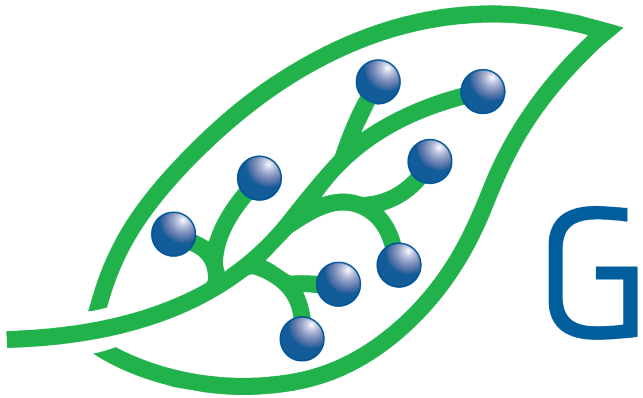

GoMapMan

https://gomapman.nib.si

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GoMapMan v1 – how it started

Motivation

- 2006ish: discovery of MapMan, translation to potato, expanding ontology…
- Problem 1: Curation of MapMan mappings in Excel
- Problem 2: Synchronization between species

GoMapMan v1:

Arabidopsis, potato, tomato, rice

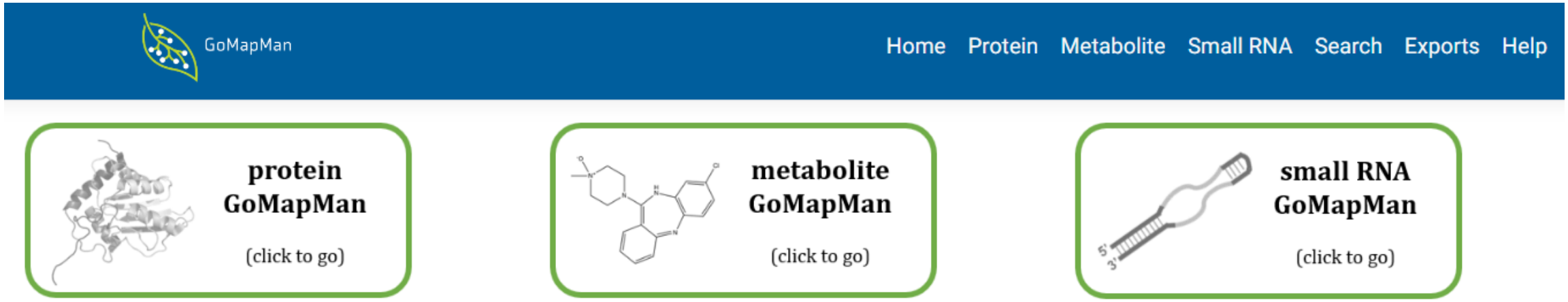
Published online 4 November 2013 *Nucleic Acids Research, 2014, Vol. 42, Database issue* ***D1167–D1175***
doi:10.1093/nar/gkt1056

GoMapMan: integration, consolidation and visualization of plant gene annotations within the MapMan ontology

Živa Ramšak[1,*], Špela Baebler[1], Ana Rotter[1], Matej Korbar[2], Igor Mozetič[2], Björn Usadel[3,4] and Kristina Gruden[1]

