

MongoDB implementation

CellBase creates one MongoDB database per species and assembly. Databases are named as follows:

cellbase_<species>_<assembly>_<cellbase-version>

For example:

```
cellbase_hsapiens_grch37_v4
cellbase_hvulgare_030312v2_v3
cellbase_lmajors_asm272v2_v3
cellbase_mmusculus_grcm38_v3
...
```

Please, note that the assembly identifier appears with all letters in lowercase and without hyphens or dots. A number of collections are created within each database, not all of them will be available for all species depending on the available data for each species:

```
gene
genome_info
genome_sequence
conservation
protein
protein_functional_prediction
protein_protein_interaction
regulatory_region
variation
clinical (only available for Human)
```

MongoDB is by definition schema-less, although documents stored under the same collection will obviously tend to have the same structure. Indexes design is based on expected most frequent queries.

Please find below collection schemas and examples of documents stored in each collection.

Collection schemas

- [gene](#)
- [genome_info](#)
- [genome_sequence](#)
- [conservation](#)
- [protein](#)
- [proteinfunctionalprediction](#)
- [proteinproteininteraction](#)
- [regulatory_region](#)
- [variation](#)
- [clinical](#)
- [Collection schemas](#)

gene

Contains gene core annotation (chromosome, start, end, transcripts, exons, etc.), but also data regarding gene-drug interactions, gene expression, etc.

```
{
  "properties": {
    "_chunkIds": {
      "items": [
        {
          "type": "string"
        }
      ],
      "type": "array"
    },
    "biotype": {
      "type": "string"
    },
    "chromosome": {
      "type": "string"
    },
    "description": {
      "type": "string"
    },
    "end": {
      "type": "integer"
    },
    "expressionValues": {
      "items": [
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          "properties": {
            "experimentId": {
              "type": "string"
            },
            "experimentalFactor": {
              "type": "string"
            },
            "expression": {
              "type": "string"
            },
            "factorValue": {
              "type": "string"
            },
            "geneName": {
              "type": "string"
            }
          }
        }
      ]
    }
  }
}
```

```

        "pvalue": {
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        },
        "technologyPlatform": {
          "type": "string"
        }
      },
      "type": "object"
    },
    "type": "array"
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  "name": {
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  "start": {
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  "status": {
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  "strand": {
    "type": "string"
  },
  "transcripts": {
    "items": [
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        "properties": {
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            "items": [
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                "type": "string"
              }
            ],
            "type": "array"
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          "cdnaSequence": {
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                  "cdnaCodingStart": {
                    "type": "integer"
                  },
                  "cdsEnd": {
                    "type": "integer"
                  },
                  "cdsStart": {
                    "type": "integer"
                  },
                  "chromosome": {
                    "type": "string"
                  },
                  "end": {
                    "type": "integer"
                  }
                }
              }
            ]
          }
        }
      }
    ]
  }
}

```

```

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        "genomicCodingStart": {
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        },
        "phase": {
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        },
        "sequence": {
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        },
        "start": {
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        },
        "strand": {
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        }
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    ],
    "type": "array"
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    "genomicCodingEnd": {
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    "genomicCodingStart": {
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    },
    "name": {
        "type": "string"
    },
    "proteinID": {
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    },
    "proteinSequence": {
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    "status": {
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    "strand": {
        "type": "string"
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    "xrefs": {
        "items": [
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                        "type": "string"
                    },
                    "dbName": {
                        "type": "string"
                    },
                    "id": {
                        "type": "string"
                    }
                }
            }
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        "type": "object"
    }
},
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},
    "type": "object"
},
    ],
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},
}

