

Tools

- **Data manipulation**

- ▶ Filter lines by keywords or numerical value
- ▶ ID Converter

- **Retrieve annotation**

- ▶ Get annotation from RNAseq/Ab-based experiments (Human species)
- ▶ Protein features (neXtProt)
- ▶ Expression level by tissue (from HPA)

- **Bioinformatic analysis tools**

- ▶ Venn diagram
- ▶ Reactome ananlysis tool
- ▶ topGO
- ▶ goProfiles

- **Other tools**

Filter lines by keywords or numerical value

- Purpose: removing unneeded data from your input
- Input file: tab-delimited file containing proteomics identification and/or quantitative results

1	2	3
Protein accession number (UniProt)	Protein name	Number of peptides (razor + unique)
P15924	Desmoplakin	69
P02538	Keratin, type II cytoskeletal 6A	53
P02768	Serum albumin	44
P08779	Keratin, type I cytoskeletal 16	29
Q02413	Desmoglein-1	24
P07355	*Annexin A2;Putative annexin A2-like protein*	22
P14923	Junction plakoglobin	22
P02788	Lactotransferrin	21
Q9HC84	Mucin-5B	21
P29508	Serpin B3	20
P63261	Actin, cytoplasmic 2	19
Q8N1N4	Keratin, type II cytoskeletal 78	18
Q04695	Keratin, type I cytoskeletal 17	18
P01876	Ig alpha-1 chain C region	16
Q01469	Fatty acid-binding protein 5, epidermal	15
P31944	Caspase-14	15
P01833	Polymeric immunoglobulin receptor	15
P06733	Alpha-enolase	15
P25311	Zinc-alpha-2-glycoprotein	15
Q15149	Plectin	15
P19013	Keratin, type II cytoskeletal 4	13
Q6KB66	Keratin, type II cytoskeletal 80	13
Q08188	Protein-glutamine gamma-glutamyltransferase E	12

Input file containing 3 columns corresponds to Table 2, 3 and 4 published in Lacombe et al,
<http://iopscience.iop.org/article/10.1088/1752-7163/aa9e71>