MySQL code for building database tables of the BNRdb

The Django models were used to build the database tables, their fields, and various constraints.

```python
class Narg(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)


class Narh(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
```

```python
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)


class Narj(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)


class Nari(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)


class Narz(models.Model):
```

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    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class Nary(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class Narw(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
```

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    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class Narv(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class Napa(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
```

```python
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class Napb(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class Napc(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
```

```python
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class Napd(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class Nirk(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
```

```python
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class NirS(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class cNorB(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
```

```python
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class qNorB(models.Model):
    Organism        =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class Norc(models.Model):
    Organism        =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
```

```python
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class NosZ(models.Model):
    Organism        =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class HzsA(models.Model):
    Organism        =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
```

```python
        Abstract = models.TextField("Abstract", max_length = 20000)
        GenFASTA = models.CharField("GenFASTA", max_length = 200)
        ProFASTA = models.CharField("ProFASTA", max_length = 200)


class HzsB(models.Model):
        Organism       =models.CharField("Organism", max_length=50)
        Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
        Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
        Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
        Microorganism = models.CharField("Microorganism", max_length = 1000)
        Clone = models.CharField("Clone", max_length = 300)
        GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
        Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
        Authors = models.CharField("Authors", max_length = 200)
        Phylum = models.CharField("Phylum", max_length = 200)
        Class = models.CharField("Class", max_length = 200)
        myOrder = models.CharField("myOrder", max_length = 200)
        Family = models.CharField("Family", max_length = 200)
        Genus = models.CharField("Genus", max_length = 200)
        Isolation_source = models.CharField("Isolation_source", max_length =
300)
        DNA_size_bp = models.CharField("DNA_size", max_length = 200)
        UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
        Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
        Protein_ID = models.CharField("Protein_ID", max_length = 200)
        Protein_Link = models.TextField("Protein_Link", max_length = 10000)
        Length_aa = models.CharField("Length_aa", max_length = 200)
        Title = models.CharField("Title", max_length = 500)
        PMID = models.CharField("PMID", max_length = 200)
        Link = models.TextField("Link", max_length = 10000)
        Research_Link = models.TextField("Research_Link", max_length = 10000)
        Abstract = models.TextField("Abstract", max_length = 20000)
        GenFASTA = models.CharField("GenFASTA", max_length = 200)
        ProFASTA = models.CharField("ProFASTA", max_length = 200)


class HzsC(models.Model):
        Organism       =models.CharField("Organism", max_length=50)
        Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
        Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
        Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
        Microorganism = models.CharField("Microorganism", max_length = 1000)
        Clone = models.CharField("Clone", max_length = 300)
        GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
        Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
        Authors = models.CharField("Authors", max_length = 200)
        Phylum = models.CharField("Phylum", max_length = 200)
        Class = models.CharField("Class", max_length = 200)
        myOrder = models.CharField("myOrder", max_length = 200)
        Family = models.CharField("Family", max_length = 200)
        Genus = models.CharField("Genus", max_length = 200)
        Isolation_source = models.CharField("Isolation_source", max_length =
300)
        DNA_size_bp = models.CharField("DNA_size", max_length = 200)
        UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
        Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
        Protein_ID = models.CharField("Protein_ID", max_length = 200)
        Protein_Link = models.TextField("Protein_Link", max_length = 10000)
        Length_aa = models.CharField("Length_aa", max_length = 200)
        Title = models.CharField("Title", max_length = 500)
        PMID = models.CharField("PMID", max_length = 200)
        Link = models.TextField("Link", max_length = 10000)
        Research_Link = models.TextField("Research_Link", max_length = 10000)
        Abstract = models.TextField("Abstract", max_length = 20000)
        GenFASTA = models.CharField("GenFASTA", max_length = 200)
        ProFASTA = models.CharField("ProFASTA", max_length = 200)
```

```python
class HzO(models.Model):
    Organism        =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class HdH(models.Model):
    Organism        =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class CcsA(models.Model):
    Organism        =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
```

```python
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class CcsB(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class CcsX(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
```

```python
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class AmoA(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class AmoB(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
```

```python
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class AmoC(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class HaO(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
```

```python
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class NxrA(models.Model):
    Organism        =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class NxrB(models.Model):
    Organism        =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
```

```python
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)


class NxrC(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)


class NxrD(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
```

```python
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class Comammox(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class McrA(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
```

```python
        Abstract = models.TextField("Abstract", max_length = 20000)