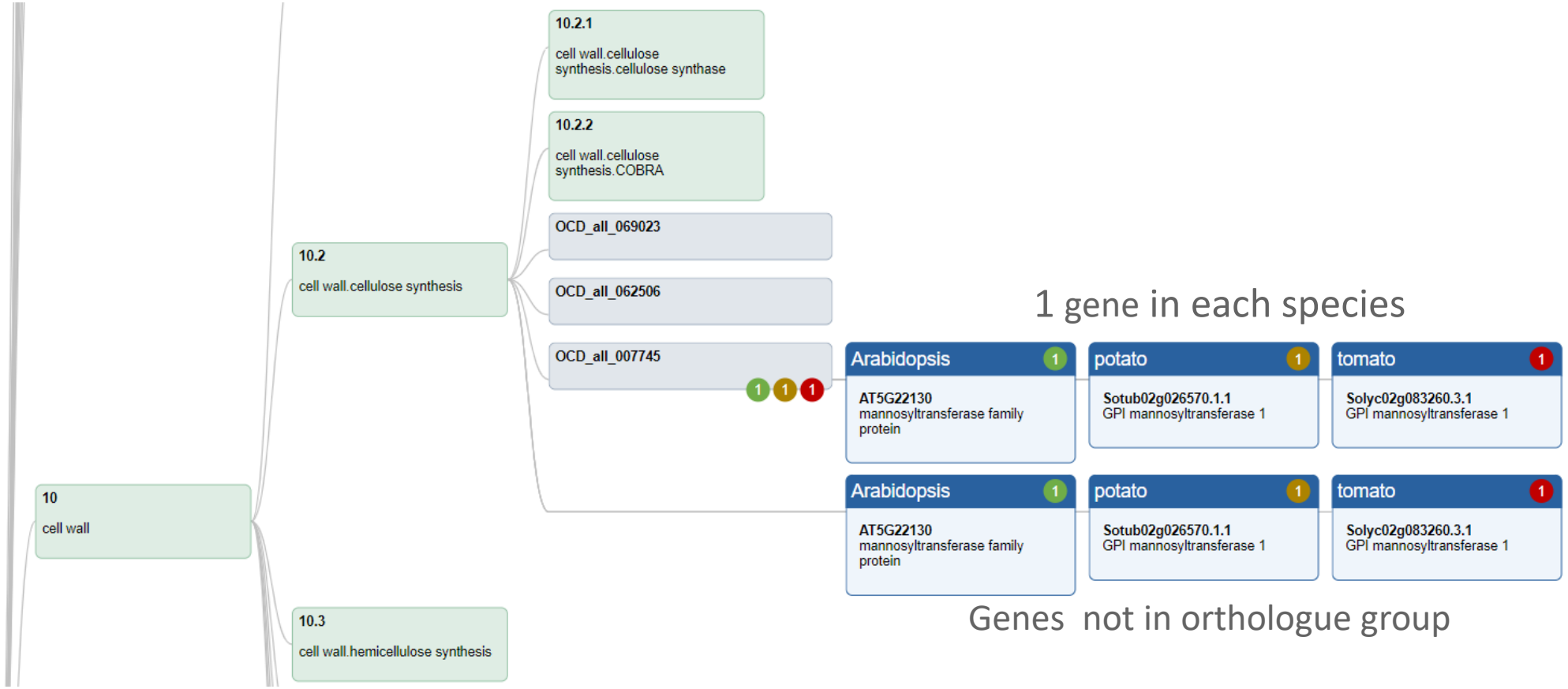
GoMapMan v2 – how it’s going

https://gomapman.nib.si



Gene ontology: MapMan v3

Browsing the PROTEIN ontology



orthologue group with genes of just one species

13 plant species

Plants

Check all | Uncheck all

☑ Arabidopsis	☑ potato	☐ grapevine	☐ rice	☐ Chlamydomonas
☐ papaya	☑ tomato	☐ black cottonwood	☐ pearl millet	
☐ sugar beet	☐ tobacco	☐ cacao tree	☐ bread wheat	

Default species

- **Arabidopsis** (*Arabidopsis thaliana*): Araport11
- **Potato** (*Solanum tuberosum*): StNIB-v1 (combining gene models PGSC v3.4 and ITAG v.1 with unigene sets POCI and StGIv13)
- **Tomato** (*Solanum lycopersicum*): ITAG Tomato Gene Models (v2.3), assembly SL2.40, annotation ITAG2.3

info on other species (with links) in HELP pages

Various (11) orthologue groupings

Ortholog type

OCD_all

PGSC/iTAG

- ITAG_orthoMCL: OrthoMCL orthologous groups by the Tomato Sequencing Consortium
- ITAG RSD: Reciprocal Shortest Distance orthologous groups; 4 plant species
- PGSC_orthoMCL: OrthoMCL orthologous groups Potato Genome Sequencing Consortium; 12 plant species

