reNEW_Group/

├── **Genomics_GNM/**

│   ├── **Project_GNM_ProjectName/**

│   │   ├── Raw_Data_RD_GNM_ProjectName_YYYYMMDD_v1/

│   │   │   └── SampleName_GNM_RD_ProjectName_YYYYMMDD_v1.fastq

│   │   ├── Processed_Data_PD_GNM_ProjectName_YYYYMMDD_v1/

│   │   │   └── SampleName_GNM_PD_ProjectName_YYYYMMDD_v1.csv

│   │   └── Reports_RPT_GNM_ProjectName_YYYYMMDD_v1.pdf

│   ├── Protocols_PTCL_GNM_YYYYMMDD.pdf

│   ├── Tools_TLC_GNM_YYYYMMDD/

│   └── Resources_RSC_GNM_YYYYMMDD/

├── **Microscopy_MIC/**

│   ├── **Project_MIC_ProjectName/**

│   │   ├── Raw_Data_RD_MIC_ProjectName_YYYYMMDD_v1/

│   │   │   └── SampleName_MIC_RD_ProjectName_YYYYMMDD_v1.tiff

│   │   ├── Processed_Data_PD_MIC_ProjectName_YYYYMMDD_v1/

│   │   │   └── SampleName_MIC_PD_ProjectName_YYYYMMDD_v1.jpg

│   │   └── Reports_RPT_MIC_ProjectName_YYYYMMDD_v1.pdf

│   ├── Protocols_PTCL_MIC_YYYYMMDD.pdf

│   ├── Tools_TLC_MIC_YYYYMMDD/

│   └── Resources_RSC_MIC_YYYYMMDD/

├── **Tissue_Culture_TC/**

│   ├── **Project_TC_ProjectName/**

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│   │   ├── Raw_Data_RD_TC_ProjectName_YYYYMMDD_v1/
│   │   │   └── SampleName_TC_RD_ProjectName_YYYYMMDD_v1.csv
│   │   ├── Processed_Data_PD_TC_ProjectName_YYYYMMDD_v1/
│   │   │   └── SampleName_TC_PD_ProjectName_YYYYMMDD_v1.csv
│   │   └── Reports_RPT_TC_ProjectName_YYYYMMDD_v1.pdf
│   ├── Protocols_PTCL_TC_YYYYMMDD.pdf
│   ├── Tools_TLC_TC_YYYYMMDD/
│   └── Resources_RSC_TC_YYYYMMDD/
└── Flow_Cytometry_FC/
    ├── Project_FC_ProjectName/
    │   ├── Raw_Data_RD_FC_ProjectName_YYYYMMDD_v1/
    │   │   └── SampleName_FC_RD_ProjectName_YYYYMMDD_v1.fcs
    │   ├── Processed_Data_PD_FC_ProjectName_YYYYMMDD_v1/
    │   │   └── SampleName_FC_PD_ProjectName_YYYYMMDD_v1.csv
    │   └── Reports_RPT_FC_ProjectName_YYYYMMDD_v1.pdf
    ├── Protocols_PTCL_FC_YYYYMMDD.pdf
    ├── Tools_TLC_FC_YYYYMMDD/
    └── Resources_RSC_FC_YYYYMMDD/
```

Here's a quick breakdown of the abbreviations:

GNM: Genomics
MIC: Microscopy
TC: Tissue Culture
FC: Flow Cytometry
RD: Raw Data
PD: Processed Data
RPT: Reports
PTCL: Protocols
TLC: Tools
RSC: Resources

In the example above, "**ProjectName**" should be replaced with a short, descriptive name for the project, and "**YYYYMMDD**" should be replaced with the date in that format. "**SampleName**" should be replaced with the specific identifier for the sample relevant to the data. "v1" denotes the file or folder version, which is essential for tracking changes over time.

The extensions of the files (like **.fastq, .tiff, .fcs, .csv, .pdf**) are based on the file type, which will depend on the kind of data and report files you are working with. Here are examples of what they could stand for:

.fastq: a standard file format for storing genetic sequence data.
.tiff or **.jpg**: standard file formats for image data, often used in microscopy.
.fcs: a file format for storing flow cytometry data.
.csv: a simple, widely used format for tabular data.
.pdf: a standard file format for text documents, such as reports or protocols.

In addition, a "**Readme**" file can be maintained in each project directory and subdirectory to explain what each file and subfolder is and to record other essential details. This system can be adapted according to the specific needs and practices of the **reNEW Research Group**.

The key is maintaining consistency with the organization's naming convention and directory structure to ensure ease of navigation, data retrieval, and understanding among all team members.