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| * Primary commands | Command | Function |
| | -in | input file |
| | -out | output file |
| | -p | protein sequences |
| | -n | nucleotide sequences |

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|--------------------|-----------------------|-----------------------------------|------------------------|---|
| Secondary commands | Dereplication | | Filteration | |
| | Command | Function | Command | Function |
| | */ -mode derep | switch to dereplication mode | */ -mode filter | switch to filter mode |
| | -min_length | minimum sequence length in output | ** -flt_file | file containing the names or fasta sequences to be filtered |
| | -multi | multiple files to process | | |
| | -fastq | to process fastq files | | |

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|-------------------|---------------|-----------------------------|----------------|-------------------------|-------------------------------------|------------------------|---|
| Tertiary commands | Dereplication | | | Name filteration | | Sequence filteration | |
| | Command | Function | longest length | Command | Function | Command | Function |
| | -optimum | for optimum length approach | | **/ -flt_by name | switch to name filteration approach | **/ -flt_by seq | switch to sequence filteration approach |
| | -prot_length | your ideal protein length | | -approach | inclusive or exclusive | -len | length of k-mer (default =6) |

* required
*/ conditional requirement
** required on secondary level
**/ conditional requirement on secondary level