1)

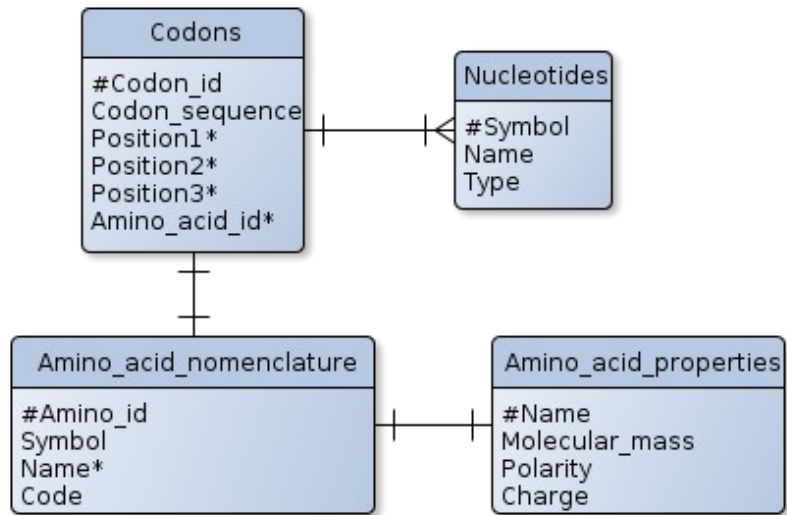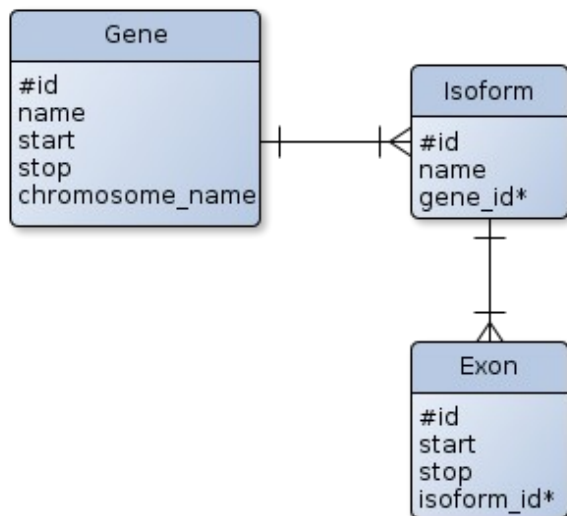**2)**
i)
Gene, Exon, Isoform

ii)

iii)
Gene(#id, name, start, stop, chromosome_name)
Isoform(#id, name, gene_id*)
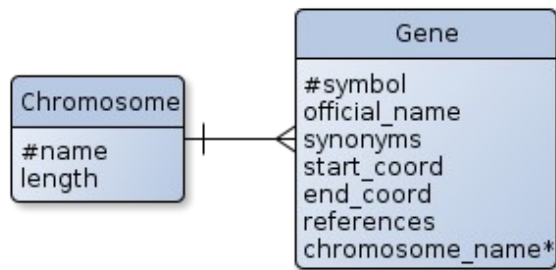Exon(#id, start, stop, isoform_id*)

3)
i)
Gene, Chromosome

ii)

iii)
Gene(#symbol, official_name, start_coord, end_coord, chromosome_name*, reference_id*)
Chromosome(#name, length)
Synonyme(#id, name, gene_id*)
Reference(#id, authors, title, journal, year, gene_id*)