        GenFASTA = models.CharField("GenFASTA", max_length = 200)
        ProFASTA = models.CharField("ProFASTA", max_length = 200)


class NoD(models.Model):
        Organism       =models.CharField("Organism", max_length=50)
        Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
        Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
        Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
        Microorganism = models.CharField("Microorganism", max_length = 1000)
        Clone = models.CharField("Clone", max_length = 300)
        GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
        Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
        Authors = models.CharField("Authors", max_length = 200)
        Phylum = models.CharField("Phylum", max_length = 200)
        Class = models.CharField("Class", max_length = 200)
        myOrder = models.CharField("myOrder", max_length = 200)
        Family = models.CharField("Family", max_length = 200)
        Genus = models.CharField("Genus", max_length = 200)
        Isolation_source = models.CharField("Isolation_source", max_length =
300)
        DNA_size_bp = models.CharField("DNA_size", max_length = 200)
        UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
        Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
        Protein_ID = models.CharField("Protein_ID", max_length = 200)
        Protein_Link = models.TextField("Protein_Link", max_length = 10000)
        Length_aa = models.CharField("Length_aa", max_length = 200)
        Title = models.CharField("Title", max_length = 500)
        PMID = models.CharField("PMID", max_length = 200)
        Link = models.TextField("Link", max_length = 10000)
        Research_Link = models.TextField("Research_Link", max_length = 10000)
        Abstract = models.TextField("Abstract", max_length = 20000)
        GenFASTA = models.CharField("GenFASTA", max_length = 200)
        ProFASTA = models.CharField("ProFASTA", max_length = 200)


class PmoA(models.Model):
        Organism       =models.CharField("Organism", max_length=50)
        Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
        Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
        Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
        Microorganism = models.CharField("Microorganism", max_length = 1000)
        Clone = models.CharField("Clone", max_length = 300)
        GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
        Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
        Authors = models.CharField("Authors", max_length = 200)
        Phylum = models.CharField("Phylum", max_length = 200)
        Class = models.CharField("Class", max_length = 200)
        myOrder = models.CharField("myOrder", max_length = 200)
        Family = models.CharField("Family", max_length = 200)
        Genus = models.CharField("Genus", max_length = 200)
        Isolation_source = models.CharField("Isolation_source", max_length =
300)
        DNA_size_bp = models.CharField("DNA_size", max_length = 200)
        UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
        Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
        Protein_ID = models.CharField("Protein_ID", max_length = 200)
        Protein_Link = models.TextField("Protein_Link", max_length = 10000)
        Length_aa = models.CharField("Length_aa", max_length = 200)
        Title = models.CharField("Title", max_length = 500)
        PMID = models.CharField("PMID", max_length = 200)
        Link = models.TextField("Link", max_length = 10000)
        Research_Link = models.TextField("Research_Link", max_length = 10000)
        Abstract = models.TextField("Abstract", max_length = 20000)
        GenFASTA = models.CharField("GenFASTA", max_length = 200)
        ProFASTA = models.CharField("ProFASTA", max_length = 200)
```

```python
class Product(models.Model):
    Organism                      = models.CharField("Microorganism",
max_length = 50)
    Microorganism                 = models.CharField("Microorganism",
max_length = 100)
    Accesion_Number               = models.CharField("Accesion_Number",
max_length = 20)
    Nucleotide_Link               = models.TextField("Nucleotide_Link",
max_length = 10000)
    Isolation_source              = models.CharField("Isolation_source",
max_length = 500)
    Energy_Source_Electron_donor  =
models.CharField("Energy_Source_Electron_donor", max_length = 500)
    Final_Product                 = models.CharField("Final_Product",
max_length = 50)
    Respiration_Fermentative_Growth  =
models.CharField("Respiration_Fermentative_Growth", max_length = 20)
    Reference                     = models.CharField("Reference", max_length
= 50)
    Nitrious_intermediate_consumed_reduced_Electron_acceptor =
models.CharField("Nitrious_intermediate_consumed_reduced_Electron_acceptor",
max_length = 20)
    Phylum                        = models.CharField("Phylum", max_length =
200)
    Class                         = models.CharField("Class", max_length =
200)
    myOrder                        = models.CharField("myOrder", max_length
= 200)
    Family                        = models.CharField("Family", max_length =
200)
    Genus                         = models.CharField("Genus", max_length =
200)
    Title                         = models.TextField("Title", max_length =
5000)
    PMID                          = models.CharField("PMID", max_length =
30)
    PubMed_Link                   = models.TextField("PubMed_Link",
max_length = 10000)
    Research_Link                 = models.TextField("Research_Link",
max_length = 10000)
    Abstract                      = models.TextField("Abstract", max_length
= 20000)

class P450nor(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
```

```python
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class GeneDenitriNirk(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class NrfA(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
```

```python
        GenFASTA = models.CharField("GenFASTA", max_length = 200)
        ProFASTA = models.CharField("ProFASTA", max_length = 200)


class NrfB(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)


class NrfC(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)


class NrfD(models.Model):
```

```python
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class NrfH(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class NirB(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
```

```python
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class NirD(models.Model):
    Organism       =models.CharField("Organism", max_length=50)
    Reaction_Stage = models.CharField("Reaction_Stage", max_length = 1000)
    Encoding_Gene  = models.CharField("Encoding_Gene", max_length  = 200)
    Enzyme_Name = models.CharField("Enzyme_Name", max_length = 500)
    Microorganism = models.CharField("Microorganism", max_length = 1000)
    Clone = models.CharField("Clone", max_length = 300)
    GenBank_ID = models.CharField("GenBank_ID", max_length = 200)
    Nucleotide_Link = models.TextField("Nucleotide_Link", max_length =
10000)
    Authors = models.CharField("Authors", max_length = 200)
    Phylum = models.CharField("Phylum", max_length = 200)
    Class = models.CharField("Class", max_length = 200)
    myOrder = models.CharField("myOrder", max_length = 200)
    Family = models.CharField("Family", max_length = 200)
    Genus = models.CharField("Genus", max_length = 200)
    Isolation_source = models.CharField("Isolation_source", max_length =
300)
    DNA_size_bp = models.CharField("DNA_size", max_length = 200)
    UniprotK = models.CharField("Uniprot_ID", max_length  = 200)
    Uniprot_Link = models.TextField("Uniprot_Link", max_length = 10000)