```

```
"type": "object"
}
```

Please, find below an example of a document stored in the gene collection. Tip: you can copy-paste the code below into a json editor to improve visualization (e.g. <http://jsoneditoronline.org/>):

```
{'status': 'KNOWN', 'end': 31381608, 'name': 'SDC3', 'source': 'Ensembl',
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'1_6271_5k', '1_6272_5k', '1_6273_5k', '1_6274_5k', '1_6275_5k',
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'experimentalFactor': 'organism_part', 'experimentId': 'E-MTAB-37',
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'experimentalFactor': 'organism_part', 'experimentId': 'E-MTAB-37',
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{'technologyPlatform': 'A-AFFY-44', 'geneName': 'ENSG00000162512',
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{'technologyPlatform': 'A-AFFY-44', 'geneName': 'ENSG00000162512',
'experimentalFactor': 'organism_part', 'experimentId': 'E-GEOD-17539',
'factorValue': 'skin', 'expression': 'DOWN', 'pvalue': 0.032277983},
{'technologyPlatform': 'A-AFFY-44', 'geneName': 'ENSG00000162512',
'experimentalFactor': 'organism_part', 'experimentId': 'E-GEOD-7307',
'factorValue': 'trigeminal ganglion', 'expression': 'UP', 'pvalue': 2.354071e-
07}, {'technologyPlatform': 'A-AFFY-44', 'geneName': 'ENSG00000162512',
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'factorValue': 'pancreas', 'expression': 'DOWN', 'pvalue': 0.0071172626},
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'factorValue': 'medulla', 'expression': 'UP', 'pvalue': 3.9396928e-13},
{'technologyPlatform': 'A-AFFY-44', 'geneName': 'ENSG00000162512',
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{'technologyPlatform': 'A-AFFY-44', 'geneName': 'ENSG00000162512',
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{'technologyPlatform': 'A-AFFY-44', 'geneName': 'ENSG00000162512',
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'factorValue': 'skeletal muscle', 'expression': 'DOWN', 'pvalue': 1.6489518e-07}, {'technologyPlatform': 'A-AFFY-44', 'geneName': 'ENSG00000162512', 'experimentalFactor': 'organism_part', 'experimentId': 'E-GEOD-7307', 'factorValue': 'cerebral cortex', 'expression': 'UP', 'pvalue': 2.6040384e-06}, {'technologyPlatform': 'A-AFFY-44', 'geneName': 'ENSG00000162512', 'experimentalFactor': 'organism_part', 'experimentId': 'E-GEOD-7307', 'factorValue': 'bone marrow', 'expression': 'DOWN', 'pvalue': 1.7366887e-05}, {'technologyPlatform': 'A-AFFY-44', 'geneName': 'ENSG00000162512', 'experimentalFactor': 'organism_part', 'experimentId': 'E-GEOD-7307', 'factorValue': 'occipital lobe', 'expression': 'UP', 'pvalue': 7.936557e-05}, {'technologyPlatform': 'A-AFFY-44', 'geneName': 'ENSG00000162512', 'experimentalFactor': 'organism_part', 'experimentId': 'E-GEOD-7307', 'factorValue': 'spinal cord', 'expression': 'UP', 'pvalue': 4.0106204e-20}, {'technologyPlatform': 'A-AFFY-44', 'geneName': 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'E-GEOD-7307', 'factorValue': 'substantia nigra pars compacta', 'expression': 'UP', 'pvalue': 8.931348e-11}, {'technologyPlatform': 'A-AFFY-44', 'geneName': 'ENSG00000162512', 'experimentalFactor': 'organism_part', 'experimentId': 'E-GEOD-7307', 'factorValue': 'tongue', 'expression': 'DOWN', 'pvalue': 0.0012368818}, {'technologyPlatform': 'A-AFFY-44', 'geneName': 'ENSG00000162512', 'experimentalFactor': 'organism_part', 'experimentId': 'E-GEOD-7307', 'factorValue': 'skin', 'expression': 'UP', 'pvalue': 0.006813136}, {'technologyPlatform': 'A-AFFY-44', 'geneName': 'ENSG00000162512', 'experimentalFactor': 'organism_part', 'experimentId': 'E-GEOD-7307', 'factorValue': 'temporal lobe', 'expression': 'UP', 'pvalue': 2.0233852e-06}, {'technologyPlatform': 'A-AFFY-44', 'geneName': 'ENSG00000162512', 'experimentalFactor': 'organism_part', 'experimentId': 'E-GEOD-7307', 'factorValue': 'tonsil', 'expression': 'DOWN', 'pvalue': 7.0418486e-05}, {'technologyPlatform': 'A-AFFY-44', 'geneName': 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'experimentalFactor': 'groups_96', 'experimentId': 'E-MTAB-62',
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'factorValue': 'cerebellum', 'expression': 'UP', 'pvalue': 0.0003318383},
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'factorValue': 'bladder', 'expression': 'DOWN', 'pvalue': 3.5734706e-15},
{ 'technologyPlatform': 'A-AFFY-33', 'geneName': 'ENSG000000162512',
'experimentalFactor': 'groups_369', 'experimentId': 'E-MTAB-62',
'factorValue': 'myometrium', 'expression': 'UP', 'pvalue': 5.5499697e-13},
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'factorValue': 'bronchial epithelium', 'expression': 'DOWN', 'pvalue':
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'ENSG000000162512', 'experimentalFactor': 'groups_369', 'experimentId': 'E-
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'ENSG000000162512', 'experimentalFactor': 'organism_part', 'experimentId': 'E-
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Please, find below an example of a document stored in the gene collection. Tip: you can copy-paste the code below into a json editor to improve visualization (e.g. <http://jsoneditoronline.org/>):

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genome_sequence

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```

[illegible]

Conservation scores per genomic position, e.g. PhastCons, PhyloP.


