Primary commands

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

Secondary commands

	Dereplication		Filtration		Exchange headers	
	Command	Function	Command	Function	Command	Function
Secondary commands	***/ -mode derep**	switch to dereplication mode	***/ -mode filter**	switch to filter mode	***/ -mode exchange_headers**	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		Command	Function	Command	Function
Tertiary commands			longest length	****/ -flt_by name**	switch to name filtration approach	****/ -flt_by seq**	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 =6)

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