    Protein_ID = models.CharField("Protein_ID", max_length = 200)
    Protein_Link = models.TextField("Protein_Link", max_length = 10000)
    Length_aa = models.CharField("Length_aa", max_length = 200)
    Title = models.CharField("Title", max_length = 500)
    PMID = models.CharField("PMID", max_length = 200)
    Link = models.TextField("Link", max_length = 10000)
    Research_Link = models.TextField("Research_Link", max_length = 10000)
    Abstract = models.TextField("Abstract", max_length = 20000)
    GenFASTA = models.CharField("GenFASTA", max_length = 200)
    ProFASTA = models.CharField("ProFASTA", max_length = 200)

class StrainsAnammox(models.Model):
    Organism                    = models.CharField("Microorganism",
max_length = 50)
    Microorganism               = models.CharField("Microorganism",
max_length = 100)
    Accesion_Number             = models.CharField("Accesion_Number",
max_length = 20)
    Nucleotide_Link             = models.TextField("Nucleotide_Link",
max_length = 10000)
```

```python
    Isolation_source               = models.CharField("Isolation_source",
max_length = 500)
    Energy_Source_Electron_donor  =
models.CharField("Energy_Source_Electron_donor", max_length = 500)
    Final_Product                  = models.CharField("Final_Product",
max_length = 50)
    Respiration_Fermentative_Growth  =
models.CharField("Respiration_Fermentative_Growth", max_length = 20)
    Reference                       = models.CharField("Reference", max_length
= 50)
    Nitrious_intermediate_consumed_reduced_Electron_acceptor =
models.CharField("Nitrious_intermediate_consumed_reduced_Electron_acceptor",
max_length = 100)
    Phylum                          = models.CharField("Phylum", max_length =
200)
    Class                           = models.CharField("Class", max_length =
200)
    myOrder                          = models.CharField("myOrder", max_length
= 200)
    Family                          = models.CharField("Family", max_length =
200)
    Genus                           = models.CharField("Genus", max_length =
200)
    Title                           = models.TextField("Title", max_length =
5000)
    PMID                            = models.CharField("PMID", max_length =
30)
    PubMed_Link                     = models.TextField("PubMed_Link",
max_length = 10000)
    Research_Link                   = models.TextField("Research_Link",
max_length = 10000)
    Abstract                        = models.TextField("Abstract", max_length
= 20000)


class Strainsdenifungi(models.Model):
    Organism                        = models.CharField("Microorganism",
max_length = 50)
    Microorganism                   = models.CharField("Microorganism",
max_length = 100)
    Accesion_Number                 = models.CharField("Accesion_Number",
max_length = 20)
    Nucleotide_Link                 = models.TextField("Nucleotide_Link",
max_length = 10000)
    Isolation_source                = models.CharField("Isolation_source",
max_length = 500)
    Energy_Source_Electron_donor  =
models.CharField("Energy_Source_Electron_donor", max_length = 500)
    Final_Product                   = models.CharField("Final_Product",
max_length = 50)
    Respiration_Fermentative_Growth  =
models.CharField("Respiration_Fermentative_Growth", max_length = 20)
    Reference                       = models.CharField("Reference", max_length
= 50)
    Nitrious_intermediate_consumed_reduced_Electron_acceptor =
models.CharField("Nitrious_intermediate_consumed_reduced_Electron_acceptor",
max_length = 100)
    Phylum                          = models.CharField("Phylum", max_length =
200)
    Class                           = models.CharField("Class", max_length =
200)
    myOrder                          = models.CharField("myOrder", max_length
= 200)
    Family                          = models.CharField("Family", max_length =
200)
    Genus                           = models.CharField("Genus", max_length =
200)
    Title                           = models.TextField("Title", max_length =
5000)
```

```python
    PMID                        = models.CharField("PMID", max_length =
30)
    PubMed_Link                 = models.TextField("PubMed_Link",
max_length = 10000)
    Research_Link               = models.TextField("Research_Link",
max_length = 10000)
    Abstract                    = models.TextField("Abstract", max_length
= 20000)

class Strinhand(models.Model):
    Organism                    = models.CharField("Microorganism",
max_length = 50)
    Microorganism               = models.CharField("Microorganism",
max_length = 100)
    Accesion_Number             = models.CharField("Accesion_Number",
max_length = 20)
    Nucleotide_Link             = models.TextField("Nucleotide_Link",
max_length = 10000)
    Isolation_source            = models.CharField("Isolation_source",
max_length = 500)
    Energy_Source_Electron_donor =
models.CharField("Energy_Source_Electron_donor", max_length = 500)
    Final_Product               = models.CharField("Final_Product",
max_length = 50)
    Respiration_Fermentative_Growth  =
models.CharField("Respiration_Fermentative_Growth", max_length = 20)
    Reference                   = models.CharField("Reference", max_length
= 50)
    Nitrious_intermediate_consumed_reduced_Electron_acceptor =
models.CharField("Nitrious_intermediate_consumed_reduced_Electron_acceptor",
max_length = 100)
    Phylum                      = models.CharField("Phylum", max_length =
200)
    Class                       = models.CharField("Class", max_length =
200)
    myOrder                     = models.CharField("myOrder", max_length
= 200)
    Family                      = models.CharField("Family", max_length =
200)
    Genus                       = models.CharField("Genus", max_length =
200)
    Title                       = models.TextField("Title", max_length =
5000)
    PMID                        = models.CharField("PMID", max_length =
30)
    PubMed_Link                 = models.TextField("PubMed_Link",
max_length = 10000)
    Research_Link               = models.TextField("Research_Link",
max_length = 10000)
    Abstract                    = models.TextField("Abstract", max_length
= 20000)

class StrainsNitrification(models.Model):
    Organism                    = models.CharField("Microorganism",
max_length = 50)
    Microorganism               = models.CharField("Microorganism",
max_length = 100)
    Accesion_Number             = models.CharField("Accesion_Number",
max_length = 20)
    Nucleotide_Link             = models.TextField("Nucleotide_Link",
max_length = 10000)
    Isolation_source            = models.CharField("Isolation_source",
max_length = 500)
    Energy_Source_Electron_donor  =
models.CharField("Energy_Source_Electron_donor", max_length = 500)
    Final_Product               = models.CharField("Final_Product",
max_length = 50)
```

```python
    Respiration_Fermentative_Growth  =
models.CharField("Respiration_Fermentative_Growth", max_length = 20)
    Reference                        = models.CharField("Reference", max_length
= 50)
    Nitrious_intermediate_consumed_reduced_Electron_acceptor =
models.CharField("Nitrious_intermediate_consumed_reduced_Electron_acceptor",
max_length = 20)
    Phylum                           = models.CharField("Phylum", max_length =
200)
    Class                            = models.CharField("Class", max_length =
200)
    myOrder                          = models.CharField("myOrder", max_length
= 200)
    Family                           = models.CharField("Family", max_length =
200)
    Genus                            = models.CharField("Genus", max_length =
200)
    Title                            = models.TextField("Title", max_length =