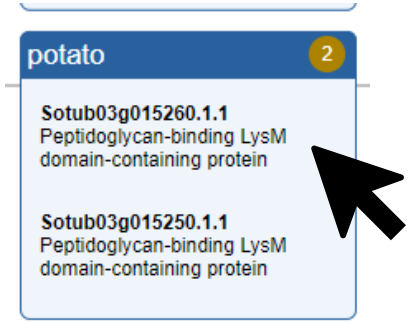
PLAZA

- PLAZA_dicots: PLAZA 3.0 dicot families
- PLAZA_monocots: PLAZA 3.0 monocot families
- PLAZA_dicots_sub: PLAZA 3.0 dicot subfamilies
- PLAZA_monocots_sub: PLAZA 3.0 monocot subfamilies

Combined (network weak components)

- **OCD_all**: ITAG_RSD + ITAG_orthoMCL + PLAZA_dicots_sub
  RECOMMENDED, selected by default
- WC_Pajek: ITAG_RSD + ITAG_orthoMCL + PGSC_orthoMCL
- OCD_PLAZAiTAG: ITAG_RSD + ITAG_orthoMCL + PLAZA_dicots_sub
- OCD_PLAZA: PLAZA_dicots_sub + PLAZA_monocots_sub

PROTEIN details



Gene details

Identifier	Sotub03g015260.1.1
Plant	potato
Related entities	MICRO.7877.C1, STMIS31TV, Sotub03g015260.1.1
Description	Peptidoglycan-binding LysM domain-containing protein
Short Name	-
Synonym	-
Source	stNIB-v1 (PGSC_DM_v3.4 and ITAG Potato Gene Model (to PGSC v2.1.11 Pseudomolecules).)
Last Modified	March 15, 2013

Ontology annotations

Click on bin to open it in ontology tree.

Bin Code	Bin Name	Bin Evidence Code
10.6	cell wall.degradation	IC

Orthologues

PGSCoMCL07354 | PGSCoMCL11254 | ITAG_RSD16094 | ITAGoMCL02944 | wc16168 | HOM03D001650 | ORTHO03D017133 | OCD_all_005239 | OCD_PLAZAiTAG_005200 | OCD_PLAZA_105806

Related entities

Entity ID	Description	Type	Source
MICRO.7877.C1	Putative dihydrodipicolinate reductase-like protein [Oryza sativa (japonica cultivar-group)]	probe	stu_Agilent_4x44k
STMIS31TV	No Hits Found	probe	stu_Agilent_4x44k
Sotub03g015260.1.1	Peptidoglycan-binding LysM domain-containing protein	gene	stu_ITAG

Annotations

GO	GO:0008150 biological_process GO:0009056 catabolic process GO:0016998 cell wall macromolecule catabolic process GO:0071554 cell wall organization or biogenesis
InterPro	IPR018392 LysM domain [domain]
PFAM	PF01476 LysM domain

