Appendix Python code for the input of excel data into database tables

The python code for the input of data into the database tables (using the BNRdb database as an example) is annotated below.

BNRDB

```python
# build.py
import pymysql as sql
import pandas as pd

class DB():
    def __init__(self, host="localhost", port=3306, db="", user="root", password="", charset="utf8"):
        self.conn = sql.connect(host=host,
                    port=port,
                    db=db   ,
                    user=user,
                    password=password,
                    charset=charset)
        self.cur = self.conn.cursor(cursor=sql.cursors.DictCursor)

    def __enter__(self):
        return self.cur

    def __exit__(self, exc_type, exc_val, exc_tb):
        self.conn.commit()
        self.cur.close()

    def get_one_data(self, query):
        self.cur.execute(query)
        return self.cur.fetchone()

    def create_table(self, table_name, query):
        self.cur.execute("DROP TABLE IF EXISTS " + table_name)
        self.cur.execute(query)

    def insert(self, data, table_name,excel_keys, is_Anammox):
        count = 0
        for i in range(0, len(data)):
            query = ""
```

```python
Organism            = str(data[excel_keys[0]][i]).
Reaction_Stage      = str(data[excel_keys[1]][i])
Encoding_Gene       = str(data[excel_keys[2]][i])
Enzyme_Name         = str(data[excel_keys[3]][i])
Microorganism       = str(data[excel_keys[4]][i])
Clone               = str(data[excel_keys[5]][i])
GenBank_ID          = str(data[excel_keys[6]][i])
Nucleotide_Link     = str(data[excel_keys[7]][i])
Authors             = str(data[excel_keys[8]][i])
Phylum              = str(data[excel_keys[9]][i])
Class               = str(data[excel_keys[10]][i])
myOrder             = str(data[excel_keys[11]][i])
Family              = str(data[excel_keys[12]][i])
Genus               = str(data[excel_keys[13]][i])
Isolation_sou       = str(data[excel_keys[14]][i])
DNA_size_bp         = str(data[excel_keys[15]][i])
UniprotK            = str(data[excel_keys[16]][i])
Uniprot_Link        = str(data[excel_keys[17]][i])
Protein_ID          = str(data[excel_keys[18]][i])
Protein_Link        = str(data[excel_keys[19]][i])
Length_aa           = str(data[excel_keys[20]][i])
Title               = str(data[excel_keys[21]][i])
PMID                = str(data[excel_keys[22]][i])
Link                = str(data[excel_keys[23]][i]).
Research_Link       = str(data[excel_keys[24]][i]).
Abstract            = str(data[excel_keys[25]][i])
GenFASTA            = str(data[excel_keys[26]][i])
ProFASTA            = str(data[excel_keys[27]][i])
query = """INSERT INTO %s (
                Organism,
                Reaction_Stage,
                Encoding_Gene,
                Enzyme_Name,
                Microorganism,
                Clone,
                GenBank_ID,
                Nucleotide_Link,
                Authors,
                Phylum,
                Class,
```

```python
                            myOrder,
                            Family,
                            Genus,
                            Isolation_source,
                            DNA_size_bp,
                            UniprotK,
                            Uniprot_Link,
                            Protein_ID,
                            Protein_Link,
                            Length_aa,
                            Title,
                            PMID,
                            Link,
                            Research_Link,
                            Abstract,
                            GenFASTA,
                            ProFASTA
                                )
                VALUES( '%s', '%s', '%s', '%s', '%s', '%s', '%s', '%s', '%s', '%s', '%s',
'%s','%s','%s',¥
                    '%s', '%s', '%s', '%s', '%s', '%s', '%s', '%s', '%s', '%s', '%s', '%s', '%s',
'%s')"""    ¥
                    % (table_name,
                        Organism,
                        Reaction_Stage,
                        Encoding_Gene,
                        Enzyme_Name,
                        Microorganism,
                        Clone,
                        GenBank_ID,
                        Nucleotide_Link,
                        Authors,
                        Phylum,
                        Class,
                        myOrder,
                        Family,
                        Genus,
                        Isolation_source,
                        DNA_size_bp,
                        UniprotK,
```

```python
                            Uniprot_Link,
                            Protein_ID,
                            Protein_Link,
                            Length_aa,
                            Title,
                            PMID,
                            Link,
                            Research_Link,
                            Abstract,
                            GenFASTA,
                            ProFASTA
                            )
        self.cur.execute(query)
        self.conn.commit()
    def update(self, key, filed, value):
        sql = sql = "UPDATE EMPLOYEE SET AGE = AGE + 1 WHERE SEX = '%c'" % ('M')
        pass

    def check(self, query):
        try:
            self.cur.execute(query)
            self.conn.commit()

        except:

            self.conn.rollback()

def Enzymes(file, sheet_name_list, DB):
    pass

if __name__ == "__main__":

    mydb = DB(db="brndb") # for bnrdb
    product_file = "DNRA_genes.xlsx" # for example, you want put nird data of
DNRA_genes.xlsx into bnrdb
    table_name = "bnrdb_app_nird"
    data = pd.read_excel(product_file, sheet_name="nirD")
    mydb.insert(data, table_name, data.keys(), is_Anammox)

```