5000)
    PMID                             = models.CharField("PMID", max_length =
30)
    PubMed_Link                      = models.TextField("PubMed_Link",
max_length = 10000)
    Research_Link                    = models.TextField("Research_Link",
max_length = 10000)
    Abstract                         = models.TextField("Abstract", max_length
= 20000)


class Strindnrafungal(models.Model):
    Organism                         = models.CharField("Microorganism",
max_length = 50)
    Microorganism                    = models.CharField("Microorganism",
max_length = 100)
    Accesion_Number                  = models.CharField("Accesion_Number",
max_length = 20)
    Nucleotide_Link                  = models.TextField("Nucleotide_Link",
max_length = 10000)
    Isolation_source                 = models.CharField("Isolation_source",
max_length = 500)
    Energy_Source_Electron_donor  =
models.CharField("Energy_Source_Electron_donor", max_length = 500)
    Final_Product                    = models.CharField("Final_Product",
max_length = 50)
    Respiration_Fermentative_Growth  =
models.CharField("Respiration_Fermentative_Growth", max_length = 20)
    Reference                        = models.CharField("Reference", max_length
= 50)
    Nitrious_intermediate_consumed_reduced_Electron_acceptor =
models.CharField("Nitrious_intermediate_consumed_reduced_Electron_acceptor",
max_length = 100)
    Phylum                           = models.CharField("Phylum", max_length =
200)
    Class                            = models.CharField("Class", max_length =
200)
    myOrder                          = models.CharField("myOrder", max_length
= 200)
    Family                           = models.CharField("Family", max_length =
200)
    Genus                            = models.CharField("Genus", max_length =
200)
    Title                            = models.TextField("Title", max_length =
5000)
    PMID                             = models.CharField("PMID", max_length =
30)
    PubMed_Link                      = models.TextField("PubMed_Link",
max_length = 10000)
    Research_Link                    = models.TextField("Research_Link",
max_length = 10000)
```

```python
    Abstract                         = models.TextField("Abstract", max_length
= 20000)


class Strindnrabac(models.Model):
    Organism                         = models.CharField("Microorganism",
max_length = 50)
    Microorganism                    = models.CharField("Microorganism",
max_length = 100)
    Accesion_Number                  = models.CharField("Accesion_Number",
max_length = 20)
    Nucleotide_Link                  = models.TextField("Nucleotide_Link",
max_length = 10000)
    Isolation_source                 = models.CharField("Isolation_source",
max_length = 500)
    Energy_Source_Electron_donor  =
models.CharField("Energy_Source_Electron_donor", max_length = 500)
    Final_Product                    = models.CharField("Final_Product",
max_length = 50)
    Respiration_Fermentative_Growth  =
models.CharField("Respiration_Fermentative_Growth", max_length = 20)
    Reference                        = models.CharField("Reference", max_length
= 50)
    Nitrious_intermediate_consumed_reduced_Electron_acceptor =
models.CharField("Nitrious_intermediate_consumed_reduced_Electron_acceptor",
max_length = 100)
    Phylum                           = models.CharField("Phylum", max_length =
200)
    Class                            = models.CharField("Class", max_length =
200)
    myOrder                           = models.CharField("myOrder", max_length
= 200)
    Family                           = models.CharField("Family", max_length =
200)
    Genus                            = models.CharField("Genus", max_length =
200)
    Title                            = models.TextField("Title", max_length =
5000)
    PMID                             = models.CharField("PMID", max_length =
30)
    PubMed_Link                      = models.TextField("PubMed_Link",
max_length = 10000)
    Research_Link                    = models.TextField("Research_Link",
max_length = 10000)
    Abstract                         = models.TextField("Abstract", max_length
= 20000)


class Aoa(models.Model):
    Organism                         = models.CharField("Microorganism",
max_length = 50)
    Microorganism                    = models.CharField("Microorganism",
max_length = 100)
    Accesion_Number                  = models.CharField("Accesion_Number",
max_length = 20)
    Nucleotide_Link                  = models.TextField("Nucleotide_Link",
max_length = 10000)
    Isolation_source                 = models.CharField("Isolation_source",
max_length = 500)
    Energy_Source_Electron_donor  =
models.CharField("Energy_Source_Electron_donor", max_length = 500)
    Final_Product                    = models.CharField("Final_Product",
max_length = 50)
    Respiration_Fermentative_Growth  =
models.CharField("Respiration_Fermentative_Growth", max_length = 20)
    Reference                        = models.CharField("Reference", max_length
= 50)
    Nitrious_intermediate_consumed_reduced_Electron_acceptor =
models.CharField("Nitrious_intermediate_consumed_reduced_Electron_acceptor",
max_length = 100)
```

```python
    Phylum                          = models.CharField("Phylum", max_length =
200)
    Class                           = models.CharField("Class", max_length =
200)
    myOrder                          = models.CharField("myOrder", max_length
= 200)
    Family                          = models.CharField("Family", max_length =
200)
    Genus                           = models.CharField("Genus", max_length =
200)
    Title                           = models.TextField("Title", max_length =
5000)
    PMID                            = models.CharField("PMID", max_length =
30)
    PubMed_Link                     = models.TextField("PubMed_Link",
max_length = 10000)
    Research_Link                   = models.TextField("Research_Link",
max_length = 10000)
    Abstract                        = models.TextField("Abstract", max_length
= 20000)

class Aob(models.Model):
    Organism                        = models.CharField("Microorganism",
max_length = 50)
    Microorganism                   = models.CharField("Microorganism",
max_length = 100)
    Accesion_Number                 = models.CharField("Accesion_Number",
max_length = 20)
    Nucleotide_Link                 = models.TextField("Nucleotide_Link",
max_length = 10000)
    Isolation_source                = models.CharField("Isolation_source",
max_length = 500)
    Energy_Source_Electron_donor    =
models.CharField("Energy_Source_Electron_donor", max_length = 500)
    Final_Product                   = models.CharField("Final_Product",
max_length = 50)
    Respiration_Fermentative_Growth   =
models.CharField("Respiration_Fermentative_Growth", max_length = 20)
    Reference                       = models.CharField("Reference", max_length
= 50)
    Nitrious_intermediate_consumed_reduced_Electron_acceptor =
models.CharField("Nitrious_intermediate_consumed_reduced_Electron_acceptor",
max_length = 100)
    Phylum                          = models.CharField("Phylum", max_length =
200)
    Class                           = models.CharField("Class", max_length =
200)
    myOrder                          = models.CharField("myOrder", max_length
= 200)
    Family                          = models.CharField("Family", max_length =
200)
    Genus                           = models.CharField("Genus", max_length =
200)
    Title                           = models.TextField("Title", max_length =
5000)
    PMID                            = models.CharField("PMID", max_length =
30)
    PubMed_Link                     = models.TextField("PubMed_Link",
