1. Design a data model for a database of mRNA expression levels. It should be fully normalized and should hold at least the following information:
   * Gene name
   * Organism
   * Gene sequence
   * Tissue
   * Expression level
   * Position of start of open reading frame
   * Position of stop of open reading frame

Assume mature mRNAs (i.e., no introns). Assume expression level is an integer value. To store string data longer than 255 characters, use the TEXT datatype. Note that to fully normalize the requested data, you will need to use more than one entity.

|  |
| --- |
| **GENES** |
| GeneId |
| TissueId |
| Expression level |

|  |
| --- |
| **SEQUENCE** |
| SequenceId |
| TissueID |
| Sequence Name |
| Position of start of open reading frame |
| Position of stop of open reading frame |

|  |
| --- |
| **ORGANISM** |
| Organism Id |
| Organism Name |

|  |
| --- |
| **TISSUE** |
| Tissue Id |
| Orgaism Id |
| Tissue Name  Tissue Type |

**Organism**

|  |  |  |
| --- | --- | --- |
| **Field name** | **Datatype** | **Notes** |
| Orgainsm ID | INT | Primary Key |
| Organism Name | VARCHAR(255) |  |

**Tissue**

|  |  |  |
| --- | --- | --- |
| **Field name** | **Datatype** | **Notes** |
| Tissue ID | INT | Primary Key |
| Organism Id | INT | Foreign key |
| Tissue Name | VARCHAR(255) |  |
| Tissue Type | VARCHAR(255) |  |

**Genes**

|  |  |  |
| --- | --- | --- |
| **Field name** | **Datatype** | **Notes** |
| Gene ID | INT | Primary Key |
| Tissue ID | INT | Foreign key |
| Expression level | VARCHAR(255) |  |

**Sequence**

|  |  |  |
| --- | --- | --- |
| **Field name** | **Datatype** | **Notes** |
| Sequence ID | INT | Primary Key |
| Tissue Id | INT | Foreign key |
| Sequence Name | VARCHAR(255) |  |
| Position of start of open reading frame | INT |  |
| Position of stop of open reading frame | INT |  |