

# Load Data

After you have generated the JSON data files (see [Building the CellBase database](#)), you can now load them in your Mongo database.

## Table of Contents:

- [Configure Database Credentials](#)
- [Load JSON files into MongoDB](#)

## Configure Database Credentials

Before loading the data into the database, your settings.xml file must have been appropriately configured indicating the database host names, ports, user and password. Here are the expected parameters:

| name                      | default         |
|---------------------------|-----------------|
| CELLBASE.DB.MONGODB.HOST  | localhost:27017 |
| CELLBASE.DB.USER          | <empty>         |
| CELLBASE.DB.PASSWORD      | <empty>         |
| CELLBASE.SERVER.REST.PORT | 9090            |

## Load JSON files into MongoDB

Use the CellBase CLI to load the data models. For example, to load all human (GRCh37) data models from the /tmp/data/cellbase/v4/homo\_sapiens\_grch37/mongodb/ created in section "Build Data Models", into the cellbase\_hsapiens\_grch37\_v4 database:

```
cellbase/build/bin$ ./cellbase.sh load -d variation --database  
cellbase_hsapiens_grch37_v4 -i /mnt/data/downloads/cellbase/v4  
/homo_sapiens_grch37/mongodb/ -L debug -Dmongodb-index-folder=/home  
/cafetero/app1/dev/cellbase/cellbase-app/app/mongodb-scripts/
```

Please, note that the whole loading and indexing process may need ~24h to complete, depending on the available hardware.

After successful load of all data, the corresponding database shall look like:

```
$ mongo mongodb-dev/cellbase_hsapiens_grch37_v4  
MongoDB shell version: 3.0.9  
connecting to: mongodb-dev/cellbase_hsapiens_grch37_v4clinical_variants  
> show collections;  
clinical_variants  
conservation  
gene  
genome_info  
genome_sequence  
metadata  
protein  
protein_functional_prediction  
protein_protein_interaction  
regulatory_region  
repeats  
variation  
variation_functional_score
```