max_length = 10000)
    Research_Link                   = models.TextField("Research_Link",
max_length = 10000)
    Abstract                        = models.TextField("Abstract", max_length
= 20000)

class Nob(models.Model):
    Organism                        = models.CharField("Microorganism",
max_length = 50)
```

```python
    Microorganism                    = models.CharField("Microorganism",
max_length = 100)
    Accesion_Number                  = models.CharField("Accesion_Number",
max_length = 20)
    Nucleotide_Link                  = models.TextField("Nucleotide_Link",
max_length = 10000)
    Isolation_source                 = models.CharField("Isolation_source",
max_length = 500)
    Energy_Source_Electron_donor  =
models.CharField("Energy_Source_Electron_donor", max_length = 500)
    Final_Product                    = models.CharField("Final_Product",
max_length = 50)
    Respiration_Fermentative_Growth  =
models.CharField("Respiration_Fermentative_Growth", max_length = 20)
    Reference                        = models.CharField("Reference", max_length
= 50)
    Nitrious_intermediate_consumed_reduced_Electron_acceptor =
models.CharField("Nitrious_intermediate_consumed_reduced_Electron_acceptor",
max_length = 100)
    Phylum                           = models.CharField("Phylum", max_length =
200)
    Class                            = models.CharField("Class", max_length =
200)
    myOrder                          = models.CharField("myOrder", max_length
= 200)
    Family                           = models.CharField("Family", max_length =
200)
    Genus                            = models.CharField("Genus", max_length =
200)
    Title                            = models.TextField("Title", max_length =
5000)
    PMID                             = models.CharField("PMID", max_length =
30)
    PubMed_Link                      = models.TextField("PubMed_Link",
max_length = 10000)
    Research_Link                    = models.TextField("Research_Link",
max_length = 10000)
    Abstract                         = models.TextField("Abstract", max_length
= 20000)

class Strainntrifungi(models.Model):
    Organism                         = models.CharField("Microorganism",
max_length = 50)
    Microorganism                    = models.CharField("Microorganism",
max_length = 100)
    Accesion_Number                  = models.CharField("Accesion_Number",
max_length = 20)
    Nucleotide_Link                  = models.TextField("Nucleotide_Link",
max_length = 10000)
    Isolation_source                 = models.CharField("Isolation_source",
max_length = 500)
    Energy_Source_Electron_donor  =
models.CharField("Energy_Source_Electron_donor", max_length = 500)
    Final_Product                    = models.CharField("Final_Product",
max_length = 50)
    Respiration_Fermentative_Growth  =
models.CharField("Respiration_Fermentative_Growth", max_length = 20)
    Reference                        = models.CharField("Reference", max_length
= 50)
    Nitrious_intermediate_consumed_reduced_Electron_acceptor =
models.CharField("Nitrious_intermediate_consumed_reduced_Electron_acceptor",
max_length = 100)
    Phylum                           = models.CharField("Phylum", max_length =
200)
    Class                            = models.CharField("Class", max_length =
200)
    myOrder                          = models.CharField("myOrder", max_length
= 200)
```

```python
    Family                         = models.CharField("Family", max_length =
200)
    Genus                          = models.CharField("Genus", max_length =
200)
    Title                          = models.TextField("Title", max_length =
5000)
    PMID                           = models.CharField("PMID", max_length =
30)
    PubMed_Link                    = models.TextField("PubMed_Link",
max_length = 10000)
    Research_Link                  = models.TextField("Research_Link",
max_length = 10000)
    Abstract                       = models.TextField("Abstract", max_length
= 20000)

class Straindamobac(models.Model):
    Organism                       = models.CharField("Microorganism",
max_length = 50)
    Microorganism                  = models.CharField("Microorganism",
max_length = 100)
    Accesion_Number                = models.CharField("Accesion_Number",
max_length = 20)
    Nucleotide_Link                = models.TextField("Nucleotide_Link",
max_length = 10000)
    Isolation_source               = models.CharField("Isolation_source",
max_length = 500)
    Energy_Source_Electron_donor  =
models.CharField("Energy_Source_Electron_donor", max_length = 500)
    Final_Product                  = models.CharField("Final_Product",
max_length = 50)
    Respiration_Fermentative_Growth  =
models.CharField("Respiration_Fermentative_Growth", max_length = 20)
    Reference                      = models.CharField("Reference", max_length
= 50)
    Nitrious_intermediate_consumed_reduced_Electron_acceptor =
models.CharField("Nitrious_intermediate_consumed_reduced_Electron_acceptor",
max_length = 100)
    Phylum                         = models.CharField("Phylum", max_length =
200)
    Class                          = models.CharField("Class", max_length =
200)
    myOrder                        = models.CharField("myOrder", max_length
= 200)
    Family                         = models.CharField("Family", max_length =
200)
    Genus                          = models.CharField("Genus", max_length =
200)
    Title                          = models.TextField("Title", max_length =
5000)
    PMID                           = models.CharField("PMID", max_length =
30)
    PubMed_Link                    = models.TextField("PubMed_Link",
max_length = 10000)
    Research_Link                  = models.TextField("Research_Link",
max_length = 10000)
    Abstract                       = models.TextField("Abstract", max_length
= 20000)

class Straindamoarc(models.Model):
    Organism                       = models.CharField("Microorganism",
max_length = 50)
    Microorganism                  = models.CharField("Microorganism",
max_length = 100)
    Accesion_Number                = models.CharField("Accesion_Number",
max_length = 20)
    Nucleotide_Link                = models.TextField("Nucleotide_Link",
max_length = 10000)
```

```python
    Isolation_source              = models.CharField("Isolation_source",
max_length = 500)
    Energy_Source_Electron_donor  =
models.CharField("Energy_Source_Electron_donor", max_length = 500)
    Final_Product                 = models.CharField("Final_Product",
max_length = 50)
    Respiration_Fermentative_Growth  =
models.CharField("Respiration_Fermentative_Growth", max_length = 20)
    Reference                     = models.CharField("Reference", max_length
= 50)
    Nitrious_intermediate_consumed_reduced_Electron_acceptor =
models.CharField("Nitrious_intermediate_consumed_reduced_Electron_acceptor",
max_length = 100)
    Phylum                        = models.CharField("Phylum", max_length =
200)
    Class                         = models.CharField("Class", max_length =
200)
    myOrder                       = models.CharField("myOrder", max_length
= 200)
    Family                        = models.CharField("Family", max_length =
200)
    Genus                         = models.CharField("Genus", max_length =
200)
    Title                         = models.TextField("Title", max_length =
5000)
    PMID                          = models.CharField("PMID", max_length =
30)
    PubMed_Link                   = models.TextField("PubMed_Link",
max_length = 10000)
    Research_Link                 = models.TextField("Research_Link",
max_length = 10000)
    Abstract                      = models.TextField("Abstract", max_length
