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



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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Contact [support@proteore.org](mailto:support@proteore.org) for any questions or concerns about the Galaxy implementation of this tool.

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





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

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- Result: a link to Reactome Web service