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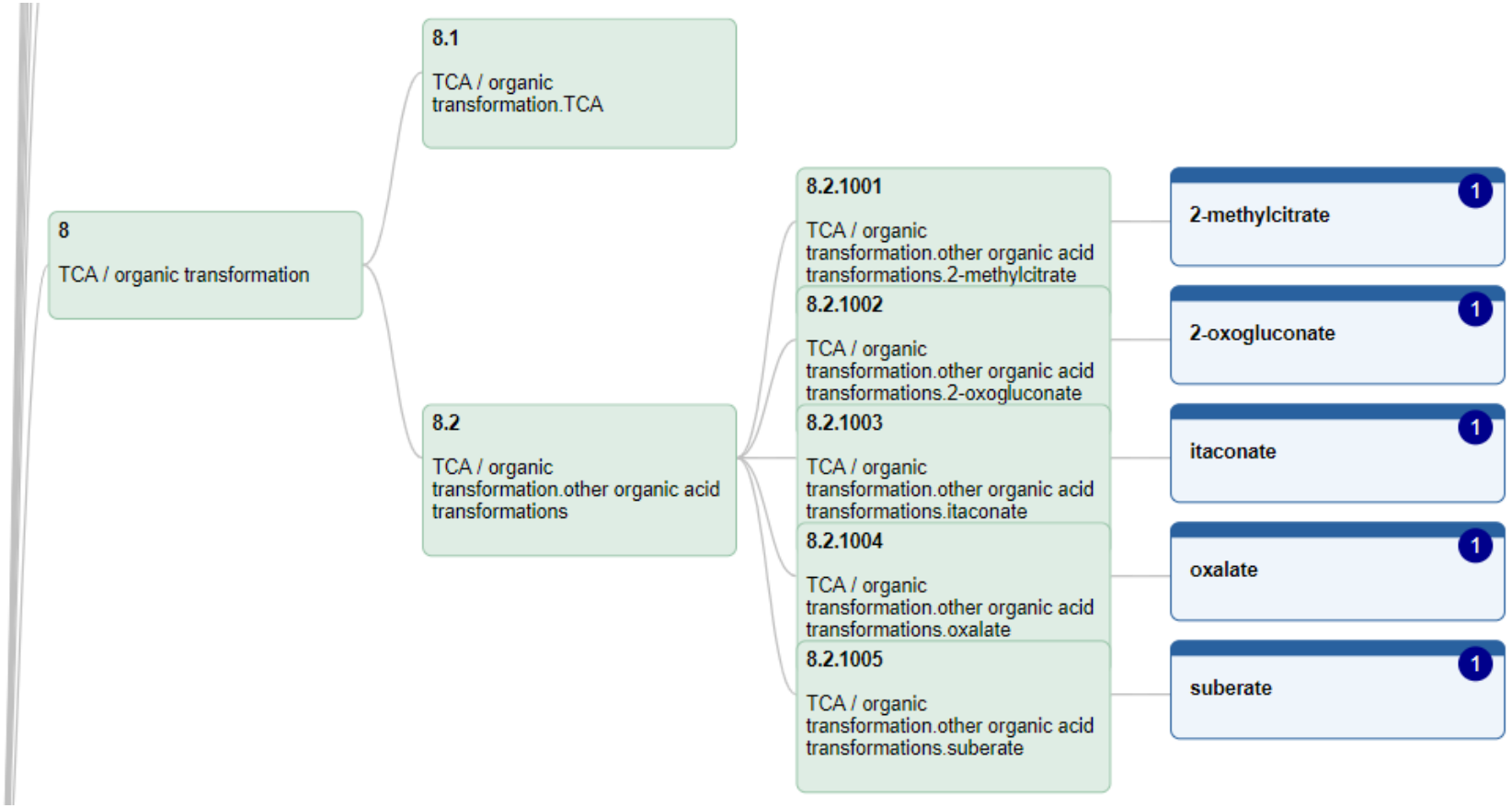
Browsing METABOLITE ontology & details



Metabolite details

Identifier	glycerate-3-phosphate
Other database ID	-
Source	MPI-MP (plant metabolites)
Last Modified	October 13, 2017

Ontology annotations

Click on bin to open it in ontology tree.