= 20000)


class WaterTreatmentPlant(models.Model):
    Influent_Source_Type   = models.CharField("Influent_Source_Type",
max_length = 200)
    Denitrification_System = models.CharField("Denitrification_System",
max_length = 200)
    Denitrifying_Reactor   = models.CharField("Denitrifying_Reactor",
max_length = 200)
    Medium                 = models.CharField("Medium", max_length = 200)
    Culture                = models.CharField("Culture", max_length = 200)
    Organism_cultured      = models.CharField("Organism_cultured",
max_length = 200)
    Respiration            = models.CharField("Respiration", max_length =
200)
    Electron_Donor         = models.TextField("Electron_Donor", max_length =
2000)
    Electron_Acceptor      = models.CharField("Electron_Acceptor",
max_length = 200)
    Input                  = models.CharField("Input", max_length = 200)
    Nitrate_Removal_Rate   = models.CharField("Nitrate_Removal_Rate",
max_length = 200)
    Denitrification_Rate   = models.CharField("Denitrification_Rate",
max_length = 200)
    Microorganism_identified = models.TextField("Microorganism_identified",
max_length = 2000)
    Molecular_Tools        = models.CharField("Molecular_Tools", max_length
= 200)
    Major_Findings         = models.CharField("Major_Findings", max_length =
2000)
    Authors                = models.CharField("Authors", max_length = 200)
    Title                  = models.TextField("Title", max_length = 5000)
    Pubmed                 = models.CharField("Pubmed", max_length = 2000)
    Link                   = models.CharField("Link", max_length = 200)
```

```python
    Abstract                = models.TextField("Abstract", max_length =
20000)

class FreshwaterSystem(models.Model):
    Influent_Source_Type    = models.CharField("Influent_Source_Type",
max_length = 200)
    Denitrification_System  = models.CharField("Denitrification_System",
max_length = 200)
    Denitrifying_Reactor    = models.CharField("Denitrifying_Reactor",
max_length = 200)
    Medium                  = models.CharField("Medium", max_length = 200)
    Culture                 = models.CharField("Culture", max_length = 200)
    Organism_cultured       = models.CharField("Organism_cultured",
max_length = 200)
    Respiration             = models.CharField("Respiration", max_length =
200)
    Electron_Donor          = models.TextField("Electron_Donor", max_length =
2000)
    Electron_Acceptor       = models.CharField("Electron_Acceptor",
max_length = 200)
    Input                   = models.CharField("Input", max_length = 200)
    Nitrate_Removal_Rate    = models.CharField("Nitrate_Removal_Rate",
max_length = 200)
    Denitrification_Rate    = models.CharField("Denitrification_Rate",
max_length = 200)
    Microorganism_identified = models.TextField("Microorganism_identified",
max_length = 2000)
    Molecular_Tools         = models.CharField("Molecular_Tools", max_length
= 200)
    Major_Findings          = models.CharField("Major_Findings", max_length =
2000)
    Authors                 = models.CharField("Authors", max_length = 200)
    Title                   = models.TextField("Title", max_length = 5000)
    Pubmed                  = models.CharField("Pubmed", max_length = 2000)
    Link                    = models.CharField("Link", max_length = 200)
    Abstract                = models.TextField("Abstract", max_length =
20000)

class MarineSystem(models.Model):
    Influent_Source_Type    = models.CharField("Influent_Source_Type",
max_length = 200)
    Denitrification_System  = models.CharField("Denitrification_System",
max_length = 200)
    Denitrifying_Reactor    = models.CharField("Denitrifying_Reactor",
max_length = 200)
    Medium                  = models.CharField("Medium", max_length = 200)
    Culture                 = models.CharField("Culture", max_length = 200)
    Organism_cultured       = models.CharField("Organism_cultured",
max_length = 200)
    Respiration             = models.CharField("Respiration", max_length =
200)
    Electron_Donor          = models.TextField("Electron_Donor", max_length =
2000)
    Electron_Acceptor       = models.CharField("Electron_Acceptor",
max_length = 200)
    Input                   = models.CharField("Input", max_length = 200)
    Nitrate_Removal_Rate    = models.CharField("Nitrate_Removal_Rate",
max_length = 200)
    Denitrification_Rate    = models.CharField("Denitrification_Rate",
max_length = 200)
    Microorganism_identified = models.TextField("Microorganism_identified",
max_length = 2000)
    Molecular_Tools         = models.CharField("Molecular_Tools", max_length
= 200)
    Major_Findings          = models.CharField("Major_Findings", max_length =
2000)
    Authors                 = models.CharField("Authors", max_length = 200)
    Title                   = models.TextField("Title", max_length = 5000)
```

```python
    Pubmed                  = models.CharField("Pubmed", max_length = 2000)
    Link                    = models.CharField("Link", max_length = 200)
    Abstract                = models.TextField("Abstract", max_length =
20000)

class GoundwaterSystem(models.Model):
    Influent_Source_Type    = models.CharField("Influent_Source_Type",
max_length = 200)
    Denitrification_System  = models.CharField("Denitrification_System",
max_length = 200)
    Denitrifying_Reactor    = models.CharField("Denitrifying_Reactor",
max_length = 200)
    Medium                  = models.CharField("Medium", max_length = 200)
    Culture                 = models.CharField("Culture", max_length = 200)
    Organism_cultured       = models.CharField("Organism_cultured",
max_length = 200)
    Respiration             = models.CharField("Respiration", max_length =
200)
    Electron_Donor          = models.TextField("Electron_Donor", max_length =
2000)
    Electron_Acceptor       = models.CharField("Electron_Acceptor",
max_length = 200)
    Input                   = models.CharField("Input", max_length = 200)
    Nitrate_Removal_Rate    = models.CharField("Nitrate_Removal_Rate",
max_length = 200)
    Denitrification_Rate    = models.CharField("Denitrification_Rate",
max_length = 200)
    Microorganism_identified = models.TextField("Microorganism_identified",
max_length = 2000)
    Molecular_Tools         = models.CharField("Molecular_Tools", max_length
= 200)
    Major_Findings          = models.CharField("Major_Findings", max_length =
2000)
    Authors                 = models.CharField("Authors", max_length = 200)
    Title                   = models.TextField("Title", max_length = 5000)
    Pubmed                  = models.CharField("Pubmed", max_length = 2000)
    Link                    = models.CharField("Link", max_length = 200)
    Abstract                = models.TextField("Abstract", max_length =
20000)

class WetlandRiparianZones(models.Model):
    Influent_Source_Type    = models.CharField("Influent_Source_Type",
max_length = 200)
    Denitrification_System  = models.CharField("Denitrification_System",
max_length = 200)
    Denitrifying_Reactor    = models.CharField("Denitrifying_Reactor",
max_length = 200)
    Medium                  = models.CharField("Medium", max_length = 200)
    Culture                 = models.CharField("Culture", max_length = 200)
    Organism_cultured       = models.CharField("Organism_cultured",
max_length = 200)
    Respiration             = models.CharField("Respiration", max_length =
200)
    Electron_Donor          = models.TextField("Electron_Donor", max_length =
2000)
    Electron_Acceptor       = models.CharField("Electron_Acceptor",
max_length = 200)
    Input                   = models.CharField("Input", max_length = 200)
    Nitrate_Removal_Rate    = models.CharField("Nitrate_Removal_Rate",
max_length = 200)
