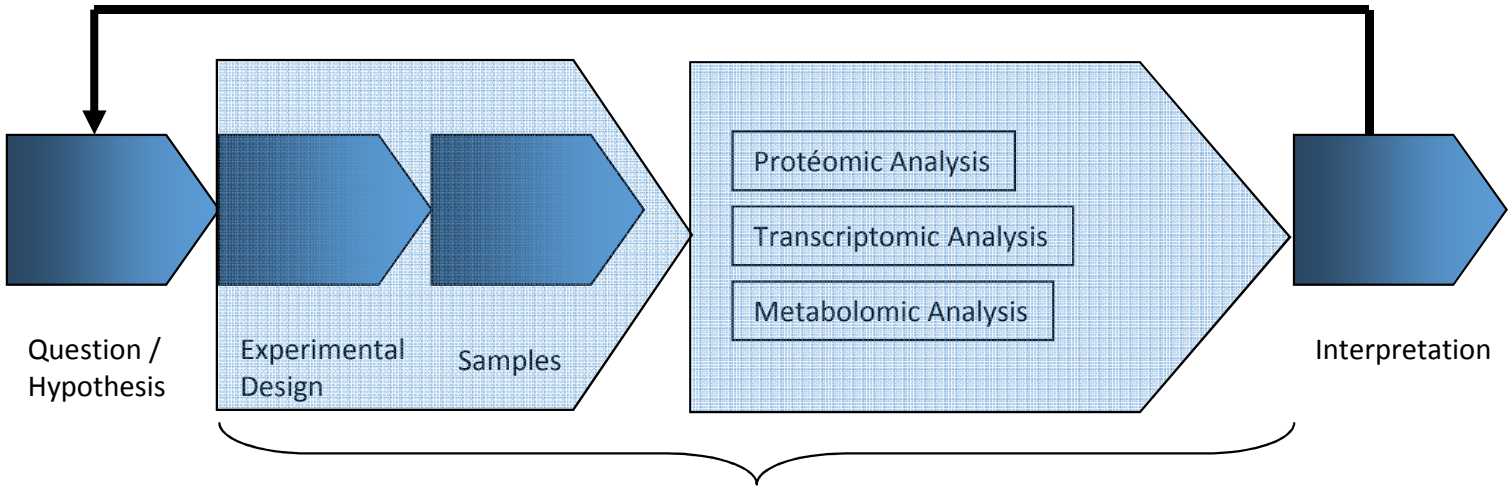
Extension of the links network …




(a) Database entries
KEGG Compound
Entry: KEGG:C00078
Name: L-tyrptophan, Tryptophan,
Formula:C11H12N2O2
Other DBs: CAS:73-22-3,
PubChemSID:3378, ChEBI:16828
ChEBI
Entry: CHEBI:16828
Name: L-tyrptophan, Trp, W, (S)-alpha-Amino-beta-(3-indolyl)-propionic acid
Formula: C11H12N2O2
Other DBs: CAS:73-22-3, KEGG:C00078
KNApSAcK
Entry: KNApSAcK:C00001396
Name: L-tyrptophan
Formula: C11H12N2O2
Other DBs: CAS:73-22-3
Organisms: Arabidopsis thaliana, Equisetum debile, Luffariella geometrica
PRIMe
Entry: PRIMe:55
Name: L-tyrptophan, L-Trp, L-alpha-Amino-3-indolepropionic acid, (S)-2-Amino-3-(3-indolyl)propionic acid, 3-beta-Indolylalanine
Formula:C11H12N2O2
Other DBs: CAS:73-22-3, KEGG:C00078, PubChemCID:6305
Mass spectra: ReSpect:PS005503, PT100533
(b) Small graphs
Tryptophan
PubChemSID:3378
KEGG:C00078
L-Tryptophan
CAS:73-22-3
(S)-alpha-Amino-beta-(3-indolyl)-propionic_acid
Trp
KEGG:C00078
ChEBI:16828
W
Tryptophan
L-Tryptophan
CAS:73-22-3
L-Tryptophan
KNApSAcK:C00001396
CAS:73-22-3
L-Trp
KEGG:C00078
PRIMe_place:c715cab
ReSpect:PS005503
3-beta-Indolylalanine
PRIMe:55
ReSpect:PT100533
L-Tryptophan
PubChemCID:6305
CAS:73-22-3
(S)-2-Amino-3-(3-indolyl)propionic_acid
L-alpha-Amino-3-indolepropionic_acid
(c) Merged network
alpha-Amino-beta-(3-indolyl)-propionic_acid
CAS:54-12-6
PubChemSID:4064
KEGG:C00806
ChEBI:27897
beta-3-indolylalanine
Tryptophan
alpha-amino-beta-3-indolepropionic_acid
PubChemSID:3378
KEGG:C00078
KNApSAcK:C00001396
Trp
ChEBI:16828
(S)-alpha-Amino-beta-(3-indolyl)-propionic_acid
L-Tryptophan
W
CAS:73-22-3
L-Trp
PRIMe:55
PRIMe_place:c715cab
(S)-2-Amino-3-(3-indolyl)propionic_acid
PubChemCID:6305
L-alpha-Amino-3-indolepropionic_acid
3-beta-Indolylalanine
ReSpect:PT100533
ReSpect:PS005503

Data commoning

Integrative Biology



biosharing

Partners, Locations (QA & QC)

STANDARDS

A catalogue of reporting standards (minimum reporting guidelines, exchange formats and terminologies) and organizations that develop these.

