
MyGene.info Documentation

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Introduction



MyGene.info provides simple-to-use REST web services to query/retrieve gene annotation data. It's designed with **simplicity** and **performance** emphasized. A typical use case is to use it to power a web application which requires querying genes and obtaining common gene annotations. For example, MyGene.info services are used to power BioGPS.

What's new in v2 API

- **ALL** species are supported now! That's more than 14,000 in total. [more]
- Gene annotation data are even more up-to-date (weekly updates).
- Gene query service supports “fields” parameter to return any fields. Previously, you need to call gene query service separately if you need more than gene symbols and names.
- Fine-tuned query algorithm to return relevant gene hits first.
- Our query backend is more scalable and extensible. Ready to expand more annotation data as we go.

Migration guide from v1 to v2 API

Still want to stick with v1 API for a while? It's still there: [v1 API](#), but annotation data there won't be updated any more.

Quick start

MyGene.info provides two simple web services: one for gene queries and the other for gene annotation retrieval. Both return results in [JSON](#) format.

3.1 Gene query service

3.1.1 URL

```
http://mygene.info/v2/query
```

3.1.2 Examples

```
http://mygene.info/v2/query?q=cdk2
http://mygene.info/v2/query?q=cdk2&species=human
http://mygene.info/v2/query?q=cdk?
http://mygene.info/v2/query?q=IL*
http://mygene.info/v2/query?q=entrezgene:1017
http://mygene.info/v2/query?q=ensemblgene:ENSG00000123374
http://mygene.info/v2/query?q=cdk2&fields=symbol,refseq
```

Hint: View nicely formatted JSON result in your browser with this handy add-on: [JSON formater](#) for Chrome or [JSONView](#) for Firefox.

3.1.3 To learn more

- You can read the full description of our query syntax [here](#).
- Try it live on [interactive API page](#).
- Play with our demo applications.
- Batch queries? Yes, you can. do it with a POST request.

3.2 Gene annotation service

3.2.1 URL

```
http://mygene.info/v2/gene/<geneid>
```

3.2.2 Examples

```
http://mygene.info/v2/gene/1017  
http://mygene.info/v2/gene/ENSG00000123374  
http://mygene.info/v2/gene/1017?fields=name,symbol,summary
```

“<geneid>” can be any of valid Entrez or Ensembl Gene ids. A retired Entrez Gene id works too if it is replaced by a new one.

3.2.3 To learn more

- You can read the full description of our query syntax [here](#).
- Try it live on [interactive API page](#).
- Play with our demo applications.
- Yes, batch queries via POST request as well.

4.1 Migration from v1 API

Migrating from v1 API to v2 API should be very trivial. Here is a summary for the changes:

4.1.1 Gene query service

URL change

Starting from v2 API, we added “/v2” as the prefix for service urls:

v1 <http://mygene.info/v1/query> or <http://mygene.info/query>

v2 <http://mygene.info/v2/query>

Returned Objects

There are some small changes in returned gene objects as summarized here:

- “rows” “hits”
- “total_rows” “total”
- “id” “_id” (“_” prefix indicates interval fields)
- “score” “_score”
- removed in v2: “homologene”, “skip”, “limit”, “etag”
- added in v2: “entrezgene” (Entrez gene id), “max_score”, “took”

You can also see the differences in the following examples:

v1: <http://mygene.info/v1/query?q=symbol:cdk2&limit=1>

```
1 {
2   "rows": [
3     {
4       "id": "1017",
5
6       "symbol": "CDK2",
7       "taxid": 9606,
8       "name": "cyclin-dependent kinase 2",
9       "homologene": {
```

```
10         "genes": [[9606,1017],[10090,12566],
11                  [10116,362817],[7227,42453],
12                  [7955,406715],[3702,824036]],
13         "id": 74409
14     },
15     "score": 72.55062866210938
16 }
17 ],
18 "total_rows": 6,
19
20
21 "skip": 0,
22 "etag": "4f1b7983a4",
23 "limit": 1
24 }
```

v2: <http://mygene.info/v2/query?q=symbol:cdk2&size=1>

```
1 {
2   "hits": [
3     {
4       "_id": "1017",
5       "entrezgene": 1017,
6       "symbol": "CDK2",
7       "taxid": 9606,
8       "name": "cyclin-dependent kinase 2",
9
10
11
12
13
14
15       "_score": 89.32175
16     }
17   ],
18   "total": 3,
19   "max_score": 89.32175,
20   "took": 4
21
22
23
24 }
```

