

# Filter lines by keywords or numerical value

- Removed lines: including 10 IDs

1	2	3
Protein accession number (UniProt)	Protein name	Number of peptides (razor + unique)
P04264	Keratin, type II cytoskeletal 1	61
P35908	Keratin, type II cytoskeletal 2 epidermal	40
P13645	Keratin, type I cytoskeletal 10	40
Q5D862	Filaggrin-2	14
Q5T749	Keratinocyte proline-rich protein	13
Q8IW75	Serpin A12	3
P81605	Dermcidin	3
P22531	Small proline-rich protein 2E	3
P59666	Neutrophil defensin 3	2
P78386	Keratin, type II cuticular Hb5	2

# ID Converter

- Purpose: converting a list of IDs into other types of public database IDs.
- Input: a list of identifiers (14 types of identifier available)

The screenshot displays the 'ID Converter' web interface. The main panel is titled 'ID Converter convert public database identifiers (Homo sapiens only for now) (Galaxy Version 0.1.0)'. It features a 'Provide your identifiers' section with a text input field and a dropdown menu. Below this is a 'Select type/source of identifier of your list' section with a dropdown menu. The 'Target type of IDs' section is expanded, showing a list of 14 target identifiers with checkboxes: neXtProt ID, Uniprot accession number, Uniprot ID, Entrez gene ID, RefSeq (NCBI) protein, GI (NCBI GI number) ID, Protein DataBank ID, GOterms (Gene Ontology) ID, Protein Information Resource ID, OMIM (Online Mendelian Inheritance in Man database) ID, Unigene ID, Ensembl gene ID, and Ensembl transcript ID. On the right, a 'History' panel shows a search bar and a list of three items: '1: Lacombe et al 2017 OK.txt', '2: Filter lines by keywords or numerical value on Lacombe et al 2017 OK.txt', and '3: Filter lines by keywords or numerical value on Lacombe et al 2017 OK.txt - Removed lines'. The interface is clean and functional, with a clear layout for input and output.