





gOPrOfiles

- Purpose: Identifying enriched biological themes, GO terms from a list of UniProt/Entrez Gene IDs
- Input: a list of UniProt or Entrez Gene IDs



Enter your ID list (only Entrez Gene ID or UniProt accession number allowed)

Copy/paste your identifiers

Copy/paste your identifiers

Input file containing your identifiers

Please select the type of your IDs list

Entrez Gene ID

Remove duplicated IDs

☐ Yes ☐ No

Please select GO terms category

☐ Select/Unselect all

- ☐ Cellular Component (CC)
- ☐ Molecular Function (MF)
- ☐ Biological Process (BP)

Level of the ontology at which the profile has to be built (the higher this number, the deeper the GO level)

2

Plot absolute or relative frequencies (not summing to 100)

☐ Yes ☐ No

Enter title of your figure

Choose graphical output (bar plots) format: png, jpeg, pdf

Rechercher des données

23/01/18

9 shown, 4 deleted

211.62 KB

[13: Venn diagram text o
utput](#)[12: Venn diagram](#)[11: Mucilli.txt](#)[10: Bredberg.txt](#)[9: Expression levels by ti
ssue \(from HPA\) on data
4](#)[4: ID Converter on data
2](#)[3: Filter lines by keywor
ds or numerical value on
Lacombe et al 2017 OK.txt - Remov
ed lines](#)[2: Filter lines by keywor
ds or numerical value on
Lacombe et al 2017 OK.txt](#)

Enter your ID list (only Entrez Gene ID or UniProt accession number allowed)

Copy/paste your identifiers

Copy/paste your identifiers

Input file containing your identifiers

Please select the type of your IDs list

Entrez Gene ID

Remove duplicated IDs

☐ Yes ☐ No

Please select GO terms category

☐ Select/Unselect all

- ☐ Cellular Component (CC)
- ☐ Molecular Function (MF)
- ☐ Biological Process (BP)

Level of the ontology at which the profile has to be built (the higher this number, the deeper the GO level)

2

Plot absolute or relative frequencies (not summing to 100)

☐ Yes ☐ No

Enter title of your figure

Choose graphical output (bar plots) format: png, jpeg, pdf

Rechercher des données

23/01/18

9 shown, 4 deleted

211.62 KB

[13: Venn diagram text o
utput](#)[12: Venn diagram](#)[11: Mucilli.txt](#)[10: Bredberg.txt](#)[9: Expression levels by ti
ssue \(from HPA\) on data
4](#)[4: ID Converter on data
2](#)[3: Filter lines by keywor
ds or numerical value on
Lacombe et al 2017 OK.txt - Remov
ed lines](#)[2: Filter lines by keywor
ds or numerical value on
Lacombe et al 2017 OK.txt](#)

Enter your ID list (only Entrez Gene ID or UniProt accession number allowed)

Copy/paste your identifiers

Copy/paste your identifiers

Input file containing your identifiers

Please select the type of your IDs list

Entrez Gene ID

Remove duplicated IDs

Yes

No

Please select GO terms category

Select/Unselect all

Cellular Component (CC)

Molecular Function (MF)

Biological Process (BP)

Level of the ontology at which the profile has to be built (the higher this number, the deeper the GO level)

2

Plot absolute or relative frequencies (not summing to 100)

Yes

No

Enter title of your figure

Choose graphical output (bar plots) format: png, jpeg, pdf



Rechercher des données

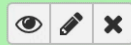
23/01/18

9 shown, 4 deleted

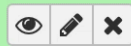
211.62 KB



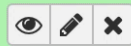
13: Venn diagram text output



12: Venn diagram



11: Mucilli.txt



10: Bredberg.txt



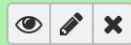
9: Expression levels by tissue (from HPA) on data 4



4: ID Converter on data 2



3: Filter lines by keywords or numerical value on Lacombe et al 2017 OK.txt - Removed lines



2: Filter lines by keywords or numerical value on Lacombe et al 2017 OK.txt



goProfiles

- Purpose: Identifying enriched biological themes, GO terms from a list of UniProt/Entrez Gene IDs
- Input: a list of UniProt or Entrez Gene IDs

The screenshot displays the goProfiles web interface, which is used for identifying enriched biological themes and GO terms from a protein list. The interface is divided into two main sections: the main input area on the left and a history panel on the right.

Main Input Area:

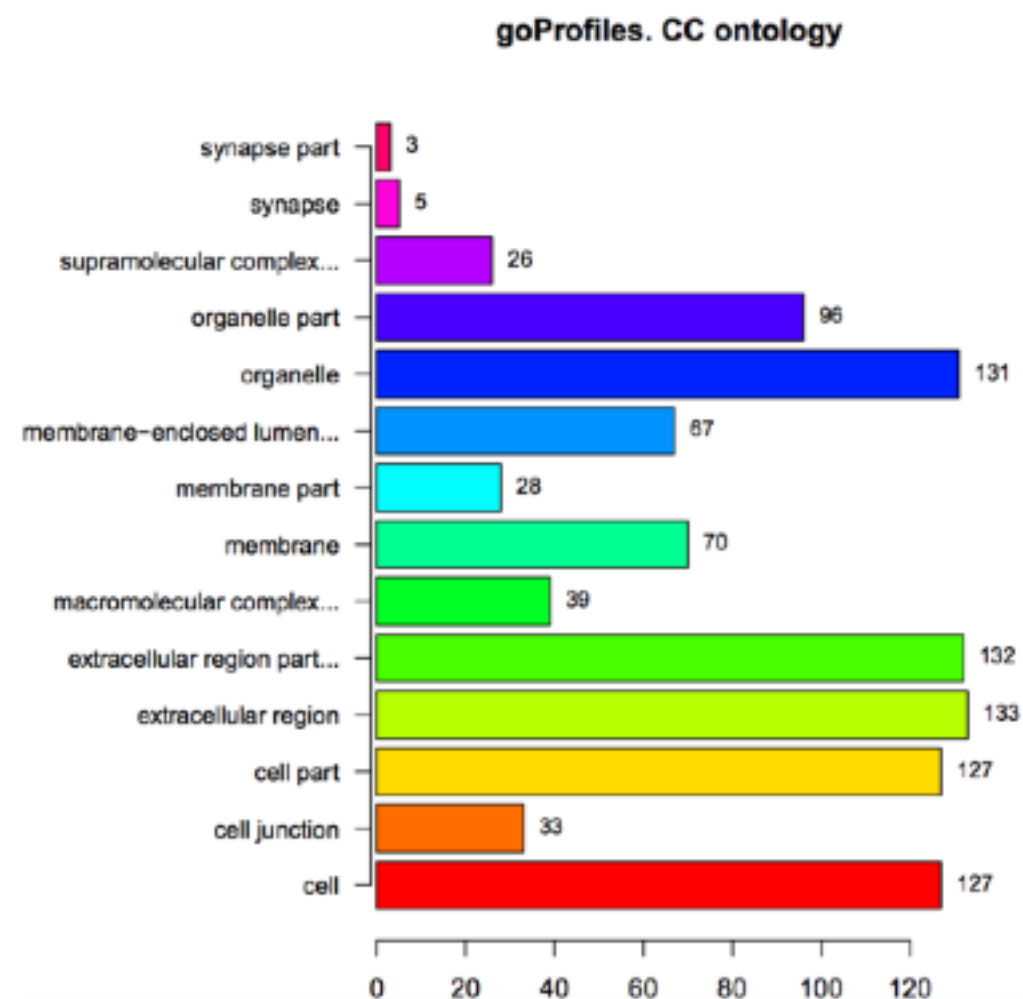
- Header:** goProfiles Identify enriched biological themes, GO terms from your protein list. (Galaxy Version 0.1.0) [Options]
- Input Section:** Enter your ID list (only Entrez Gene ID or UniProt accession number allowed). It includes a text input field with a search icon and a dropdown menu with the option "Copy/paste your identifiers".
- ID Type Selection:** Please select the type of your IDs list. A dropdown menu shows "Entrez Gene ID".
- Duplicate Removal:** Remove duplicated IDs. Buttons for "Yes" and "No".
- GO Terms Category:** Please select GO terms category. A checkbox for "Select/Unselect all" is present. Below it, three checkboxes are listed: "Cellular Component (CC)", "Molecular Function (MF)", and "Biological Process (BP)".
- Ontology Level:** Level of the ontology at which the profile has to be built (the higher this number, the deeper the GO level). A dropdown menu shows "2".
- Plotting Options:** Plot absolute or relative frequencies (not summing to 100). Buttons for "Yes" and "No".
- Figure Title:** Enter title of your figure. A text input field.
- Output Format:** Choose graphical output (bar plots) format: png, jpeg, pdf. A dropdown menu.

History Panel:

- Header:** History [Refresh] [Settings] [Close]
- Search:** Rechercher des données [Search Icon]
- Current View:** 23/01/18, 9 shown, 4 deleted, 211.62 KB. [Check] [Trash] [Comment]
- History List:**
 - 13: Venn diagram text output [Eye] [Edit] [X]
 - 12: Venn diagram [Eye] [Edit] [X]
 - 11: Mucilli.txt [Eye] [Edit] [X]
 - 10: Bredberg.txt [Eye] [Edit] [X]
 - 9: Expression levels by tissue (from HPA) on data 4 [Eye] [Edit] [X]
 - 4: ID Converter on data 2 [Eye] [Edit] [X]
 - 3: Filter lines by keywords or numerical value on Lacombe et al 2017 OK.txt - Removed lines [Eye] [Edit] [X]
 - 2: Filter lines by keywords or numerical value on Lacombe et al 2017 OK.txt [Eye] [Edit] [X]

goProfiles

- Results: plot and textual output for each GO categories chosen



1	2	3
CC.Description	CC.GOID	CC.Frequency
cell	GO:0005623	127
cell junction	GO:0030054	33
cell part	GO:0044464	127
extracellular region	GO:0005576	133
extracellular region part	GO:0044421	132
macromolecular complex	GO:0032991	39
membrane	GO:0016020	70
membrane part	GO:0044425	28
membrane-enclosed lumen	GO:0031974	67
organelle	GO:0043226	131
organelle part	GO:0044422	96
supramolecular complex	GO:0099080	26
synapse	GO:0045202	5
synapse part	GO:0044456	3
MF.Description	MF.GOID	MF.Frequency
antioxidant activity	GO:0016209	8
binding	GO:0005488	127
catalytic activity	GO:0003824	60
molecular function regulator	GO:0098772	27
molecular transducer activity	GO:0060089	9
nucleic acid binding transcription factor activity	GO:0001071	1
signal transducer activity	GO:0004871	4
structural molecule activity	GO:0005198	27
transcription factor activity, protein binding	GO:0000988	1
transporter activity	GO:0005215	7

This tool uses R/Bioconductor package goProfiles - Sanchez A, Ocana J and Salicru M (2016). goProfiles: goProfiles: an R package for the statistical analysis of functional profiles. R package version 1.38.0.