4.1.2 Gene annotation service

URL change

Starting from v2 API, we added “/v2” as the prefix for service urls:

v1 <http://mygene.info/v1/gene> or <http://mygene.info/gene>

v2 <http://mygene.info/v2/gene>

Returned Objects

The returned objects are essentially back-compatible in v2, except that gene object in v2 contains even more fields as we expand underlying annotation data.

4.2 Gene annotation data

4.2.1 Data sources

We currently obtain the gene annotation data from several public data resources and keep them up-to-date, so that you don't have to do it:

Source	Update frequency	Notes
NCBI Entrez	weekly snapshot	
Ensembl	whenever a new release is available	Ensembl Pre! and EnsemblGenomes are not included at the moment
Uniprot	whenever a new release is available	
NetAffy	whenever a new release is available	
PharmGKB	whenever a new release is available	
UCSC	whenever a new release is available	For "exons" field
CPDB	whenever a new release is available	For "pathway" field

The most updated data information can be accessed [here](#).

4.2.2 Gene object

Gene annotation data are both stored and returned as a gene object, which is essentially a collection of fields (attributes) and their values:

```
{
  "_id": "1017"
  "taxid": 9606,
  "symbol": "CDK2",
  "entrezgene": 1017,
  "name": "cyclin-dependent kinase 2",
  "genomic_pos": {
    "start": 56360553,
    "chr": "12",
    "end": 56366568,
    "strand": 1
  }
}
```

The example above omits most of available fields. For a full example, you can just check out a few gene examples: [CDK2](#), [ADA](#). Or, did you try our [interactive API page](#) yet?

4.2.3 Species

We support **ALL** species annotated by NCBI and Ensembl. All of our services allow you to pass a "species" parameter to limit the query results. "species" parameter accepts taxonomy ids as the input. You can look for the taxonomy ids

for your favorite species from [NCBI Taxonomy](#).

For convenience, we allow you to pass these *common names* for commonly used species (e.g. “species=human,mouse,rat”):

Common name	Genus name	Taxonomy id
human	Homo sapiens	9606
mouse	Mus musculus	10090
rat	Rattus norvegicus	10116
fruitfly	Drosophila melanogaster	7227
nematode	Caenorhabditis elegans	6239
zebrafish	Danio rerio	7955
thale-cress	Arabidopsis thaliana	3702
frog	Xenopus tropicalis	8364
pig	Sus scrofa	9823

If needed, you can pass “species=all” to query against all available species, although, we recommend you to pass specific species you need for faster response.

4.2.4 Genome assemblies

Our gene query service supports genome interval queries. We import genomic location data from Ensembl, so all species available there are supported. You can find their reference genome assemblies information [here](#).

This table lists the genome assemblies for commonly-used species:

Common name	Genus name	Genome assembly
human	Homo sapiens	GRCh38 (hg38), also support hg19
mouse	Mus musculus	GRCm38 (mm10), also support mm9
rat	Rattus norvegicus	Rnor_5.0 (rn4)
fruitfly	Drosophila melanogaster	BDGP5 (dm3)
nematode	Caenorhabditis elegans	WBcel235 (ce10)
zebrafish	Danio rerio	Zv9 (danRer6)
frog	Xenopus tropicalis	JGI_4.2 (xenTro2)
pig	Sus scrofa	Sscrofa10.2 (susScr2)

4.2.5 Available fields

The table below lists of all of the possible fields that could be in a gene object.

4.3 Gene query service

This page describes the reference for MyGene.info gene query web service. It’s also recommended to try it live on our [interactive API page](#).