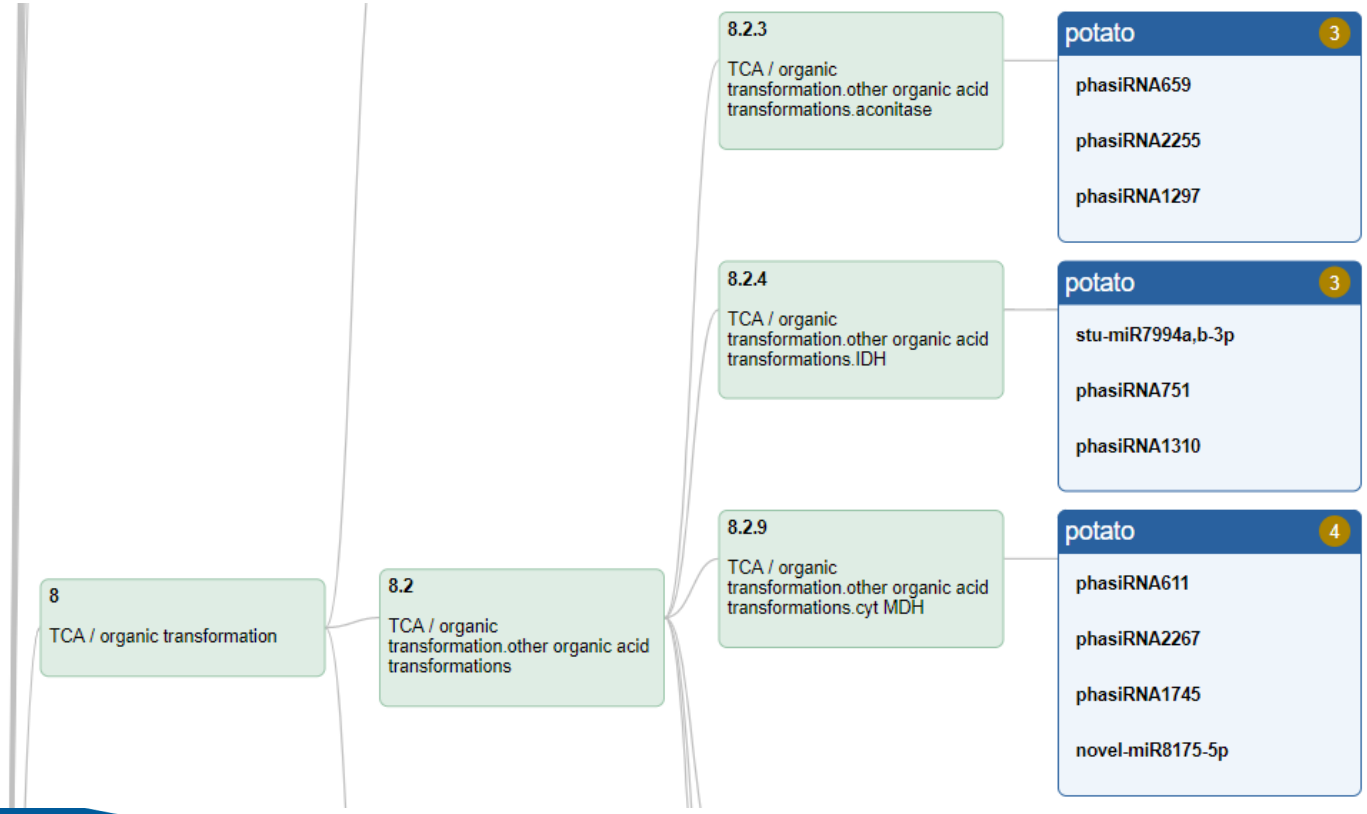
Bin Code	Bin Name
1.3.1006	PS.calvin cycle.glycerate-3-phosphate
4.1005	glycolysis.glycerate-3-phosphate

Just one “species”

Browsing sRNA ontology & annotation

sRNA inherits ontology position of the target gene

Only for potato (Križnik, FrontPlantSci 2018)



sRNA details

Identifier	stu-miR164a-3p
Plant	potato
Description	stu-miR164a-3p
Source	stu-MIR (miRNAs from potato, merger between miRBase and our own predictions)
Last Modified	October 13, 2017

Ontology annotations

Click on bin to open it in ontology tree.

Bin Code	Bin Name
5.1	fermentation.LDH
17.5.1.2	hormone metabolism.ethylene.synthesis-degradation.1-aminocyclopropane-1-carboxylate oxidase
17.5.2	hormone metabolism.ethylene.signal transduction
20.2.1	stress.abiotic.heat
27.3.19	RNA.regulation of transcription.EIN3-like (EIL) transcription factor family
27.3.32	RNA.regulation of transcription.WRKY domain transcription factor family
27.3.59	RNA.regulation of transcription.methyl binding domain proteins
27.3.63	RNA.regulation of transcription.PHD finger transcription factor
29.2.2	protein.synthesis.ribosome biogenesis

Search

○ Protein ○ Small RNA ◉ Metab

Enter your keywords

fructose

Search

Search in: ☑ Metabolite identifier ☑ Short name/Synonyms ☑ Description

Items per page 100

«« « 1 » »»

