

Web API

In addition to the web interface, one can access Cas-Database via web API (Application Programming Interface). All data is returned in JSON (JavaScript Object Notation) format.

1. Retrieving an organism list

Request

Method	URL
GET	http://www.rgenome.net/cas-database/organisms/

Parameter	Description
organism_type	If specified, only the organisms with this type of organism are selected. Currently 1 for Vertebrates, 2 for Plants, 3 for Insects, and 4 for Others.

Response

Response
<pre>{ "organisms": [{"type": <organism type>, "id": <organism id>, "name": <organism name>}, ...] }</pre>
Example (http://www.rgenome.net/cas-database/organisms/)
<pre>{ "organisms": [{"type": "vertebrate", "id": 1, "name": "Homo sapiens (GRCh38/hg38) - Human"}, {"type": "plant", "id": 2, "name": "Arabidopsis thaliana (TAIR10)"}, {"type": "plant", "id": 3, "name": "Musa acuminata (MA1) - Banana"}, {"type": "plant", "id": 4, "name": "Vitis vinifera (IGGP_12X) - European grapevine"}, {"type": "vertebrate", "id": 5, "name": "Rattus norvegicus (Rnor 6.0) - Rat"}, {"type": "vertebrate", "id": 6, "name": "Mus musculus (GRCm38/mm10) - Mouse"}, {"type": "plant", "id": 7, "name": "Solanum lycopersicum (SL 2.5) - Tomato"}, {"type": "vertebrate", "id": 8, "name": "Danio rerio (GRCz10) - Zebrafish"}, {"type": "insect", "id": 9, "name": "Drosophila melanogaster (BDGP6) - Fruit fly"}, {"type": "other", "id": 10, "name": "Caenorhabditis elegans (WBcel235)"}, {"type": "plant", "id": 11, "name": "Glycine max (JGI v1.0) - Soybean"}, {"type": "vertebrate", "id": 12, "name": "Sus scrofa (Ensembl v10.2) - Pig"}] }</pre>

2. Retrieving a gene list

Request

Method	URL
GET	<a href="http://www.rgenome.net/cas-database/organisms/<organism_id>/genes/">http://www.rgenome.net/cas-database/organisms/<organism_id>/genes/

Parameter	Description
page	Page number to retrieve.
query	Searching query for genes. If specified, only genes with query in symbol or Ensemble id are returned.
all	Flag to retrieve all genes without pagination. 1 is true, and 0 is false.

Response

Response

```

{
  "links": {
    "next": <URL of next page, if available>,
    "previous": <URL of previous page, if available>
  }
  "page_count": <number of available pages>,
  "gene_count": <number of all found genes>,
  "genes": [
    {
      "id": <gene ID in number>,
      "symbol": <symbol of gene>,
      "ensembl_id": <Ensembl ID of gene>,
      "description": <description of gene>,
      "biotype": <type of gene>
    },
    ...
  ]
}

```

Example (<http://www.rgenome.net/cas-database/organisms/1/genes/?page=1&query=c4bp>)

```

{"page_count": 1, "gene_count": 2, "genes": [{"symbol": "C4BPA", "ensembl_id": "ENSG00000123838", "id": 18037, "biotype": "Protein coding", "description": "complement component 4 binding protein, alpha [Source:HGNC Symbol;Acc:HGNC:1325]"}, {"symbol": "C4BPB", "ensembl_id": "ENSG00000123843", "id": 15648, "biotype": "Protein coding", "description": "complement component 4 binding protein, beta [Source:HGNC Symbol;Acc:HGNC:1328]}]}

```

3. Retrieving a target list

Request

Method	URL
GET	<a href="http://www.rgenome.net/cas-database/genes/<gene_id>/targets/">http://www.rgenome.net/cas-database/genes/<gene_id>/targets/

Parameter	Description
filter_mis0	Filtering query for the count of 0 mismatches, specified in number. Trailing '+' or '-' sign to the number specifies ranges of count, e.g. mismatch count of equals to 2 or above would be '2+'.
filter_mis1	Filtering query for the count of 1 mismatch, specified in number. Trailing '+' or '-' sign to the number specifies ranges of count.
filter_mis2	Filtering query for the count of 2 mismatches, specified in number. Trailing '+' or '-' sign to the number specifies ranges of count.
filter_maxcoverage	Flag for selection of the targets with maximum transcript coverage. 1 is true, 0 is false.
filter_gc	Flag for filtering GC contents. If set, the targets with GC contents below 20 or above 80 are neglected. 1 is true, 0 is false.
filter_trepeat	Flag for filtering Thymine repeats. If set, the targets with more than 4 Thymines are neglected. 1 is true, 0 is false.
filter_oof	Filtering query for the Microhomology-associated out-of-frame score, specified in number. If set, only the targets above this criterion are selected.
filter_cdsposition	Filtering query for the relative CDS position, specified in number. If set, only the targets below this criterion are selected.
max_count	If specified, the optimal targets up to this value among the filtered targets are selected. The targets are selected to have minimal off-target numbers and also maximum Microhomology-associated out-of-frame score.