    Denitrification_Rate    = models.CharField("Denitrification_Rate",
max_length = 200)
    Microorganism_identified = models.TextField("Microorganism_identified",
max_length = 2000)
    Molecular_Tools         = models.CharField("Molecular_Tools", max_length
= 200)
    Major_Findings          = models.CharField("Major_Findings", max_length =
2000)
```

```python
    Authors                  = models.CharField("Authors", max_length = 200)
    Title                    = models.TextField("Title", max_length = 5000)
    Pubmed                   = models.CharField("Pubmed", max_length = 2000)
    Link                     = models.CharField("Link", max_length = 200)
    Abstract                 = models.TextField("Abstract", max_length =
20000)

class SulphurRemoval(models.Model):
    Influent_Source_Type    = models.CharField("Influent_Source_Type",
max_length = 200)
    Denitrification_System = models.CharField("Denitrification_System",
max_length = 200)
    Denitrifying_Reactor    = models.CharField("Denitrifying_Reactor",
max_length = 200)
    Medium                   = models.CharField("Medium", max_length = 200)
    Culture                  = models.CharField("Culture", max_length = 200)
    Organism_cultured        = models.CharField("Organism_cultured",
max_length = 200)
    Respiration              = models.CharField("Respiration", max_length =
200)
    Electron_Donor           = models.TextField("Electron_Donor", max_length =
2000)
    Nitrate_Removal_Rate    = models.CharField("Nitrate_Removal_Rate",
max_length = 200)
    Denitrification_Rate    = models.CharField("Denitrification_Rate",
max_length = 200)
    Major_Findings           = models.CharField("Major_Findings", max_length =
2000)
    Authors                  = models.CharField("Authors", max_length = 200)
    Title                    = models.TextField("Title", max_length = 5000)
    Pubmed                   = models.CharField("Pubmed", max_length = 2000)
    Link                     = models.CharField("Link", max_length = 200)
    Abstract                 = models.TextField("Abstract", max_length =
20000)

class Systemnitrification(models.Model):
    Influent = models.CharField("Influent", max_length = 500)
    System   = models.CharField("System", max_length = 500)
    Reactor  = models.CharField("Reactor", max_length = 500)
    Medium   = models.CharField("Medium", max_length = 500)
    Culture  = models.CharField("Culture", max_length = 500)
    Microorganism_identified = models.CharField("Microorganism_identified",
max_length = 500)
    Respiration = models.CharField("Respiration", max_length = 500)
    Electron_donor = models.CharField("Electron_donor", max_length = 500)
    Electron_acceptor = models.CharField("Electron_acceptor", max_length =
500)
    PH       = models.CharField("PH", max_length = 50)
    Ammonia_removal_rate = models.CharField("Ammonia_removal_rate",
max_length = 50)
    Nitrate_removal_rate = models.CharField("Nitrate_removal_rate",
max_length = 50)
    Ammonia_Removal_efficiency =
models.CharField("Ammonia_Removal_efficiency", max_length = 50)
    Nitrate_Removal_efficiency =
models.CharField("Nitrate_Removal_efficiency", max_length = 50)
    Total_Nitrogen_Removal = models.CharField("Total_Nitrogen_Removal",
max_length = 50)
    Carbon_Source = models.CharField("Carbon_Source", max_length = 500)
    Final_products = models.CharField("Final_products", max_length = 200)
    Major_findings = models.TextField("Major_findings", max_length = 20000)
    Authors = models.CharField("Authors", max_length = 50)
    Title = models.CharField("Title", max_length = 500)
    Pubmed_Link = models.CharField("Pubmed_Link", max_length = 500)
    Research_Link = models.CharField("Research_Link", max_length = 500)
    Abstract = models.TextField("Abstract", max_length = 20000)

class SystemComammox(models.Model):
```

```python
    Influent = models.CharField("Influent", max_length = 500)
    System  = models.CharField("System", max_length = 500)
    Reactor = models.CharField("Reactor", max_length = 500)
    Medium  = models.CharField("Medium", max_length = 500)
    Culture = models.CharField("Culture", max_length = 500)
    Microorganism_identified = models.CharField("Microorganism_identified",
max_length = 500)
    Respiration = models.CharField("Respiration", max_length = 500)
    Electron_donor = models.CharField("Electron_donor", max_length = 500)
    Electron_acceptor = models.CharField("Electron_acceptor", max_length =
500)
    PH       = models.CharField("PH", max_length = 50)
    Temperature = models.CharField("Temperature", max_length = 50)
    HRT = models.CharField("HRT", max_length = 200)
    NH4_Influent = models.CharField("NH4_Influent", max_length = 200)
    NO2_Influent = models.CharField("NO2_Influent", max_length = 200)
    NO3_Influent = models.CharField("NO3_Influent", max_length = 200)
    NH4_Effluent = models.CharField("NH4_Effluent", max_length = 200)
    NO2_Effluent = models.CharField("NO2_Effluent", max_length = 200)
    NO3_Effluent = models.CharField("NO3_Effluent", max_length = 200)
    NH4_removal = models.CharField("NH4_removal", max_length = 200)
    NO2_removal = models.CharField("NO2_removal", max_length = 200)
    NO3_removal = models.CharField("NO3_removal", max_length = 200)
    TN_Removal_rate = models.CharField("TN_Removal_rate", max_length = 200)
    Authors = models.CharField("Authors", max_length = 200)
    Title = models.CharField("Title", max_length = 200)
    Pubmed_Link = models.CharField("Pubmed_Link", max_length = 200)
    Research_Link = models.CharField("Research_Link", max_length = 200)
    Abstract = models.TextField("Abstract", max_length = 20000)

class SystemHAND(models.Model):
    Influent = models.CharField("Influent", max_length = 500)
    System  = models.CharField("System", max_length = 500)
    Reactor = models.CharField("Reactor", max_length = 500)
    Medium  = models.CharField("Medium", max_length = 500)
    Culture = models.CharField("Culture", max_length = 500)
    Microorganism_identified = models.CharField("Microorganism_identified",
max_length = 500)
    Respiration = models.CharField("Respiration", max_length = 500)
    Electron_donor = models.CharField("Electron_donor", max_length = 500)
    Electron_acceptor = models.CharField("Electron_acceptor", max_length =
500)
    PH       = models.CharField("PH", max_length = 50)
    Temperature = models.CharField("Temperature", max_length = 50)
    HRT = models.CharField("HRT", max_length = 200)
    NH4_Influent = models.CharField("NH4_Influent", max_length = 200)
    NO2_Influent = models.CharField("NO2_Influent", max_length = 200)
    NO3_Influent = models.CharField("NO3_Influent", max_length = 200)
    NH4_Effluent = models.CharField("NH4_Effluent", max_length = 200)
    NO2_Effluent = models.CharField("NO2_Effluent", max_length = 200)
    NO3_Effluent = models.CharField("NO3_Effluent", max_length = 200)
    NH4_removal = models.CharField("NH4_removal", max_length = 200)
    NO2_removal = models.CharField("NO2_removal", max_length = 200)
    NO3_removal = models.CharField("NO3_removal", max_length = 200)
    TN_Removal_rate = models.CharField("TN_Removal_rate", max_length = 200)
    Authors = models.CharField("Authors", max_length = 200)
    Title = models.CharField("Title", max_length = 200)
    Pubmed_Link = models.CharField("Pubmed_Link", max_length = 200)
    Research_Link = models.CharField("Research_Link", max_length = 200)
    Abstract = models.TextField("Abstract", max_length = 20000)

class SystemDNRA(models.Model):
    Influent = models.CharField("Influent", max_length = 500)
    System  = models.CharField("System", max_length = 500)
    Reactor = models.CharField("Reactor", max_length = 500)