4.3.1 Service endpoint

<code>http://mygene.info/v2/query</code>
--

4.3.2 GET request

Query parameters

q

Required, passing user query. The detailed query syntax for parameter “q” we explained *below*.

fields

Optional, can be a comma-separated fields to limit the fields returned from the matching gene hits. The supported field names can be found from any gene object (e.g. [gene 1017](#)). Note that it supports dot notation as well, e.g., you can pass “refseq.rna”. If “fields=all”, all available fields will be returned. Default: “symbol,name,taxid,entrezgene”.

species

Optional, can be used to limit the gene hits from given species. You can use “common names” for nine common species (human, mouse, rat, fruitfly, nematode, zebrafish, thale-cress, frog and pig). All other species, you can provide their taxonomy ids. See more details here. Multiple species can be passed using comma as a separator. Passing “all” will query against all available species. Default: human,mouse,rat.

size

Optional, the maximum number of matching gene hits to return (with a cap of 1000 at the moment). Default: 10.

from

Optional, the number of matching gene hits to skip, starting from 0. Default: 0

Hint: The combination of “size” and “from” parameters can be used to get paging for large query:

q=cdk*&size=50	first 50 hits
q=cdk*&size=50&from=50	the next 50 hits

sort

Optional, the comma-separated fields to sort on. Prefix with “-” for descending order, otherwise in ascending order. Default: sort by matching scores in descending order.

facets

Optional, a single field or comma-separated fields to return facets, for example, “facets=taxid”, “facets=taxid,type_of_gene”. See *examples of faceted queries here*.

species_facet_filter

Optional, relevant when faceting on species (i.e., “facets=taxid” are passed). It’s used to pass species filter without changing the scope of faceting, so that the returned facet counts won’t change. Either species name or taxonomy id can be used, just like “*species*” parameter above. See *examples of faceted queries here*.

entrezonly

Optional, when passed as “true” or “1”, the query returns only the hits with valid Entrez gene ids. Default: false.

ensemblonly

Optional, when passed as “true” or “1”, the query returns only the hits with valid Ensembl gene ids. Default: false.

callback

Optional, you can pass a “**callback**” parameter to make a [JSONP](#) call.

dotfield

Optional, can be used to control the format of the returned fields when passed “fields” parameter contains dot notation, e.g. “fields=refseq.rna”. If “dotfield” is true, the returned data object contains a single “refseq.rna” field, otherwise, a single “refseq” field with a sub-field of “rna”. Default: true.

filter

Alias for “fields” parameter.

limit

Alias for “size” parameter.

skip

Alias for “from” parameter.

email

Optional, if you are regular users of our services, we encourage you to provide us an email, so that we can better track the usage or follow up with you.

Query syntax

Examples of query parameter “q”:

Simple queries

search for everything:

q=cdk2	search for any fields
q=tumor suppressor	default as "AND" for all query terms
q="cyclin-dependent kinase"	search for the phrase

Fielded queries

```
q=entrezgene:1017
q=symbol:cdk2
q=refseq:NM_001798
```

Field	Description	Examples
entrezgene	Entrez gene id	q=entrezgene:1017
ensemblgene	Ensembl gene id	q=ensemblgene:ENSG00000123374
symbol	official gene symbol	q=symbol:cdk2
name	gene name	q=name:cyclin-dependent
alias	gene alias	q=alias:p33
summary	gene summary text	q=summary:insulin
refseq	NCBI RefSeq id (both rna and proteins)	q=refseq:NM_001798 q=refseq:NP_439892
unigene	NCBI UniGene id	q=unigene:Hs.19192
homologene	NCBI HomoloGene id	q=homologene:74409
accession	NCBI GeneBank Accession number	q=accession:AA810989
ensembltranscript	Ensembl transcript id	q=ensembltranscript:ENST00000266970
ensemblprotein	Ensembl protein id	q=ensemblprotein:ENSP00000243067
uniprot	UniProt id	q=uniprot:P24941
ipi (deprecated!)	IPI id	q=ipi:IPI00031681
pdb	PDB id	q=pdb:1AQ1
prosite	Prosite id	q=prosite:PS50011
pfam	PFam id	q=pfam:PF00069
interpro	InterPro id	q=interpro:IPR008351
mim	OMIM id	q=mim:116953
pharmgkb	PharmGKB id	q=pharmgkb:PA101
reporter	Affymetrix probeset id	q=reporter:204252_at
reagent	GNF reagent id	q=reagent:GNF282834
go	Gene Ontology id	q=go:0000307
hgnc	HUGO Gene Nomenclature Committee	q=hgnc:1771
hprd	Human Protein Reference Database	q=hprd:00310
mgc	Mouse Genome Informatics	q=mgc:MGIV:88339
rgb	Rat Genome Database	q=rgd:620620