➔ Link data in the context of metadata

➔ Positive and lasting impact on the value of scientific results

Data commoning

➔ Ensure consistency between the metadata

Contexts of the minimun information to be reported

MIBBI: http://mibbi.org

biosharing

Communication Formats

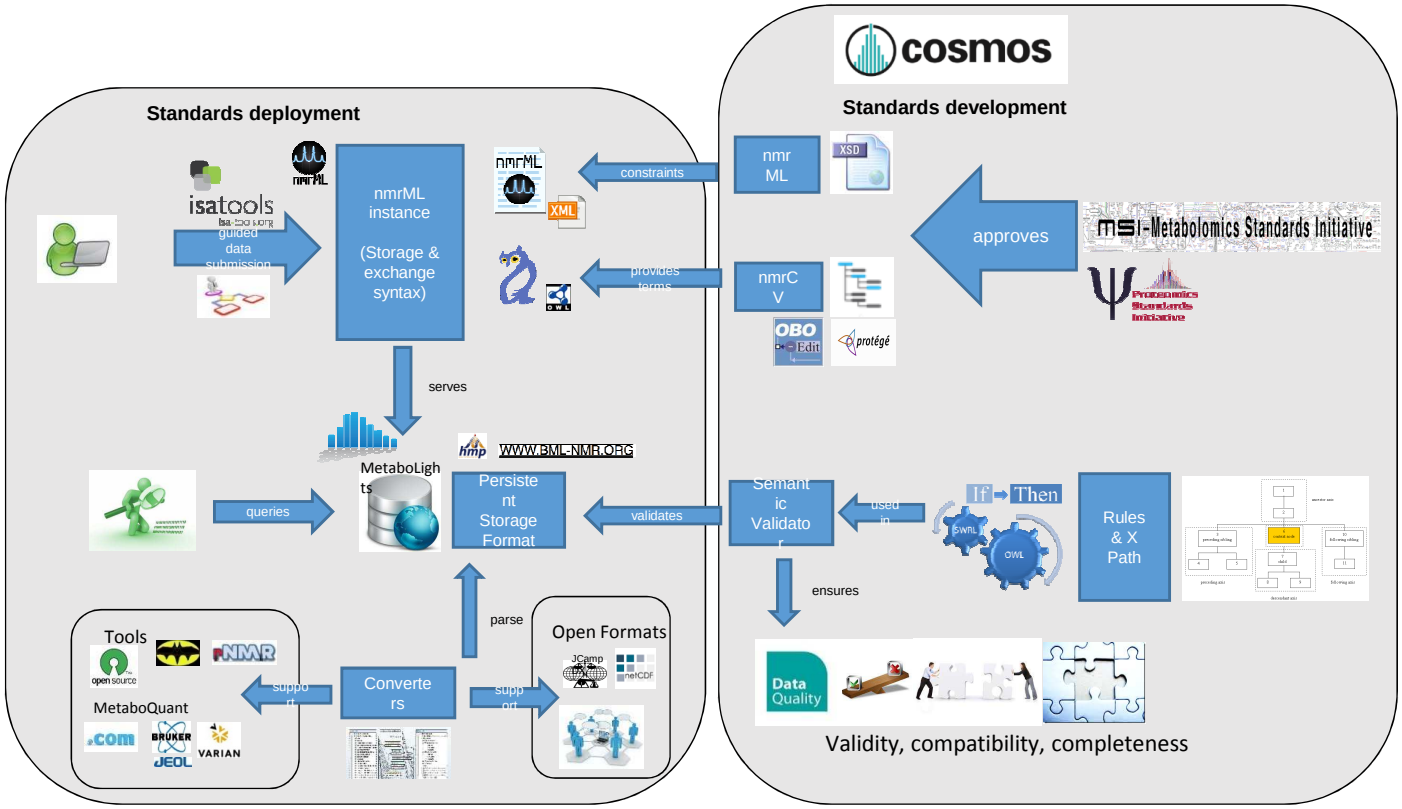
ISA-tab
http://isatab.sf.net

Terminologies of description

OBO foundry
http://obofoundry.org

COSMOS data annotation, verification, and distribution workflow

ISA-Tab



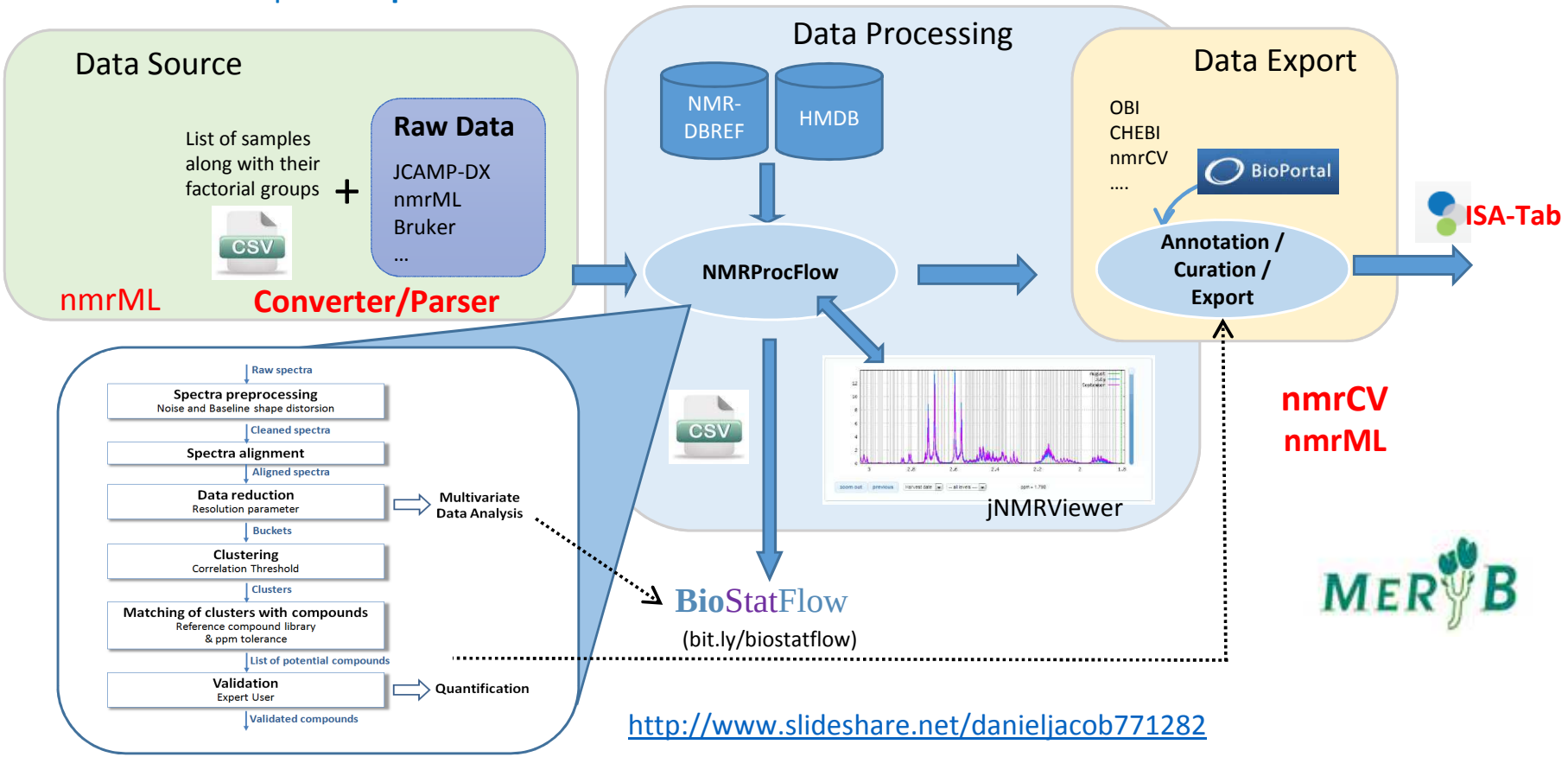
nmrML

nmrCV

Converter/Parser

NMRProcFlow