```
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```

Please, find below an example of a document stored in the gene collection. Tip: you can copy-paste the code below into a json editor to improve visualization (e.g. <http://jsoneditoronline.org/>):

```
{'end': 2269999, '_chunkIds': ['8_1134_2k'], 'chunkId': 1134, 'start':
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0.06, 0.057, 0.052, 0.054, 0.054, 0.052, 0.038, 0.03, 0.02, 0.006, 0.001,
0.001, 0.001, 0.0, 0.001, 0.001, 0.003, 0.004, 0.007, 0.008, 0.009, 0.009,
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0.015, 0.011, 0.006, 0.004, 0.005, 0.005, 0.004, 0.006, 0.006, 0.007, 0.007,
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```

protein

Protein annotation from UniProt and InterPro.

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```

```

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Please, find below an example of a document stored in the gene collection. Tip: you can copy-paste the code below into a json editor to improve visualization (e.g. <http://jsoneditoronline.org/>):

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proteinfunctionalprediction

Variant effect prediction scores such as SIFT or Polyphen for each aminoacid change.

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}
```



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    }
  },
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}

```

```

    }
  },
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    "ps": {
      "type": "number"
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  },
  "type": "object"
},
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      "type": "integer"
    },
    "ps": {
      "type": "number"
    }
  },
  "type": "object"
},
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    },
    "ps": {
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    }
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}
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        "pe": {
          "type": "integer"
        },
        "ps": {
          "type": "number"
        }
      },
      "type": "object"
    },
    "C": {
      "properties": {
        "pe": {
          "type": "integer"
        },
        "ps": {
          "type": "number"
        }
      },
      "type": "object"
    },
    "D": {
      "properties": {
        "pe": {
          "type": "integer"
        },
        "ps": {
          "type": "number"
        }
      },
      "type": "object"
    },
    "E": {
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        "pe": {
          "type": "integer"
        },
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          "type": "number"
        }
      },
      "type": "object"
    }
  },
  "type": "object"
}

```

```

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      "ps": {
        "type": "number"
      }
    },
    "type": "object"
  },
  "N": {
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      "pe": {
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      }
    },
  },

```

```

      "ps": {
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      }
    },
    "type": "object"
  },
  "P": {
    "properties": {
      "pe": {
        "type": "integer"
      },
      "ps": {
        "type": "number"
      }
    },
    "type": "object"
  },
  "Q": {
    "properties": {
      "pe": {
        "type": "integer"
      },
      "ps": {
        "type": "number"
      }
    },
    "type": "object"
  },
  "R": {
    "properties": {
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      },
      "ps": {
        "type": "number"
      }
    },
    "type": "object"
  },
  "S": {
    "properties": {
      "pe": {
        "type": "integer"
      },
      "ps": {
        "type": "number"
      }
    },
    "type": "object"
  },
  "T": {
    "properties": {
      "pe": {
        "type": "integer"
      },
      "ps": {
        "type": "number"
      }
    },
    "type": "object"
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        "type": "integer"
      },
      "ps": {
        "type": "number"
      }
    },
    "type": "object"
  },
  "W": {
    "properties": {
      "pe": {
        "type": "integer"
      },
      "ps": {
        "type": "number"
      }
    },
    "type": "object"
  },
  "Y": {

```

```

    "properties": {
      "pe": {
        "type": "integer"
      },
      "ps": {
        "type": "number"
      }
    },
    "type": "object"
  },
  "type": "object"
},
"checksum": {
  "type": "string"
},
"size": {
  "type": "integer"
},
"transcriptId": {
  "type": "string"
}
},
"type": "object"
}

