

# client-configuration.yml

## Overview

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This is the default client configuration file you would get if not maven properties have been set up during the building (see [Configuration](#)). Most of this settings apply to command line.

```
logLevel: "INFO"
logFile: null

## number of seconds that session remains open
sessionDuration: 1200

## Default study when -s, --study are empty, e.g. "reference_grch37:
1kg_phase3"
defaultStudy: ""

## Alias to different studies, these can be fully qualified: user@project:
study
alias:
  1kg_grch37: hgvauser@reference_grch37:1kg_phase3
  1kg_grch38: reference_grch38:1kg_phase3

## The default organism values can be defined here.
organism:
  taxonomyCode: ${OPENCQA.CLIENT.ORGANISM.TAXONOMY_CODE}
  scientificName: ${OPENCQA.CLIENT.ORGANISM.SCIENTIFIC_NAME}
  commonName: ${OPENCQA.CLIENT.ORGANISM.COMMON_NAME}
  assembly: ${OPENCQA.CLIENT.ORGANISM.ASSEMBLY}

## REST client configuration options
rest:
  host: "${OPENCQA.CLIENT.REST.HOST}"
  batchQuerySize: 200
  timeout: ${OPENCQA.CLIENT.REST.TIMEOUT}
  defaultLimit: 2000

## gRPC configuration options
grpc:
  host: "${OPENCQA.CLIENT.GRPC.HOST}"

## Configure the default behaviour when query variants
variant:
  unknownGenotype: "0/0"
# each study can have a different format
includeFormats:
  1kg_grch37: "GT,AD,DP,GQ"
```

Where:

- **sessionDuration**: the number of seconds the session will be opened in the command line without any interaction
- **defaultStudy**: the study to be used when no study is provided
- **alias**: you can define study aliases, sometimes *project* and *study* alias can be too long or maybe there are studies with the same name in different projects. With the study **alias** setting you can define short names for fully qualified names at OpenCGA: *user@project:alias*
- **organism**: default organism to be used when creating new Projects, remember that all studies in the same project belong to the same species and assembly
- **rest**: the credentials to RESTful web services. *host* parameter contains the URL and the port.
- **grpc**: *host* for gRPC server, this contains URL and port
- **variant**: specific section for variants. *unknownGenotype* defines the default genotype to be returned for missing genotypes. *includeFormats* define the sample format data to be returned from the variant query service