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

<table>
<thead>
<tr>
<th>Method</th>
<th>URL</th>
</tr>
</thead>
<tbody>
<tr>
<td>GET</td>
<td><a href="http://www.rgenome.net/cas-database/organisms/">http://www.rgenome.net/cas-database/organisms/</a></td>
</tr>
</tbody>
</table>

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

```
{
  "organisms": [
    {"type": "organism type", "id": <organism id>, "name": <organism name>},
    ...]
}
```

Example [http://www.rgenome.net/cas-database/organisms/](http://www.rgenome.net/cas-database/organisms/)

```json
["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 (UGI v1.0) - Soybean"}, {"type": "vertebrate", "id": 12, "name": "Sus scrofa (Ensembl v10.2) - Pig"}]]
```

2. Retrieving a gene list

Request

<table>
<thead>
<tr>
<th>Method</th>
<th>URL</th>
</tr>
</thead>
<tbody>
<tr>
<td>GET</td>
<td><a href="http://www.rgenome.net/cas-database/organisms/">http://www.rgenome.net/cas-database/organisms/</a>&lt;organism_id&gt;/genes/</td>
</tr>
</tbody>
</table>

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
3. Retrieving a target list

**Request**

<table>
<thead>
<tr>
<th>Method</th>
<th>URL</th>
</tr>
</thead>
<tbody>
<tr>
<td>GET</td>
<td><a href="http://www.rgenome.net/cas-database/organisms/">http://www.rgenome.net/cas-database/organisms/</a>&lt;gene_id&gt;/targets/</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>filter_mis0</td>
<td>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+’.</td>
</tr>
<tr>
<td>filter_mis1</td>
<td>Filtering query for the count of 1 mismatch, specified in number. Trailing ‘+’ or ‘-’ sign to the number specifies ranges of count.</td>
</tr>
<tr>
<td>filter_mis2</td>
<td>Filtering query for the count of 2 mismatches, specified in number. Trailing ‘+’ or ‘-’ sign to the number specifies ranges of count.</td>
</tr>
<tr>
<td>filter_maxcoverage</td>
<td>Flag for selection of the targets with maximum transcript coverage. 1 is true, 0 is false.</td>
</tr>
<tr>
<td>filter_gc</td>
<td>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.</td>
</tr>
<tr>
<td>filter_trepeats</td>
<td>Flag for filtering Thymine repeats. If set, the targets with more than 4 Thymines are neglected. 1 is true, 0 is false.</td>
</tr>
<tr>
<td>filter_oof</td>
<td>Filtering query for the Microhomology-associated out-of-frame score, specified in number. If set, only the targets above this criterion are selected.</td>
</tr>
<tr>
<td>filter_cdsposition</td>
<td>Filtering query for the relative CDS position, specified in number. If set, only the targets below this criterion are selected.</td>
</tr>
<tr>
<td>max_count</td>
<td>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.</td>
</tr>
</tbody>
</table>

**Response**
### Response

```json
{
  "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": [34], "id": "id", "chromosome": "chr7", "cds_percentages": ["ENST00000408906": 20.9401709402]}, {"gc_contents": 20.0, "strand": "+", "oof_score": 65.821194708, "sequence": "AGCACGAAATATCAATGATGG", "coverage": 1, "position": 144050597, "offtarget_counts": [35], "id": "id", "chromosome": "chr7", "cds_percentages": ["ENST00000408906": 21.4743589744]}, {"gc_contents": 50.0, "strand": "+", "oof_score": 65.9402947474, "sequence": "GCCAAGGTTTGTCAGCATCTTGG", "coverage": 1, "position": 144050633, "offtarget_counts": [40], "id": "id", "chromosome": "chr7", "cds_percentages": ["ENST00000408906": 25.3205128205]}, {"gc_contents": 50.0, "strand": "+", "oof_score": 64.873991398, "sequence": "AGTCCTGGCTGTCACTTCTTGGG", "coverage": 1, "position": 144050826, "offtarget_counts": [41], "id": "id", "chromosome": "chr7", "cds_percentages": ["ENST00000408906": 47.1153846154}], "target_counts": ["ENST00000408906": 152, "filtered_count": 4]}
```

4. Retrieving an off-target list

### Request

<table>
<thead>
<tr>
<th>Method</th>
<th>URL</th>
</tr>
</thead>
<tbody>
<tr>
<td>GET</td>
<td><a href="http://www.rgenome.net/cas-database/genes/">http://www.rgenome.net/cas-database/genes/</a>&lt;gene_id&gt;/targets/&lt;target_id&gt;/offtargets/</td>
</tr>
</tbody>
</table>

### Parameter

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>page</td>
<td>Page number to retrieve.</td>
</tr>
<tr>
<td>count</td>
<td>If specified, only the off-targets with the mismatch count of this value are selected.</td>
</tr>
<tr>
<td>all</td>
<td>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.</td>
</tr>
</tbody>
</table>

### Response
Response

```json
{
    "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/](http://www.rgenome.net/cas-database/genes/100/targets/1/offtargets/))

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