```

Please, find below an example of a document stored in the gene collection. Tip: you can copy-paste the code below into a json editor to improve visualization (e.g. <http://jsoneditoronline.org/>):

```

{'size': 5, 'checksum': 'bbac0f119ec291d3260463db5c0aa0d9', 'aaPositions':
{'1': {'A': {'ps': 0.644, 'pe': 1}, 'C': {'ps': 0.963, 'pe': 0}, 'E': {'ps':
0.669, 'pe': 1}, 'D': {'ps': 0.898, 'pe': 1}, 'G': {'ps': 0.792, 'pe': 1},
'F': {'ps': 0.887, 'pe': 1}, 'I': {'ps': 0.78, 'pe': 1}, 'H': {'ps': 0.951,
'pe': 0}, 'K': {'ps': 0.472, 'pe': 1}, 'M': {'ps': None, 'pe': None}, 'L':
{'ps': 0.415, 'pe': 2}, 'N': {'ps': 0.794, 'pe': 1}, 'Q': {'ps': 0.734, 'pe':
1}, 'P': {'ps': 0.928, 'pe': 0}, 'S': {'ps': 0.644, 'pe': 1}, 'R': {'ps':
0.039, 'pe': 2}, 'T': {'ps': 0.706, 'pe': 1}, 'W': {'ps': 0.983, 'pe': 0},
'V': {'ps': 0.706, 'pe': 1}, 'Y': {'ps': 0.928, 'pe': 0}}, '3': {'A': {'ps':
0.659, 'pe': 1}, 'C': {'ps': 0.975, 'pe': 0}, 'E': {'ps': 0.808, 'pe': 1},
'D': {'ps': 0.853, 'pe': 1}, 'G': {'ps': 0.792, 'pe': 1}, 'F': {'ps': 0.827,
'pe': 1}, 'I': {'ps': 0.906, 'pe': 1}, 'H': {'ps': 0.936, 'pe': 0}, 'K':
{'ps': 0.808, 'pe': 1}, 'M': {'ps': 0.976, 'pe': 0}, 'L': {'ps': 0.685, 'pe':
1}, 'N': {'ps': 0.923, 'pe': 0}, 'Q': {'ps': 0.952, 'pe': 0}, 'P': {'ps':
0.058, 'pe': 2}, 'S': {'ps': None, 'pe': None}, 'R': {'ps': 0.93, 'pe': 0},
'T': {'ps': 0.785, 'pe': 1}, 'W': {'ps': 0.976, 'pe': 0}, 'V': {'ps': 0.808,
'pe': 1}, 'Y': {'ps': 0.096, 'pe': 2}}, '2': {'A': {'ps': 0.994, 'pe': 0},
'C': {'ps': 0.999, 'pe': 0}, 'E': {'ps': 0.999, 'pe': 0}, 'D': {'ps': 0.999,
'pe': 0}, 'G': {'ps': 0.998, 'pe': 0}, 'F': {'ps': 0.998, 'pe': 0}, 'I':
{'ps': None, 'pe': None}, 'H': {'ps': 0.999, 'pe': 0}, 'K': {'ps': 0.999,
'pe': 0}, 'M': {'ps': 0.999, 'pe': 0}, 'L': {'ps': 0.986, 'pe': 0}, 'N':
{'ps': 0.999, 'pe': 0}, 'Q': {'ps': 0.999, 'pe': 0}, 'P': {'ps': 0.999, 'pe':
0}, 'S': {'ps': 0.998, 'pe': 0}, 'R': {'ps': 0.999, 'pe': 0}, 'T': {'ps':
0.997, 'pe': 0}, 'W': {'ps': 0.999, 'pe': 0}, 'V': {'ps': 0.986, 'pe': 0},
'Y': {'ps': 0.999, 'pe': 0}}, '5': {'A': {'ps': 0.792, 'pe': 1}, 'C': {'ps':
0.982, 'pe': 0}, 'E': {'ps': 0.976, 'pe': 0}, 'D': {'ps': 0.976, 'pe': 0},
'G': {'ps': 0.965, 'pe': 0}, 'F': {'ps': 0.904, 'pe': 1}, 'I': {'ps': None,
'pe': None}, 'H': {'ps': 0.982, 'pe': 0}, 'K': {'ps': 0.949, 'pe': 0}, 'M':
{'ps': 0.951, 'pe': 0}, 'L': {'ps': 0.078, 'pe': 2}, 'N': {'ps': 0.975, 'pe':
0}, 'Q': {'ps': 0.976, 'pe': 0}, 'P': {'ps': 0.976, 'pe': 0}, 'S': {'ps':
0.963, 'pe': 0}, 'R': {'ps': 0.976, 'pe': 0}, 'T': {'ps': 0.915, 'pe': 0},
'W': {'ps': 0.982, 'pe': 0}, 'V': {'ps': 0.437, 'pe': 2}, 'Y': {'ps': 0.976,
'pe': 0}}, '4': {'A': {'ps': 0.955, 'pe': 0}, 'C': {'ps': 0.99, 'pe': 0},
'E': {'ps': 0.981, 'pe': 0}, 'D': {'ps': 0.987, 'pe': 0}, 'G': {'ps': 0.972,
'pe': 0}, 'F': {'ps': 0.78, 'pe': 1}, 'I': {'ps': 0.972, 'pe': 0}, 'H':
{'ps': 0.987, 'pe': 0}, 'K': {'ps': 0.981, 'pe': 0}, 'M': {'ps': 0.99, 'pe':
0}, 'L': {'ps': 0.889, 'pe': 1}, 'N': {'ps': 0.987, 'pe': 0}, 'Q': {'ps':
0.987, 'pe': 0}, 'P': {'ps': 0.987, 'pe': 0}, 'S': {'ps': 0.98, 'pe': 0},
'R': {'ps': 0.987, 'pe': 0}, 'T': {'ps': 0.981, 'pe': 0}, 'W': {'ps': 0.219,
'pe': 2}, 'V': {'ps': 0.955, 'pe': 0}, 'Y': {'ps': None, 'pe': None}}},
'transcriptId': 'ENST00000430747'}

