

MYSQL code for building database tables of the bECdb

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

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```python
class Compounds(models.Model):
 classification = models.CharField(max_length=100)
 category = models.CharField(max_length=100)
 year = models.CharField(max_length=100)
 compound = models.CharField(max_length=100)
 synonyms = models.CharField(max_length=1000)
 information = models.TextField(max_length=65536)
 myreferences = models.TextField(max_length=65536)
 references_link = models.CharField(max_length=2000)
 cas_number = models.CharField(max_length=100)
 ec_number = models.CharField(max_length=100)
 StockholmAnnexCode = models.CharField(max_length=100)
 mykey = models.CharField(max_length=2000)
 molecular = models.CharField(max_length=2000)
 weight = models.CharField(max_length=50)
 Solubility = models.CharField(max_length=2000)
 smile = models.CharField(max_length=2000)
 similarity = models.CharField(max_length=2000)
 products = models.CharField(max_length=2000)
 products_links = models.TextField(max_length=2000)
 cas_numbers_related = models.CharField(max_length=2000)
 weights_related = models.CharField(max_length=2000)
 formula_related = models.CharField(max_length=2000)
 dsstox_related = models.CharField(max_length=2000)
 persistence = models.CharField(max_length=2000)
 specific_exemptions = models.CharField(max_length=2000)
 acceptable_purposes = models.CharField(max_length=2000)
 conventions = models.CharField(max_length=2000)
 conventions_link = models.CharField(max_length=2000)
 ECHA = models.CharField(max_length=2000)
 ECHA_link = models.CharField(max_length=2000)
 PubChem = models.CharField(max_length=200)
 PubChem_link = models.CharField(max_length=200)
 ddstox = models.CharField(max_length=200)
 ddstox_link = models.CharField(max_length=2000)
 KEGG = models.CharField(max_length=200)
 KEGG_link = models.CharField(max_length=2000)
 chemspider = models.CharField(max_length=200)
 chemspider_link = models.CharField(max_length=2000)

class Bacteria(models.Model):
 compound = models.CharField(max_length=200)
 organism = models.CharField(max_length=200)
 accession_number = models.CharField(max_length=200)
 my_16S_number_link = models.CharField(max_length=2000)
 microorganism = models.CharField(max_length=200)
 fasta_link = models.CharField(max_length=2000)
 metabolized = models.CharField(max_length=200)
 biodegradation_rate = models.CharField(max_length=200)
 primary_intermediate = models.CharField(max_length=200)
 final_reduced_form = models.CharField(max_length=200)
 enzyme_activity_detected = models.CharField(max_length=200)
 degradation_technique = models.CharField(max_length=200)
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respiration = models.CharField(max_length=200)
respiring_condition = models.CharField(max_length=200)
carbon_source = models.CharField(max_length=200)
continent = models.CharField(max_length=200)
country = models.CharField(max_length=200)
isolation_source = models.CharField(max_length=200)
habitat_notes = models.CharField(max_length=2000)
title = models.TextField(max_length=20000)
pmid = models.CharField(max_length=200)
myreference = models.CharField(max_length=2000)
link = models.CharField(max_length=2000)

class Archaea(models.Model):
 compound = models.CharField(max_length=200)
 organism = models.CharField(max_length=200)
 accession_number = models.CharField(max_length=200)
 my_16S_number_link = models.CharField(max_length=2000)
 microorganism = models.CharField(max_length=200)
 fasta_link = models.CharField(max_length=2000)
 metabolized = models.CharField(max_length=2000)
 biodegradation_rate = models.CharField(max_length=200)
 primary_intermediate = models.CharField(max_length=200)
 final_reduced_form = models.CharField(max_length=200)
 enzyme_activity_detected = models.CharField(max_length=200)
 degradation_technique = models.CharField(max_length=200)
 respiration = models.CharField(max_length=200)
 respiring_condition = models.CharField(max_length=200)
 carbon_source = models.CharField(max_length=200)
 continent = models.CharField(max_length=200)
 country = models.CharField(max_length=200)
 isolation_source = models.CharField(max_length=200)
 habitat_notes = models.CharField(max_length=2000)
 title = models.TextField(max_length=20000)
 pmid = models.CharField(max_length=200)
 myreference = models.CharField(max_length=2000)
 link = models.CharField(max_length=2000)

class Fungi(models.Model):
 compound = models.CharField(max_length=200)
 organism = models.CharField(max_length=200)
 accession_number = models.CharField(max_length=200)
 my_16S_number_link = models.CharField(max_length=2000)
 microorganism = models.CharField(max_length=200)
 fasta_link = models.CharField(max_length=2000)
 metabolized = models.CharField(max_length=2000)
 biodegradation_rate = models.CharField(max_length=200)
 primary_intermediate = models.CharField(max_length=200)
 final_reduced_form = models.CharField(max_length=200)
 enzyme_activity_detected = models.CharField(max_length=200)
 degradation_technique = models.CharField(max_length=200)
 respiration = models.CharField(max_length=200)
 respiring_condition = models.CharField(max_length=200)
 carbon_source = models.CharField(max_length=200)
 continent = models.CharField(max_length=200)
 country = models.CharField(max_length=200)
 isolation_source = models.CharField(max_length=200)
 habitat_notes = models.CharField(max_length=2000)
 title = models.TextField(max_length=20000)
 pmid = models.CharField(max_length=200)
 myreference = models.CharField(max_length=2000)
 link = models.CharField(max_length=2000)