1.fructose

Description:

Shortname: none

Bin codes: 2.2.1.1001

2.fructose 6-phosphate

Description:

Shortname: none

Bin codes: 1.3.1002, 2.1.1.1001, 2.1.2.1002

3.fructose-1,6-biphosphate

Description:

Shortname: none

Bin codes: 1.3.1003

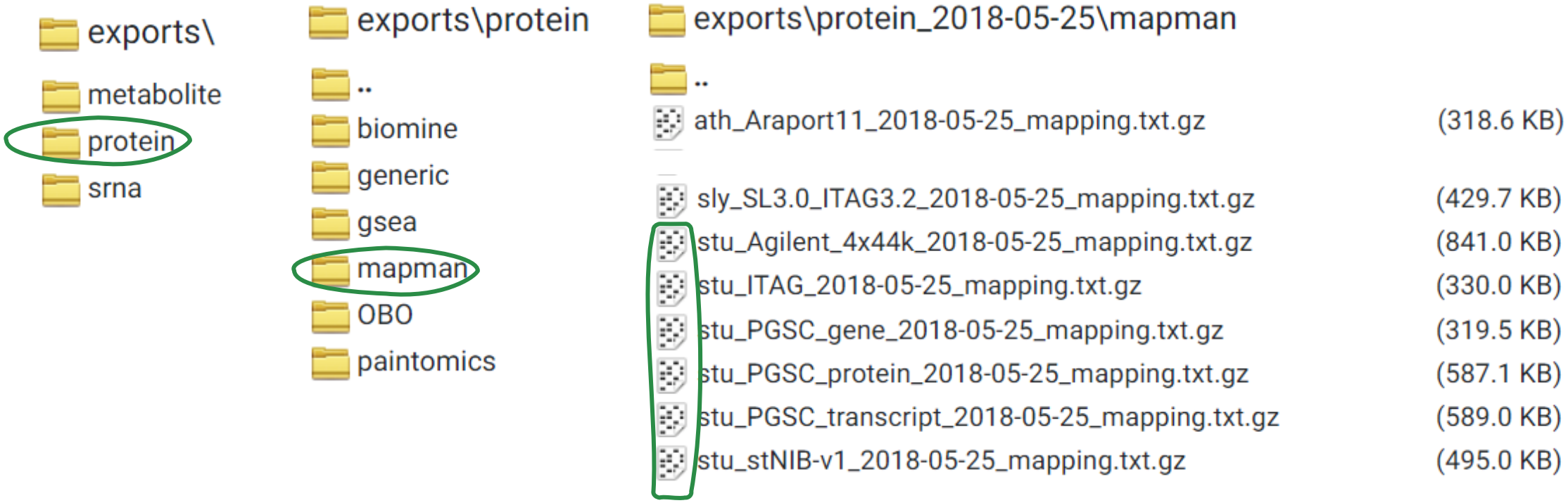
4.fructose-2,6-biphosphate

Description:

Shortname: none

Bin codes: 2.1.1.1002

Exports


exports\
metabolite
protein
srna
exports\protein
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biomine
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gsea
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paintomics
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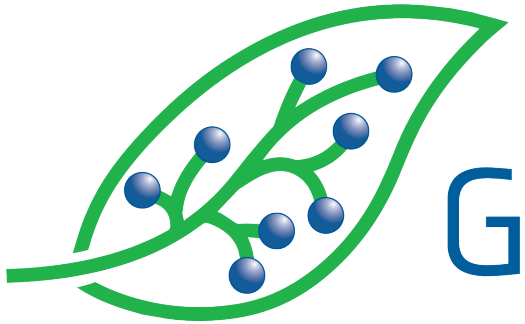
stu_PGSC_transcript_2018-05-25_mapping.txt.gz (589.0 KB)
stu_stNIB-v1_2018-05-25_mapping.txt.gz (495.0 KB)

Questions?

https://gomapman.nib.si
gomapman@nib.si



GoMapMan

Slovenian Research and Innovation Agency

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