```

proteinproteininteraction

PPI data from Intact.

```

{
  "properties": {
    "authors": {
      "items": [

```

```

        {
            "type": "string"
        }
    ],
    "type": "array"
},
"detectionMethod": {
    "items": [
        {
            "properties": {
                "name": {
                    "type": "string"
                },
                "psimi": {
                    "type": "string"
                }
            },
            "type": "object"
        }
    ],
    "type": "array"
},
"interactorA": {
    "properties": {
        "biologicalRole": {
            "items": [
                {
                    "properties": {
                        "name": {
                            "type": "string"
                        },
                        "psimi": {
                            "type": "string"
                        }
                    },
                    "type": "object"
                }
            ],
            "type": "array"
        },
        "dbName": {
            "type": "string"
        },
        "id": {
            "type": "string"
        },
        "moleculeType": {
            "properties": {
                "name": {
                    "type": "string"
                },
                "psimi": {
                    "type": "string"
                }
            },
            "type": "object"
        },
        "xrefs": {
            "items": [
                {
                    "properties": {
                        "dbName": {
                            "type": "string"
                        },
                        "description": {
                            "type": "string"
                        },
                        "id": {
                            "type": "string"
                        }
                    },
                    "type": "object"
                }
            ],
            "type": "array"
        }
    },
    "type": "object"
},
"interactorB": {
    "properties": {
        "biologicalRole": {
            "items": [
                {

```

```

        "properties": {
          "name": {
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          },
          "psimi": {
            "type": "string"
          }
        },
        "type": "object"
      },
      "type": "array"
    },
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    "id": {
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    },
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        },
        "psimi": {
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        }
      },
      "type": "object"
    },
    "xrefs": {
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              "type": "string"
            },
            "description": {
              "type": "string"
            },
            "id": {
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            }
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          "type": "object"
        }
      ],
      "type": "array"
    },
    "type": "object"
  },
  "pubmed": {
    "type": "string"
  },
  "score": {
    "items": [
      {
        "properties": {
          "score": {
            "type": "number"
          },
          "type": {
            "type": "string"
          }
        },
        "type": "object"
      }
    ],
    "type": "array"
  },
  "source": {
    "items": [
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        "properties": {
          "name": {
            "type": "string"
          },
          "psimi": {
            "type": "string"
          }
        },
        "type": "object"
      }
    ],
    "type": "array"
  }
}

```



```

    },
    "type": "array"
  },
  "status": {
    "type": "string"
  },
  "type": {
    "items": [
      {
        "properties": {
          "name": {
            "type": "string"
          },
          "psimi": {
            "type": "string"
          }
        },
        "type": "object"
      }
    ],
    "type": "array"
  },
  "xrefs": {
    "items": [
      {
        "properties": {
          "dbName": {
            "type": "string"
          },
          "id": {
            "type": "string"
          }
        },
        "type": "object"
      }
    ],
    "type": "array"
  }
},
"type": "object"
}