    Medium  = models.CharField("Medium", max_length = 500)
    Culture = models.CharField("Culture", max_length = 500)
```

```python
    Microorganism_identified = models.CharField("Microorganism_identified",
max_length = 500)
    Respiration = models.CharField("Respiration", max_length = 500)
    Electron_donor = models.CharField("Electron_donor", max_length = 500)
    Electron_acceptor = models.CharField("Electron_acceptor", max_length =
500)
    PH       = models.CharField("PH", max_length = 50)
    Temperature = models.CharField("Temperature", max_length = 50)
    HRT = models.CharField("HRT", max_length = 200)
    NO3_Influent = models.CharField("NO3_Influent", max_length = 200)
    NH4_accumulation = models.CharField("NH4_accumulation", max_length =
200)
    NO2_removal = models.CharField("NO2_Effluent", max_length = 200)
    NH4_Accumulation_rate = models.CharField("NH4_Accumulation_rate",
max_length = 200)
    Authors = models.CharField("Authors", max_length = 200)
    Title = models.CharField("Title", max_length = 200)
    Pubmed_Link = models.CharField("Pubmed_Link", max_length = 200)
    Research_Link = models.CharField("Research_Link", max_length = 200)
    Abstract = models.TextField("Abstract", max_length = 20000)

class SystemDAMO(models.Model):
    Influent = models.CharField("Influent", max_length = 500)
    System   = models.CharField("System", max_length = 500)
    Reactor  = models.CharField("Reactor", max_length = 500)
    Medium   = models.CharField("Medium", max_length = 500)
    Culture  = models.CharField("Culture", max_length = 500)
    Microorganism_identified = models.CharField("Microorganism_identified",
max_length = 500)
    Respiration = models.CharField("Respiration", max_length = 500)
    Electron_donor = models.CharField("Electron_donor", max_length = 500)
    Electron_acceptor = models.CharField("Electron_acceptor", max_length =
500)
    PH       = models.CharField("PH", max_length = 50)
    Temperature = models.CharField("Temperature", max_length = 50)
    HRT = models.CharField("HRT", max_length = 200)
    NH4_Influent = models.CharField("NH4_Influent", max_length = 200)
    NO2_Influent = models.CharField("NO2_Influent", max_length = 200)
    NO3_Influent = models.CharField("NO3_Influent", max_length = 200)
    NH4_Effluent = models.CharField("NH4_Effluent", max_length = 200)
    NO2_Effluent = models.CharField("NO2_Effluent", max_length = 200)
    NO3_Effluent = models.CharField("NO3_Effluent", max_length = 200)
    NH4_removal = models.CharField("NH4_removal", max_length = 200)
    NO2_removal = models.CharField("NH2_removal", max_length = 200)
    NO3_removal = models.CharField("NO3_removal", max_length = 200)
    TN_Removal_rate = models.CharField("TN_Removal_rate", max_length = 200)
    Authors = models.CharField("Authors", max_length = 200)
    Title = models.CharField("Title", max_length = 200)
    Pubmed_Link = models.CharField("Pubmed_Link", max_length = 200)
    Research_Link = models.CharField("Research_Link", max_length = 200)
    Abstract = models.TextField("Abstract", max_length = 20000)

class SystemFNT(models.Model):
    Influent = models.CharField("Influent", max_length = 500)
    System   = models.CharField("System", max_length = 500)
    Reactor  = models.CharField("Reactor", max_length = 500)
    Medium   = models.CharField("Medium", max_length = 500)
    Culture  = models.CharField("Culture", max_length = 500)
    Fungal_species = models.CharField("Fungal_species", max_length = 500)
    Respiration = models.CharField("Respiration", max_length = 500)
    Electron_donor = models.CharField("Electron_donor", max_length = 500)
    Electron_acceptor = models.CharField("Electron_acceptor", max_length =
500)
    PH = models.CharField("PH", max_length = 50)
    Temperature = models.CharField("Temperature", max_length = 50)
    HRT = models.CharField("HRT", max_length = 200)
    Inoculum = models.CharField("Inoculum", max_length = 200)
    Aeration_rate = models.CharField("Aeration_rate", max_length = 200)
```

```python
    Incubation = models.CharField("Incubation", max_length = 200)
    biomass = models.CharField("biomass", max_length = 200)
    Ammonia_removal_rate = models.CharField("Ammonia_removal_rate",
max_length = 200)
    Nitrate_removal_rate = models.CharField("Nitrate_removal_rate",
max_length = 200)
    Nitrate_removal_efficiencies =
models.CharField("Nitrate_removal_efficiencies", max_length = 200)
    Ammonia_removal_efficiency =
models.CharField("Ammonia_removal_efficiency", max_length = 200)
    COD = models.CharField("COD", max_length = 200)
    COD_reduction = models.CharField("COD_reduction", max_length = 200)
    Authors = models.CharField("Authors", max_length = 200)
    Title = models.CharField("Title", max_length = 200)
    Pubmed_Link = models.CharField("Pubmed_Link", max_length = 200)
    Research_Link = models.CharField("Research_Link", max_length = 200)
    Abstract = models.TextField("Abstract", max_length = 20000)

class Multiomic(models.Model):
    bioproject_id = models.CharField('bioproject_id', max_length=50)
    accession_id =  models.CharField('accession_id', max_length=50)
    sequence_id  = models.CharField('sequence_id', max_length=50)
    sra_id       = models.CharField('sra_id', max_length=50)
    strategy     = models.CharField('strategy', max_length=100)
    platform     = models.CharField('platform', max_length=50)
    selection    = models.CharField('selection', max_length=50)
    data_type    = models.CharField('data_type', max_length=2000)
    organism     = models.CharField('sra_organismid', max_length=50)
    title        = models.TextField('title', max_length=20000)
    author       = models.CharField('author', max_length=100)
    reference    = models.CharField('reference', max_length=1000)
    process      = models.CharField('process', max_length=200)
    library_source = models.CharField('library_source', max_length=200)

class Systemanammox(models.Model):
    Influent = models.CharField("Influent", max_length = 500)
    System   = models.CharField("System", max_length = 500)
    Reactor  = models.CharField("Reactor", max_length = 500)
    Medium   = models.CharField("Medium", max_length = 500)
    Culture  = models.CharField("Culture", max_length = 500)
    Microorganism_identified = models.CharField("Microorganism_identified",
max_length = 500)
    Respiration = models.CharField("Respiration", max_length = 500)
    Electron_donor = models.CharField("Electron_donor", max_length = 500)
    Electron_acceptor = models.CharField("Electron_acceptor", max_length =
500)
    PH       = models.CharField("PH", max_length = 50)
    sludge_concentration = models.CharField("sludge_concentration",
max_length = 50)
    HRT = models.CharField("HRT", max_length = 50)
    NH4Influent = models.CharField("NH4Influent", max_length = 50)
    NO2Influent = models.CharField("NO2Influent", max_length = 50)
    SO4Influent = models.CharField("SO4Influent", max_length = 50)
    NH4Removal_efficiency = models.CharField("NH4Removal_efficiency",
max_length = 50)
    NO2Removal_efficiency = models.CharField("NO2Removal_efficiency",
max_length = 50)
    SO4Removal_efficiency = models.CharField("SO4Removal_efficiency",
max_length = 50)
    NLR = models.CharField("NLR", max_length = 50)
    NRR = models.CharField("NRR", max_length = 50)
    Major_findings = models.TextField("Major_findings", max_length = 20000)
    Authors = models.CharField("Authors", max_length = 50)
    Title = models.CharField("Title", max_length = 50)
    Pubmed_Link = models.CharField("Pubmed_Link", max_length = 500)
    Research_Link = models.CharField("Research_Link", max_length = 500)
    Abstract = models.TextField("Abstract", max_length = 20000)
```