

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

Secondary commands	Dereplication		Filtration		Exchange headers	
	Command	Function	Command	Function	Command	Function
	*/ -mode <b>derep</b>	switch to dereplication mode	*/ -mode <b>filter</b>	switch to filter mode	*/ -mode <b>exchange_headers</b>	switch to exchange headers mode
	*/ -org_order	preserve the original order of sequences				
	-min_length	minimum sequence length in output	** -flt_file	file contains the names or fasta sequences to be filtered	** -ex_file	csv file contains the old and the new words to be exchanged in FASTA headers
	-multi	multiple files to process				
	-fastq	to process fastq files				

Tertiary commands	Dereplication			Name filtration		Sequence filtration	
	Command	Function	longest length	Command	Function	Command	Function
	-len	length of k-mer (default =28)		**/ -flt_by <b>name</b>	switch to name filtration approach	**/ -flt_by <b>seq</b>	switch to sequence filtration approach
	-optimum	for optimum length approach		**/ -kw	Filter by keywords (separated by a comma) in your FASTA headers either inclusive or exclusive	**/ -org_order	preserve the original order of sequences
	-prot_length	your ideal protein length		-approach	inclusive or exclusive	-len	length of k-mer (default=28)

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