```

Please, find below an example of a document stored in the gene collection. Tip: you can copy-paste the code below into a json editor to improve visualization (e.g. <http://jsoneditoronline.org/>):

```

{
  "status": "curated",
  "xrefs": [
    {
      "id": "MINT-5214823",
      "dbName": "mint"
    },
    {
      "id": "EBI-495141",
      "dbName": "intact",
      "detectionMethod": [
        {
          "psimi": "MI:0030",
          "name": "cross-linking study",
          "pubmed": "11717445",
          "interactorA": {
            "moleculeType": {
              "psimi": "MI:0326",
              "name": "protein",
              "biologicalRole": [
                {
                  "psimi": "MI:0499",
                  "name": "unspecified role"
                }
              ],
              "xrefs": [
                {
                  "id": "Q92851-3",
                  "dbName": "uniprotkb",
                  "id": "EBI-495122",
                  "dbName": "intact",
                  "id": "q92851-3",
                  "dbName": "display_long",
                  "id": "10-C",
                  "dbName": "isoform synonym",
                  "id": "CASP10",
                  "dbName": "gene name",
                  "id": "CASP10",
                  "dbName": "display_short",
                  "id": "MCH4",
                  "dbName": "gene name synonym",
                  "id": "Apoptotic protease Mch-4",
                  "dbName": "gene name synonym",
                  "id": "FAS-associated death domain protein interleukin-1B-converting enzyme 2",
                  "dbName": "gene name synonym",
                  "id": "ICE-like apoptotic protease 4",
                  "dbName": "gene name synonym",
                  "description": "caspa_human",
                  "id": "EBI-495095",
                  "dbName": "intact",
                  "id": "Q92851-3",
                  "dbName": "uniprotkb",
                  "interactorB": {
                    "moleculeType": {
                      "psimi": "MI:0326",
                      "name": "protein",
                      "biologicalRole": [
                        {
                          "psimi": "MI:0499",
                          "name": "unspecified role"
                        }
                      ],
                      "xrefs": [
                        {
                          "id": "Q92851-3",
                          "dbName": "uniprotkb",
                          "id": "EBI-495122",
                          "dbName": "intact",
                          "id": "q92851-3",
                          "dbName": "display_long",
                          "id": "10-C",
                          "dbName": "isoform synonym",
                          "id": "CASP10",
                          "dbName": "gene name",
                          "id": "CASP10",
                          "dbName": "display_short",
                          "id": "MCH4",
                          "dbName": "gene name synonym",
                          "id": "Apoptotic protease Mch-4",
                          "dbName": "gene name synonym",
                          "id": "FAS-associated death domain protein interleukin-1B-converting enzyme 2",
                          "dbName": "gene name synonym",
                          "id": "ICE-like apoptotic protease 4",
                          "dbName": "gene name synonym",
                          "description": "caspa_human",
                          "id": "EBI-495095",
                          "dbName": "intact",
                          "id": "Q92851-3",
                          "dbName": "uniprotkb",
                          "score": [
                            {
                              "score": 0.4,
                              "type": "intact-miscore"
                            }
                          ],
                          "source": [
                            {
                              "psimi": "MI:0471",
                              "name": "MINT",
                              "authors": "Wang et al. (2001)",
                              "type": [
                                {
                                  "psimi": "MI:0915",
                                  "name": "physical association"
                                }
                              ]
                            }
                          ]
                        }
                      ]
                    }
                  }
                }
              ]
            }
          }
        }
      ]
    }
  ]
}

```

regulatory_region

Regulatory annotation.

```

{
  "properties": {
    "_chunkIds": {
      "items": [
        {
          "type": "string"
        }
      ],
      "type": "array"
    },
    "alias": {
      "type": "string"
    },
    "cellTypes": {
      "items": [
        {
          "type": "string"
        }
      ],
      "type": "array"
    },
    "chromosome": {
      "type": "string"
    },
    "chunkIds": {
      "items": [
        {
          "type": "string"
        }
      ],
      "type": "array"
    },
    "end": {
      "type": "integer"
    },
    "featureClass": {
      "type": "string"
    },
    "featureType": {
      "type": "string"
    },
    "frame": {
      "type": "string"
    },
    "name": {
      "type": "string"
    },
    "score": {
      "type": "string"
    },
    "source": {
      "type": "string"
    },
    "start": {
      "type": "integer"
    },
    "strand": {
      "type": "string"
    }
  },
  "type": "object"
}

```

Please, find below an example of a document stored in the gene collection. Tip: you can copy-paste the code below into a json editor to improve visualization (e.g. <http://jsoneditoronline.org/>):

```

{'alias': 'HUVEC_CTCF_ENCODE_Uw_SWEMBL_R015', 'featureType':
'TF_binding_site', 'chunkIds': ['19_133_2k'], 'end': 267744, 'name': 'CTCF',
'start': 267159, 'frame': '.', '_chunkIds': ['19_133_2k'], 'cellTypes':
['HUVEC'], 'source': 'SWEmbl_R015', 'score': '.', 'strand': '.',
'featureClass': 'Transcription Factor', 'chromosome': '19'}

```

variation

Genomic variant data from ENSEMBL variation. Includes CellBase variant annotation and population frequencies from ExAC, 1K genomes phase 1 and 3, GoNL, UK10K, etc.

```

{
  "properties": {
    "alleleString": {
      "type": "string"
    }
  }
}

