1. DEG analysis with limma and volcano plot  
        R code, data input, and output.

Please see the folder "LIMMA\_volcano\_plot".

2. Input data for:  
        STRING PPI network

AJUBA, CDH3, CEMIP, CHI3L1, CLDN1, COL11A1, CTHRC1, CXCL8, DPEP1, EGFL6, EPHX4, FOXQ1, INHBA, KRT23, MMP7, MSX2, TACSTD2, TESC, TRIM29, ADH1C, BEST2, CA1, CA4, CD177, CDKN2B, CEACAM7, CLCA4, CLDN8, CNTN3, CWH43, GCG, GREM2, GUCA2A, GUCA2B, HSD17B2, LAMA1, MS4A12, MT1M, NXPE4, PCK1, PYY, SCARA5, SI, SLC30A10, SST, STMN2, TNFRSF17, TRPM6, UGT2A3, and ZG16.

Simply visit the [STRING website](https://cn.string-db.org/cgi/input?sessionId=bbUO3IK1nLPn&input_page_active_form=multiple_identifiers) and insert these genes name, finally create the tsv file and download.

        Enrichr pathway enrichment analysis

AJUBA, CDH3, CEMIP, CHI3L1, CLDN1, COL11A1, CTHRC1, CXCL8, DPEP1, EGFL6, EPHX4, FOXQ1, INHBA, KRT23, MMP7, MSX2, TACSTD2, TESC, TRIM29, ADH1C, BEST2, CA1, CA4, CD177, CDKN2B, CEACAM7, CLCA4, CLDN8, CNTN3, CWH43, GCG, GREM2, GUCA2A, GUCA2B, HSD17B2, LAMA1, MS4A12, MT1M, NXPE4, PCK1, PYY, SCARA5, SI, SLC30A10, SST, STMN2, TNFRSF17, TRPM6, UGT2A3, and ZG16.

Using the [Enrichr webtool](https://maayanlab.cloud/Enrichr/) to perform the GO and KEGG pathway analysis. Simply insert these gene names to the box.

        Regulatory network analysis

CXCL8, CEMIP, MMP7, CA4, ADH1C, GUCA2A, GUCA2B, ZG16, CLCA4, MS4A12 and CLDN1

Using the [NetworkAnalyst](https://www.networkanalyst.ca/NetworkAnalyst/uploads/ListUploadView.xhtml) webtool to perform the regulatory network analysis. Simply insert these gene names to the box and select Specify organism to H. sapiens (Human) and Set ID type to Entrez ID.

        Disease-cKGs enrichment analysis

CXCL8, CEMIP, MMP7, CA4, ADH1C, GUCA2A, GUCA2B, ZG16, CLCA4, MS4A12 and CLDN1

Using the [Enrichr webtool](https://maayanlab.cloud/Enrichr/) to perform the Disease-cKGs enrichment analysis. Simply insert these gene names to the box and select the Diseases/Drugs then Disease-cKGs.

3. Prognostic power analysis  
        R code, data input, and output  
Please see the folder " Prognostic\_power\_analysis ".

4. Detailed analysis of Molecular docking simulation for exploring candidate drugs  
        code, data input, and output

Please see the folder " Docking " and this folder contain two folders (Proposed genes and Published genes). Each folder contains proposed gene (input file “gene name”.pdbqt), drugs (input files are “drug name”.pdbqt and output files are “drug name”\_out.pdbqt and .log (extension)), and code is Vina\_linux.pl.