Response

Response

```
{
  "targets": [
    {
      "id": <target ID in gene>,
      "chromosome": <chromosome name>,
      "position": <position of target>,
      "gc_contents": <GC contents of target>,
      "strand": <strand information of target>,
      "oof_score": <Microhomology-associated out-of-frame score>,
      "sequence": <sequence of target>,
      "coverage": <exon coverage>,
      "cds_percentages": {
        <Ensembl ID of transcript>: <relative position in CDS>,
        ...
      },
      "offtarget_counts": [
        <count of off-targets with mismatch 0>,
        <count of off-targets with mismatch 1>,
        <count of off-targets with mismatch 2>
      ]
    },
    ...
  ],
  "target_counts": {
    <Ensembl ID of transcript>: {
      "total_count": <count of all targets in the transcript>,
      "filtered_count": <count of filtered targets in the transcript>
    }
  }
}
```

Example (http://www.rgenome.net/cas-database/genes/100/targets/?filter_mis0=1&filter_mis1=0&filter_mis2=0)

```
{"targets": [{"gc_contents": 40.0, "strand": "-", "oof_score": 74.2595596756, "sequence": "ACGAAATATCAATGATGGCCAGG", "coverage": 1, "position": 144050592, "offtarget_counts": [1, 0, 0], "id": 34, "chromosome": "chr7", "cds_percentages": {"ENST00000408906": 20.9401709402}}, {"gc_contents": 30.0, "strand": "-", "oof_score": 65.821194708, "sequence": "AGCATACGAAATATCAATGATGG", "coverage": 1, "position": 144050597, "offtarget_counts": [1, 0, 0], "id": 35, "chromosome": "chr7", "cds_percentages": {"ENST00000408906": 21.4743589744}}, {"gc_contents": 50.0, "strand": "-", "oof_score": 65.9402947474, "sequence": "GCCAAGGTTTGTGTCAGCATCTTGG", "coverage": 1, "position": 144050633, "offtarget_counts": [1, 0, 0], "id": 40, "chromosome": "chr7", "cds_percentages": {"ENST00000408906": 25.3205128205}}, {"gc_contents": 50.0, "strand": "+", "oof_score": 64.873991398, "sequence": "AGTCCTGGCTGTCACTTCTTGGG", "coverage": 1, "position": 144050826, "offtarget_counts": [1, 0, 0], "id": 59, "chromosome": "chr7", "cds_percentages": {"ENST00000408906": 47.1153846154}}, {"target_counts": {"ENST00000408906": {"total_count": 152, "filtered_count": 4}}}]
```

4. Retrieving an off-target list

Request

Method	URL
GET	<a href="http://www.rgenome.net/cas-database/genes/<gene_id>/targets/<target_id>/offtargets/">http://www.rgenome.net/cas-database/genes/<gene_id>/targets/<target_id>/offtargets/

Parameter	Description
page	Page number to retrieve.
count	If specified, only the off-targets with the mismatch count of this value are selected.
all	Flag to retrieve all off-targets without pagination. If the number of off-targets is more than 1000, then this option is neglected. 1 is true, and 0 is false.

Response

Response

```
{
  "links": {
    "next": <URL of next page, if available>,
    "previous": <URL of previous page, if available>
  }
  "page_count": <number of available pages>,
  "offtarget_count": <number of all found genes>,
  "offtargets": [
    {
      "sequence": <sequence of the off-target>,
      "chromosome": <chromosome name>,
      "position": <position of the off-target>,
      "strand": <strand information>,
      "mismatch_count": <count of mismatches in the off-target>,
      "region": <genomic region of the cleavage site>
    },
    ...
  ]
}
```

Example (<http://www.rgenome.net/cas-database/genes/100/targets/1/offtargets/>)

```
{"page_count": 1, "offtargets": [{"chromosome": "chr2", "sequence": "GCATGACAAAATaAGACAGGG", "region": "Intergenic", "strand": "+", "position": 126565746, "mismatch_count": 2}, {"chromosome": "chr3", "sequence": "tCATGACAAAAATCAGAAACAG", "region": "Intergenic", "strand": "+", "position": 163991276, "mismatch_count": 2}, {"chromosome": "chr7", "sequence": "GCATGACAAAAATCAGACATGG", "region": "CDS", "strand": "+", "position": 144050399, "mismatch_count": 0}], "offtarget_count": 3}
```