```

```

},
"alternate": {
  "type": "string"
},
"ancestralAllele": {
  "type": "string"
},
"chromosome": {
  "type": "string"
},
"chunkIds": {
  "items": [
    {
      "type": "string"
    }
  ],
  "type": "array"
},
"consequenceTypes": {
  "items": [
    {
      "type": "string"
    }
  ],
  "type": "array"
},
"displayConsequenceType": {
  "type": "string"
},
"end": {
  "type": "integer"
},
"evidence": {
  "type": "string"
},
"id": {
  "type": "string"
},
"minorAllele": {
  "type": "string"
},
"minorAlleleFreq": {
  "type": "string"
},
"phenotype": {
  "type": "null"
},
"populationFrequencies": {
  "items": [],
  "type": "array"
},
"reference": {
  "type": "string"
},
"samples": {
  "type": "null"
},
"start": {
  "type": "integer"
},
"strand": {
  "type": "string"
},
"transcriptVariations": {
  "items": [
    {
      "properties": {
        "alleleString": {
          "type": "string"
        },
        "cdnaEnd": {
          "type": "integer"
        },
        "cdnaStart": {
          "type": "integer"
        },
        "cdsEnd": {
          "type": "integer"
        },
        "cdsStart": {
          "type": "integer"
        },
        "codonAlleleString": {
          "type": "string"
        }
      }
    }
  ]
}

```

```

    },
    "consequenceTypes": {
      "items": [
        {
          "type": "string"
        }
      ],
      "type": "array"
    },
    "distanceToTranscript": {
      "type": "integer"
    },
    "hgvsGenomic": {
      "type": "string"
    },
    "hgvsProtein": {
      "type": "string"
    },
    "hgvsTranscript": {
      "type": "string"
    },
    "peptideAlleleString": {
      "type": "string"
    },
    "polyphenPrediction": {
      "type": "string"
    },
    "polyphenScore": {
      "type": "number"
    },
    "siftPrediction": {
      "type": "string"
    },
    "siftScore": {
      "type": "number"
    },
    "somatic": {
      "type": "string"
    },
    "transcriptId": {
      "type": "string"
    },
    "translationEnd": {
      "type": "integer"
    },
    "translationStart": {
      "type": "integer"
    }
  },
  "type": "object"
},
"validationStatus": {
  "type": "string"
},
"xrefs": {
  "items": [
    {
      "properties": {
        "crossReference": {
          "type": "string"
        },
        "dataBase": {
          "type": "string"
        },
        "version": {
          "type": "string"
        }
      }
    }
  ],
  "type": "array"
},
"transcriptId": {
  "type": "string"
},
"translationEnd": {
  "type": "integer"
},
"translationStart": {
  "type": "integer"
}
}

```

Please, find below an example of a document stored in the gene collection. Tip: you can copy-paste the code below into a json editor to improve visualization (e.g. <http://jsoneditoronline.org/>):

```
{'reference': 'A', 'validationStatus': '', 'evidence':
'Multiple_observations', 'populationFrequencies': [],
'displayConsequenceType': 'intron_variant', 'id': 'rs600183', 'chromosome':
'HSCHR19LRC_PGF2_CTG1', 'end': 54989681, 'alternate': 'G', 'minorAllele': '',
'start': 54989681, 'consequenceTypes': ['intron_variant'], 'phenotype': None,
'samples': None, 'type': 'SNV', 'xrefs': [{'crossReference': 'rs2364439',
'version': '138', 'dataBase': 'Archive dbSNP'}], 'ancestralAllele': '',
'alleleString': 'A/G', 'strand': '1', 'chunkIds':
['HSCHR19LRC_PGF2_CTG1_10997_5k'], 'transcriptVariations': [{'siftScore':
0.0, 'cdnaStart': 0, 'codonAlleleString': '', 'transcriptId':
'ENST00000576413', 'translationStart': 0, 'hgvsProtein': '', 'cdsEnd': 0,
'cdnaEnd': 0, 'somatic': '0', 'distanceToTranscript': 10278,
'consequenceTypes': ['intron_variant'], 'peptideAlleleString': '',
'translationEnd': 0, 'cdsStart': 0, 'polyphenPrediction': '',
'hgvsTranscript': 'ENST00000576413.1:c.35-4618G>A', 'hgvsGenomic': '',
'alleleString': 'G/A', 'polyphenScore': 0.0, 'siftPrediction': ''},
{'siftScore': 0.0, 'cdnaStart': 0, 'codonAlleleString': '', 'transcriptId':
'ENST00000573202', 'translationStart': 0, 'hgvsProtein': '', 'cdsEnd': 0,
'cdnaEnd': 0, 'somatic': '0', 'distanceToTranscript': 9986,
'consequenceTypes': ['intron_variant'], 'peptideAlleleString': '',
'translationEnd': 0, 'cdsStart': 0, 'polyphenPrediction': '',
'hgvsTranscript': 'ENST00000573202.1:c.356-7090G>A', 'hgvsGenomic': '',
'alleleString': 'G/A', 'polyphenScore': 0.0, 'siftPrediction': ''},
{'siftScore': 0.0, 'cdnaStart': 0, 'codonAlleleString': '', 'transcriptId':
'ENST00000575687', 'translationStart': 0, 'hgvsProtein': '', 'cdsEnd': 0,
'cdnaEnd': 0, 'somatic': '0', 'distanceToTranscript': 1768,
'consequenceTypes': ['intron_variant'], 'peptideAlleleString': '',
'translationEnd': 0, 'cdsStart': 0, 'polyphenPrediction': '',
'hgvsTranscript': 'ENST00000575687.2:c.929-482G>A', 'hgvsGenomic': '',
'alleleString': 'G/A', 'polyphenScore': 0.0, 'siftPrediction': ''},
{'siftScore': 0.0, 'cdnaStart': 0, 'codonAlleleString': '', 'transcriptId':
'ENST00000572500', 'translationStart': 0, 'hgvsProtein': '', 'cdsEnd': 0,
'cdnaEnd': 0, 'somatic': '0', 'distanceToTranscript': 1768,
'consequenceTypes': ['intron_variant'], 'peptideAlleleString': '',
'translationEnd': 0, 'cdsStart': 0, 'polyphenPrediction': '',
'hgvsTranscript': 'ENST00000572500.2:c.*296-482G>A', 'hgvsGenomic': '',
'alleleString': 'G/A', 'polyphenScore': 0.0, 'siftPrediction': ''}],
'minorAlleleFreq': ''}
```

