





Porteiras

- Purpose: Annotating your protein list using features retrieved from neXtProt database
- Input: a list of neXtProt or UniProt IDs



Select your type of input file

Input file containing your identifiers (neXtProt or Uniprot ID)

Choose a file that contains your list of IDs



34: Get annotation from RNAseq/Ab-based experiments (Human species) on data 4

This file must imperatively have 1 column filled with IDs consistent with the neXtprot database (Uniprot accession number or neXtProt ID). If this is not the case, please use the ID_Converter tool.

Please specify the column where are your IDs (e.g : Enter c1 for column n°1)

c1

Does your file have a header?

Yes

Type of your input ids

Uniprot accession number

Select features of interest (compulsory step)

Physico-Chemical Features

☐ Select/Unselect all

- ☐ Sequence Length
- ☐ Molecular Weight
- ☐ Isoelectric point
- ☐ Number of transmembrane domains
- ☐ Protein Existence (evidence score from 1 to 5)

Choose the information you want to add to your data from Nextprot

Localization

Rechercher des données

23/01/18

21 shown, 10 [deleted](#), 3 [hidden](#)

2.22 MB



[34: Get annotation from RNAseq/Ab-based experiments \(Human species\) on data 4](#)



[33: Dotplot output for to pGO analysis MF category Y](#)



[32: Barplot output for to pGO analysis MF category Y](#)



[31: Text output for topG O analysis MF category](#)



[30: Dotplot output for to pGO analysis CC category Y](#)



[29: Barplot output for to pGO analysis CC category Y](#)



[28: Text output for topG O analysis CC category](#)



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Protein Features (neXtProt) Annotate your protein list using features retrieved from neXtProt database.

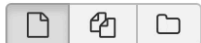
Options

(Galaxy Version 0.1.0)

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Does your file have a header?

Yes

Type of your input ids

Uniprot accession number

Select features of interest (compulsory step)

Physico-Chemical Features

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- ☐ Molecular Weight
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Choose the information you want to add to your data from Nextprot

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Protein features

- Purpose: Annotating your protein list using features retrieved from neXtProt database
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Protein Features (neXtProt) Annotate your protein list using features retrieved from neXtProt database. (Galaxy Version 0.1.0) Options

Select your type of input file

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c1

Does your file have a header?

Yes

Type of your input ids

Uniprot accession number

Select features of interest (compulsory step)

Physico-Chemical Features

☐ Select/Unselect all

☐ Sequence Length

☐ Molecular Weight

☐ Isoelectric point

☐ Number of transmembrane domains

☐ Protein Existence (evidence score from 1 to 5)

Choose the information you want to add to your data from Nextprot

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Protein features

- Result: information from neXtProt added into the end of input file

SeqLength	MW	IsoPoint	TMDomains	ProteinExistence	Chr
SeqLength	MW	IsoPoint	TMDomains	ProteinExistence	Chr
1454	161107	5.5	0	PE1	12
911	104854	5.27	0	PE1	19
334	37329	8.98	0	PE1	9
188	21008	5.07	0	PE1	7
701	80356	7.57	0	PE1	17
2602	278164	5.47	0	PE1	3
380	42905	6.34	0	PE1	18
346	35971	8.05	0	PE1	19
332	36689	8.44	0	PE1	11
154	15936	5.7	0	PE1	21
289	32118	6.45	0	PE1	14
417	44615	8.3	0	PE1	X
406	45205	6.13	0	PE1	16
418	46737	5.37	0	PE1	14
423	47651	5.33	0	PE1	14
141	16214	4.95	0	PE1	20
141	16388	6.73	0	PE1	20
98	11006	5.38	0	PE1	3
Protein not found in Nextprot	Protein not found in Nextprot	Protein not found in Nextprot	Protein not found in Nextprot	Protein not found in Nextprot	Protein not found in Nextprot
Protein not found in Nextprot	Protein not found in Nextprot	Protein not found in Nextprot	Protein not found in Nextprot	Protein not found in Nextprot	Protein not found in Nextprot

Annotations have been retrieved from the neXtProt database (Gaudet et al., 2017)