

Genbanks_Ecs	
genbank_id *	INTEGER (Foreign key Genbanks.genbank_id)
ec_id *	INTEGER (Foreign key Ecs.ec_id)

Ecs	
ec_id	INTEGER (Primary key, autoincrement)
ec_number *	TEXT

Genbanks_CazyFamilies	
genbank_id *	INTEGER (Foreign key Genbanks.genbank_id)
family_id *	INTEGER (Foreign key CazyFamilies.family)

CazyFamilies	
family_id	INTEGER (Primary key, autoincrement)
family *	VARCHAR
subfamily *	VARCHAR

NcbiTaxs	
ncbi_tax_id	INTEGER (Primary key, autoincrement)
kingdom	Type
phylum	Type
tax_class	Type
tax_order	Type
family	Type
genus	VARCHAR
species	VARCHAR

GtdbTaxs	
gtdb_tax_id	INTEGER (Primary key, autoincrement)
kingdom	VARCHAR
phylum	VARCHAR
tax_class	VARCHAR
tax_order	VARCHAR
family	VARCHAR
genus*	VARCHAR
species*	INTEGER
gtdb_release	INTEGER

Uniprots	
genbank_id	INTEGER (Foreign key Genbanks.genbank_id)
uniprot_id	INTEGER (Primary key, autoincrement)
uniprot_accession *	VARCHAR (UniProt: entry id)
uniprot_name	VARCHAR (UniProt: entry name)
sequence	VARCHAR
seq_update_date	VARCHAR

Genbanks	
genbank_id	INTEGER (Primary key, autoincrement)
genbank_accession *	VARCHAR
sequence	VARCHAR
seq_update_date	VARCHAR
taxonomy_id	INTEGER (Foreign key Taxs.taxonomy_id)
ncbi_id	INTEGER(Foreign key NcbiTaxs.ncbi_id)

Genbanks_Pdbs	
genbank_id *	INTEGER (Foreign key Genbanks.genbank_id)
pdb_id *	INTEGER (Foreign key Pdbs.pdb_id)

Pdbs	
pdb_id	INTEGER (Primary key, autoincrement)
pdb_accession *	VARCHAR

Taxs	
taxonomy_id	INTEGER (Primary key, autoincrement)
genus *	VARCHAR
species *	VARCHAR
kingdom_id	INTEGER (Foreign key Kingdoms.kingdom_id)

Kingdoms	
kingdom_id	INTEGER (Primary key, autoincrement)
kingdom *	VARCHAR

Genbanks_Genomes	
genbank_id *	INTEGER (Foreign key Genbanks.genbank_id)
genome_id *	INTEGER (Foreign key Genomes.genome_id)

Genomes	
genome_id	INTEGER (Primary key, autoincrement)
assembly_name *	VARCHAR
gbk_version_accession *	VARCHAR
gbk_ncbi_id	INTEGER
refseq_version_accession *	VARCHAR
refseq_ncbi_id	INTEGER
gtdb_tax_id	INTEGER (Foreign key GtdbTaxs.gtdb_tax_id)