clinical

Clinical variants from databases such as ClinVar, COSMIC or GWAS catalog.

```
{
  "properties": {
    "accessionNumber": {
      "type": "string"
    },
    "age": {
      "type": "number"
    },
    "alternate": {
      "type": "string"
    },
    "chromosome": {
      "type": "string"
    },
    "comments": {
      "type": "string"
    },
    "end": {
      "type": "integer"
    },
    "geneCDSLength": {
      "type": "integer"
    },
    "geneName": {
      "type": "string"
    },
    "genomewideScreen": {
      "type": "string"
    },
    "hgncId": {
      "type": "string"
    },
    "histologySubtype": {
      "type": "string"
    },
  },
}
```

```

    "idSample": {
      "type": "string"
    },
    "idStudy": {
      "type": "integer"
    },
    "id_tumour": {
      "type": "string"
    },
    "mutationAA": {
      "type": "string"
    },
    "mutationCDS": {
      "type": "string"
    },
    "mutationDescription": {
      "type": "string"
    },
    "mutationGRCh37GenomePosition": {
      "type": "string"
    },
    "mutationGRCh37Strand": {
      "type": "string"
    },
    "mutationID": {
      "type": "string"
    },
    "mutationSomaticStatus": {
      "type": "string"
    },
    "mutationZygosity": {
      "type": "string"
    },
    "primaryHistology": {
      "type": "string"
    },
    "primarySite": {
      "type": "string"
    },
    "reference": {
      "type": "string"
    },
    "sampleName": {
      "type": "string"
    },
    "sampleSource": {
      "type": "string"
    },
    "siteSubtype": {
      "type": "string"
    },
    "snp": {
      "type": "boolean"
    },
    "start": {
      "type": "integer"
    },
    "tumourOrigin": {
      "type": "string"
    }
  },
  "type": "object"
}

```

Please, find below an example of a document stored in the gene collection. Tip: you can copy-paste the code below into a json editor to improve visualization (e.g. <http://jsoneditoronline.org/>):

```

{
  'histologySubtype': 'adenocarcinoma',
  'reference': 'A',
  'mutationGRCh37Strand': '-',
  'comments': 'Stage:IIA',
  'hgncId': '11548',
  'sampleSource': 'NS',
  'chromosome': 'X',
  'geneName': 'TAF7L',
  'end': 100531072,
  'alternate': 'G',
  'tumourOrigin': 'NS',
  'id_tumour': '1566056',
  'start': 100531072,
  'primarySite': 'large_intestine',
  'siteSubtype': 'colon',
  'geneCDSLength': 1389,
  'genomewideScreen': 'y',
  'primaryHistology': 'carcinoma',
  'mutationGRCh37GenomePosition': '23:100531072-100531072',
  'idStudy': 376,
  'sampleName': 'TCGA-D5-6930-01',
  'mutationCDS': 'c.1200A>G',
  'snp': false,
  'age': 67.0,
  'idSample': '1651269',
  'accessionNumber': 'ENST00000372907',
  'mutationAA': 'p.K400K',
  'mutationDescription': 'Substitution - coding silent',
  'mutationSomaticStatus': 'Reported in another cancer sample as somatic',
  'mutationID': '25490',
  'mutationZygosity': 'het'
}

```