

Protein features

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

SeqLength	MW	IsoPoint	TMDomains	ProteinExistence	Chr
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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)

Reactome analysis tool

- Purpose: querying Reactome with your list of IDs
- Input: a list of identifiers (UniProt, Entrez Gene IDs or Gene Name)

Reactome Analysis Tools query Reactome with your IDs list (Galaxy Version 0.1.0) Options

Input identifiers (Uniprot accession number (e.g. P01023), Entrez gene ID (e.g.7157) or gene name (e.g. AQP7))

Copy/paste your list of IDs

Enter list of identifiers

Execute

Reactome software provides service of creating diagram representing the relations between the biological processes. This tool allows linking to Reactome web service with pre-loaded data from a list of IDs, a file containing IDs or from a column of a complexed file.

For the rows that have more than 1 ID, only the first one is taken into account Supported IDs: Uniprot accession number (e.g. P01023), Entrez gene ID (e.g.7157), gene name (e.g. AQP7)

Authors
Fabregat et al. 2017 PMID: 29145629 (<https://www.ncbi.nlm.nih.gov/pubmed/29145629>)
Milacic et al. 2012 PMID:24213504 (<https://www.ncbi.nlm.nih.gov/pubmed/24243840>)

Galaxy integration
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Sandra Dérozier, Olivier Rué, Christophe Caron, Valentin Loux INRA, Paris-Saclay University, MAIAGE Unit, Migale Bioinformatics platform,
Contact support@proteore.org for any questions or concerns about the Galaxy implementation of this tool.

History

Rechercher des données

23/01/18
22 shown, 10 deleted, 3 hidden
2.25 MB

35: Add information from neXtProt

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

33: Dotplot output for to pGO analysis MF category

32: Barplot output for to pGO analysis MF category

31: Text output for topGO analysis MF category

30: Dotplot output for to pGO analysis CC category

29: Barplot output for to pGO analysis CC category