SeqQual pipeline / program (prog) name*	usage**	arguments (arg)	description (Record of actions and parameters printed into log.txt)	Shell examples ***
print_log-ace_changename.pl	**(perl ~/SeqQual/prog arg >> log.txt) = *(A)***		change ace name	2.1-ace-only.sh
print_log-largeace_split.pl	***(A)***		split large ace	2.3-ace-qual.sh
print_log-largephd_split.pl	"		split large phd files	2.3-ace-qual.sh
print_log-acedealing-qual.pl	"		dealing with ace and qual files	2.3-ace-qual.sh
print_log-aceonly.pl	"		dealing with ace files which have no other related files	2.3-ace-qual.sh
print_log-aln-diploid-ab1.pl	"	polyphred score, polyphred quality and 18 parameters for phrap	diploid_ab1; phrap parameters used in phrap, polyphred pamaters used in polyphred	1.1-diploid-ab1.sh
print_log-aln-haploid-ab1.pl	"	18 parameters from Phrap	haploid_ab1; phrap parameters used in phap	1.2-haploid-ab1.sh
print_log-arlequin-diploid.pl	"	up to 20 group names	writing arlequin input files from diploid data; and up to 20 group numbers or names used	*fasta-*data.sh
print_log-arlequin-haploid.pl	"	up to 20 group names	write arlequin input files for haploid data; and up to 20 group numbers or names used	*fasta-*data.sh
print_log-fasta.pl	"		dealing with fasta alignment files	*fasta-*data.sh
print_log-remove1.pl	"		remove bad positions with only "?" and "-"	1.1-diploid-ab1.sh, 1.2-haploid-ab1.pl
print_log-renamephd.pl	"		rename phd files	1.1-diploid-ab1.sh, 1.2-haploid-ab1.pl
print_log-replace.pl	"	max length of "isolated nucleotides"	replace isolated nucleotides which are surrouned by "?"; the max length of "isolated nucleotides" (which is used by the script)	1.1-diploid-ab1.sh
print_log-truncate.pl	"	number of nucleotides in the column from which truncate process is done	truncate; the number of nucleotides in the column from which the truncate process is done	1.1-diploid-ab1.sh
print_log-userphd-diploid-ab1.pl	"		inserting user phd/poly files	1.1-diploid-ab1.sh
print_log-userphd-haploid-ab1.pl	"		inserting user phd files	1.2-haploid-ab1.sh
print_log-write_aln-diploid.pl	"	phred score, genotype score	write fasta alignment from ace, phd, polyphred.out; phred score and genotype score used	1.1-diploid-ab1.sh
print_log-write_aln-qual.pl	"	phred score	write fasta alignment , phd score used	2.3-ace-qual.sh
print_log-write_aln-haploid.pl	"	phred score	write fasta alignment , phd score used	1.2-haploid-ab1.sh
print_log-write_haplotypealn.pl	"		write haploid phase unknown alignment files from diploid alignment files	*fasta-*data.sh
print_log-write_SNP-diploid.pl	"	phred score, genotype score	write SNP aligment; phred score, genotype score	*fasta-*data.sh
print_log-write_SNP-fasta_aln.pl	"		write SNP alignment	*fasta-*data.sh
print_log-write_unaln-diploid.pl	"	phred score, genotype score	write unaligned fasta files; phred score, genotype score	*fasta-*data.sh
print_log-write_unaln-haploid.pl	"	phred score	write unaligned fasta files; phred score	*fasta-*data.sh
print_log-write_unaln-fasta.pl	"		write unaligned fasta files	*fasta-*data.sh
take_log_to_output.pl	"		take log.txt to folder Output, check name to log_data&time.txt	1.1-diploid-ab1.sh, 1.2-haploid-ab1.sh, *fasta-*data.sh

***** **all print_log scripts relate to the print_source scripts of the same names and can be used along with them**

****** **all scripts append log information to the log.txt file**

******* **all shell scripts can be run by typing "source *.sh"**