* Primary commands

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

Secondary commands

	Dereplication		Filtration	
	Command	Function	Command	Function
	*/ -mode derep	switch to dereplication mode	*/ -mode filter	switch to filter mode
	*/ -org_order	preserve the original order of sequences		
	-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		

Tertiary commands

	Dereplication			Name filtration		Sequence filtration	
	Command	Function	longest length	Command	Function	Command	Function
				**/ -flt_by name	switch to name filtration approach	**/ -flt_by seq	switch to sequence filteration 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