An efficient spectra processing workflow for metabolite identification from 1H-NMR metabolomics data
from **Raw Data** up to the **peaks list** and the **metabolites identification**

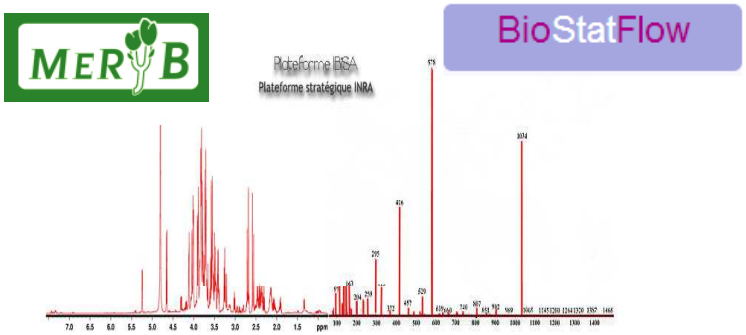


http://www.slideshare.net/danieljacob771282

Jacob D. *et al*, (March 2013) Analytical and Bioanalytical Chemistry. DOI:10.1007/s00216-013-6852-y

Remerciements :

UMR1332 BFP /
PMFB
Stéphane Bernillon
Catherine Deborde
Yves Gibon
Mickaël Maucourt
Annick Moing
Dominique Rolin



http://bit.ly/meryb
http://bit.ly/biostatflow
https://code.google.com/p/nmr-viewer/

INRA SCIENCE & IMPACT

cgfb MÉTABOLOME