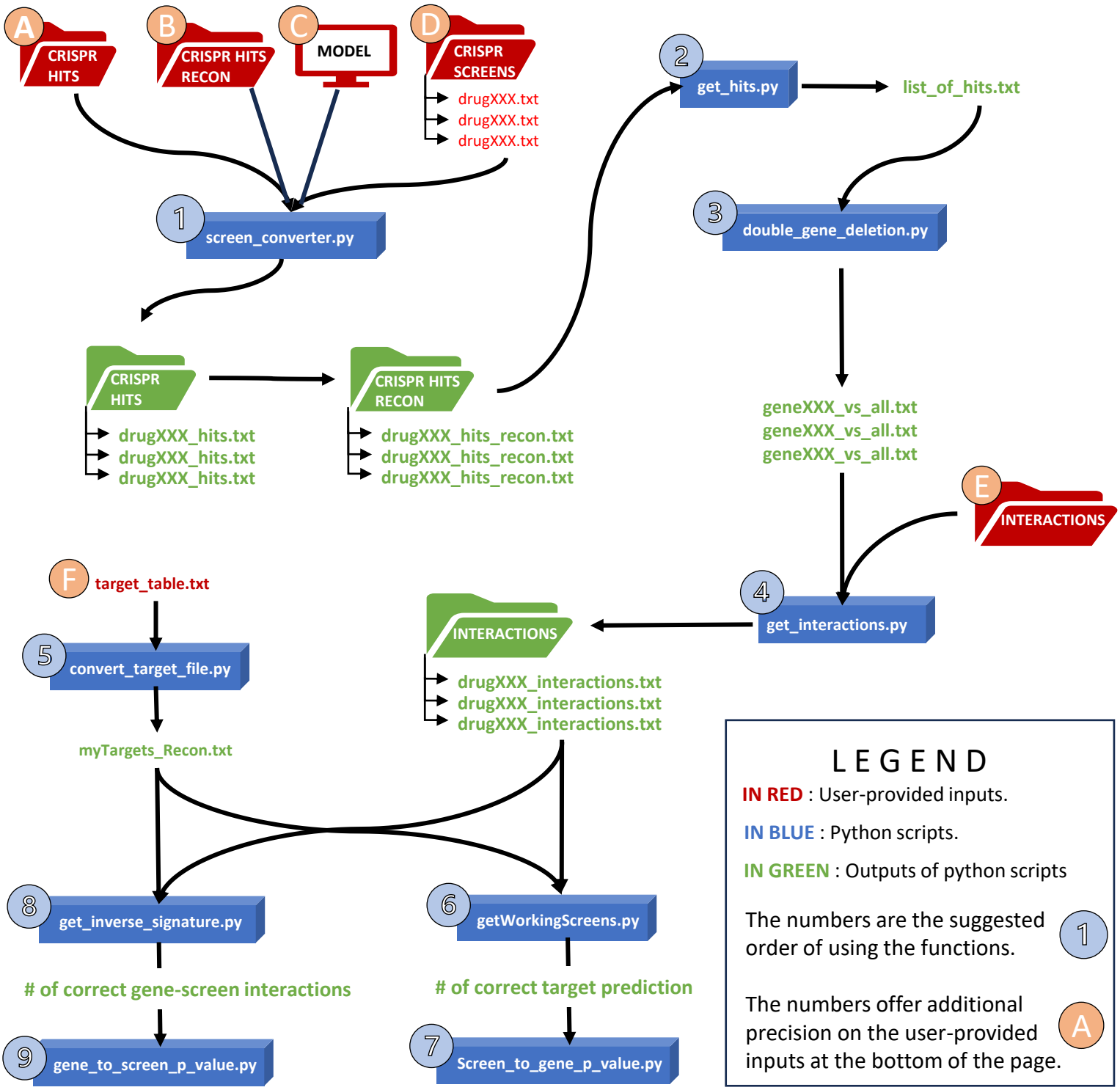

Additional information

- **A** The directory of the folder in which the list of hits of each drug will be placed. It should be empty.
- **B** The directory of the folder in which the list of hits converted to BiGG ID of each drug will be placed. It should be empty.
- **C** The metabolic model of class cobra.core.Model which resembles the cell line with which the CRISPR screen have been executed. It can be outputted from the 'make_model' folder.
- **D** The directory of the folder containing the CRISPR screens of each drug. It should contain a tab delimited txt file for each drug. An example of such a txt file is provided under '1_methyl_nicotinamide.txt'.
- **E** The directory of the 'interaction' folder. This folder should be empty, and will be filled with one txt file per drug containing candidate target genes, i.e. genes that are thought to be interacting with CRISPR hits.
- **F** A txt file containing a list of the CRISPR screens and their associated known molecular target. An example is provided under 'target_table.txt'. The user can also provide a file in the format of the 'myTargets_Recon.txt' example, and not use the 'convert_target_file script'.

Additional information is provided within the python function file themselves.