iv)
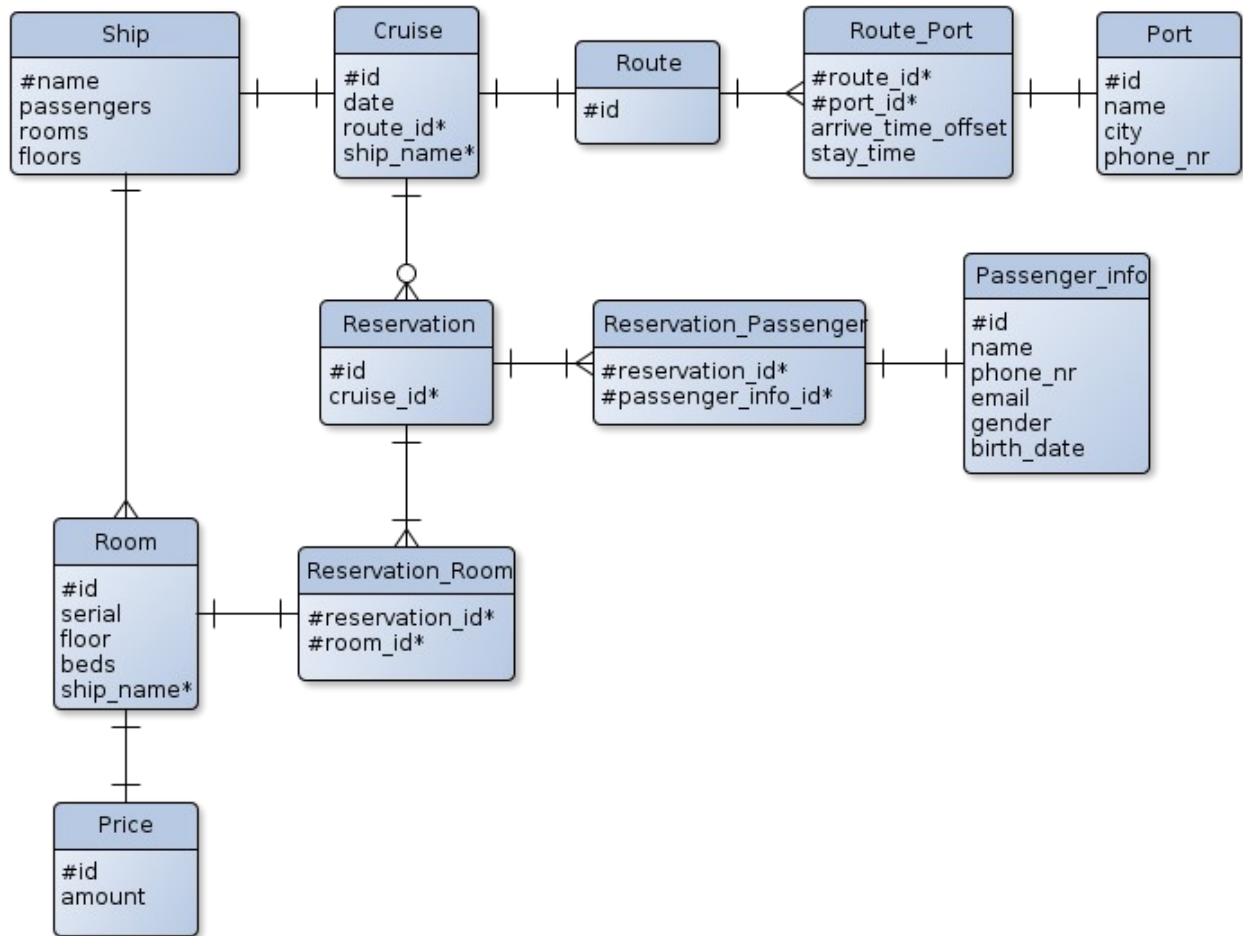Gene(#symbol, official_name, start_coord, end_coord, chromosome_name*)
Chromosome(#name, length)
Synonyme(#id, name, gene_id*)
Reference(#id, authors, title, journal, year)
Gene_Reference(#gene_symbol, #reference_id)

4)

5)

i)
The table has no primary key.
If a truck has more than one assignment, leading to multiple rows of the same registration_number, then the registration_number can't act as primary key.
The truck "info" will also lead to a lot of unnecessary data replication.
Also, you can't have a many-to-many relation with a single table. An assignment can have multiple trucks, and a truck can have multiple assignments.

ii)
Registration_number -> Registration_year
Registration_number -> Model
Registration_number -> Maximum_weight

iii)
{registration_number, assignment_number}

iv)
Truck(#id, Registration_number, Registration_year, Model, Maximum_weight)
Truck_Assignment(#Truck_id*, #Assignment_number*)