

prepare_probeslist_for_part2_from_lreens_output

↪ input
selected_probes.txt
output →
probes.fasta

merge_LHS_RHS_for_each_gene
↪ input
probes.fasta
output →
merged_sequences.txt

trim_from_Atail_for_cross_hybridization_check
↪ input
merged_sequences.txt
output →
cleaned_sequences.fasta

trim_from_prefix_for_cross_hybridization_check
↪ input
cleaned_sequences.fasta
output →
cleaned_sequences_from_prefix.fasta

blast_for_cross_hybridization_check
↪ input
cleaned_sequences_from_prefix.fasta
output →
blast_cross_results/results_env_nt_nt.txt blast_cross_results/results_nt_prok_nt.txt blast_cross_results/results_nt_viruses_nt.txt

filter_hits
↪ input
blast_cross_results/results_env_nt_nt.txt blast_cross_results/results_nt_prok_nt.txt blast_cross_results/results_nt_viruses_nt.txt probes.fasta
output →
filtered_probes.fasta

generate_output_after_cross_check
↪ input
filtered_probes.fasta
output →
output_after_cross_check_combined.xlsx output_after_cross_check_lhs.xlsx output_after_cross_check_rhs.xlsx

all
↪ input
output_after_cross_check_combined.xlsx output_after_cross_check_lhs.xlsx output_after_cross_check_rhs.xlsx