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

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		

Tertiary commands	Dereplication			Name filtration		Sequence filtration	
	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 =20)

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