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class Algae(models.Model):
 compound = models.CharField(max_length=200)
 aphial_id = models.CharField(max_length=200)
 link = models.CharField(max_length=200)
 organism = models.CharField(max_length=200)
 accession_number = models.CharField(max_length=200)
 my_16S_number_link = models.CharField(max_length=2000)
 microorganism = models.CharField(max_length=200)
 fasta_link = models.CharField(max_length=2000)
 metabolized = models.CharField(max_length=200)
 primary_intermediate = models.CharField(max_length=200)
 final_reduced_form = models.CharField(max_length=200)
 enzyme_activity_detected = models.CharField(max_length=200)
 type_of_bioremediation = models.CharField(max_length=200)
 tissues = models.CharField(max_length=200)
 continent = models.CharField(max_length=200)
 country = models.CharField(max_length=200)
 isolation_source = models.CharField(max_length=200)
 habitat_notes = models.CharField(max_length=2000)
 title = models.TextField(max_length=20000)
 pmid = models.CharField(max_length=200)
 myreference = models.CharField(max_length=2000)
 research_link = models.CharField(max_length=2000)

class Gene(models.Model):
 compound = models.CharField(max_length=200)
 substrate = models.CharField(max_length=200)
 pathway_map = models.CharField(max_length=200)
 enzyme = models.CharField(max_length=200)
 encoding_gene = models.CharField(max_length=200)
 myfunction = models.CharField(max_length=500)
 ec_number = models.CharField(max_length=500)
 ec_link = models.CharField(max_length=500)
 kegg_orthology = models.CharField(max_length=500)
 kegg_link = models.CharField(max_length=500)
 organism = models.CharField(max_length=500)
 gene_bank_id = models.CharField(max_length=200)
 nucleotide_link = models.CharField(max_length=200)
 microorganism = models.CharField(max_length=200)
 gene_fasta = models.CharField(max_length=200)
 uniProt_id = models.CharField(max_length=200)
 uniProt_link = models.CharField(max_length=200)
 protein_id = models.CharField(max_length=200)
 protein_link = models.CharField(max_length=200)
 pro_fasta = models.CharField(max_length=200)
 continent = models.CharField(max_length=200)
 country = models.CharField(max_length=200)
 isolation_source = models.CharField(max_length=200)
 habitat_notes = models.CharField(max_length=200)
 title = models.CharField(max_length=200)
 pmid = models.CharField(max_length=200)
 myreference = models.CharField(max_length=200)
 research_link = models.CharField(max_length=200)

class Intermediate(models.Model):
 specifics_of_degradation = models.CharField(max_length=1000,
default="N/A")
 pop_degraded = models.CharField(max_length=1000, default="N/A")

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 pop_degradation_pathway = models.CharField(max_length=1000,
default="N/A")
 intermediate_Name = models.CharField(max_length=1000)
 cas_number = models.CharField(max_length=1000, default="N/A")
 molecular_formula = models.CharField(max_length=1000,
default="N/A")
 molecular_weight = models.CharField(max_length=1000,
default="N/A")
 smiles = models.CharField(max_length=1000, default="N/A")
 structure = models.CharField(max_length=1000, default="N/A")
 pubChem_cid = models.CharField(max_length=1000, default="N/A")
 pubChem_cid_link = models.CharField(max_length=1000,
default="N/A")
 kegg_id = models.CharField(max_length=1000, default="N/A")
 kegg_id_link = models.CharField(max_length=1000, default="N/A")
 ChempSpider_id = models.CharField(max_length=1000, default="N/A")
 ChempSpider_id_link = models.CharField(max_length=1000,
default="N/A")

class Pathway_literature(models.Model):
 pathway_name = models.CharField(max_length=200)
 compound_degraded = models.CharField(max_length=200)
 mydescription = models.TextField(max_length=20000)
 titles = models.TextField(max_length=20000)
 links = models.TextField(max_length=20000)
 authors = models.TextField(max_length=20000)
 abstracts = models.TextField(max_length=65536)
class Enzyme(models.Model):
 enzyme_name = models.CharField(max_length=200)
 ec_number = models.CharField(max_length=200)
 enzyme_class = models.CharField(max_length=200)
 encoding_gene = models.CharField(max_length=200)
 mydescription = models.TextField(max_length=20000)
 synonyms = models.CharField(max_length=2000)
 degradation_pathway = models.CharField(max_length=200)
 reaction_catalyzed = models.CharField(max_length=200)
 brend = models.CharField(max_length=200)
 brend_link = models.CharField(max_length=200)
 kegg_orthology_id = models.CharField(max_length=200)
 kegg_orthology_link = models.CharField(max_length=200)
 expasy = models.CharField(max_length=200)
 expasy_link = models.CharField(max_length=200)
 enzyme_database = models.CharField(max_length=200)
 enzyme_link = models.CharField(max_length=200)
 organism = models.CharField(max_length=200)
 mystatus = models.CharField(max_length=200)
 gene_cluster = models.CharField(max_length=200)
 subunit = models.CharField(max_length=200)
 protein_name = models.CharField(max_length=200)
 genbank_id = models.CharField(max_length=200)
 genbank_link = models.CharField(max_length=200)
 protein_id = models.CharField(max_length=200)
 protein_link = models.CharField(max_length=200)
 uniProtKB_id = models.CharField(max_length=200)
 uniProtKB_link = models.CharField(max_length=200)
 authors = models.CharField(max_length=200)
 titles = models.TextField(max_length=20000)
 pmid = models.CharField(max_length=200)
 pmid_link = models.CharField(max_length=200)
 research_Link = models.CharField(max_length=200)
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