Continued on next page

Table 4.1 – continued from previous page

Field	Description	Examples
flybase	A Database of Drosophila Genes & Genomes	q=flybase:FBgn0004107&species=fruitfly
wormbase	C elegans and related nematodes database	q=wormbase:WBGene00057218&species=31234
zfin	Zebrafish Information Network	q=zfin:ZDB-GENE-980526-104&species=zebrafish
tair	Arabidopsis Information Resource	q=tair:AT3G48750&species=thale-cress
xenbase	Xenopus laevis and Xenopus tropicalis biology and genomics resource	q=xenbase:XB-GENE-1001990&species=frog
mirbase	database of published miRNA sequences and annotation	q=mirbase:MI0017267
retired	Retired Entrez gene id, including those with replaced gene ids.	q=retired:84999

Available fields

Genome interval query

When we detect your query (“q” parameter) contains a genome interval pattern like this one:

```
chrX:151,073,054-151,383,976
```

we will do the genome interval query for you. Besides above interval string, you also need to specify “species” parameter (with the default as human). These are all accepted queries:

```
q=chrX:151073054-151383976&species:9606
q=chrX:151,073,054-151,383,976&species:human
```

Hint: As you can see above, the genomic locations can include commas in it.

See also:

Genome assembly information

Wildcard queries

Wildcard character “*” or “?” is supported in either simple queries or fielded queries:

q=CDK?	single character wildcard
q=symbol:CDK?	single character wildcard within "symbol" field
q=IL*R	multiple character wildcard

Note: Wildcard character can not be the first character. It will be ignored.

Boolean operators and grouping

You can use **AND/OR/NOT** boolean operators and grouping to form complicated queries:

q=tumor AND suppressor	AND operator
q=CDK2 OR BTK	OR operator
q="tumor suppressor" NOT receptor	NOT operator
q=(interleukin OR insulin) AND receptor	the use of parentheses

Returned object

A GET request like this:

```
http://mygene.info/v2/query?q=symbol:cdk2
```

should return hits as:

```
{
  "hits": [
    {
      "name": "cyclin-dependent kinase 2",
      "_score": 87.76775,
      "symbol": "CDK2",
      "taxid": 9606,
      "entrezgene": 1017,
      "_id": "1017"
    },
    {
      "name": "cyclin-dependent kinase 2",
      "_score": 79.480484,
      "symbol": "Cdk2",
      "taxid": 10090,
      "entrezgene": 12566,
      "_id": "12566"
    },
    {
      "name": "cyclin dependent kinase 2",
      "_score": 62.286797,
      "symbol": "Cdk2",
      "taxid": 10116,
      "entrezgene": 362817,
      "_id": "362817"
    }
  ],
  "total": 3,
  "max_score": 87.76775,
  "took": 4
}
```

Faceted queries

If you need to perform a faceted query, you can pass an optional “*facets*” parameter. For example, if you want to get the facets on species, you can pass “*facets=taxid*”:

A GET request like this:

```
http://mygene.info/v2/query?q=cdk2&size=1&facets=taxid
```

should return hits as:

```
{
  "hits": [
    {
      "entrezgene":1017,
      "name":"cyclin-dependent kinase 2",
      "_score":400.43347,
      "symbol":"CDK2",
      "_id":"1017",
      "taxid":9606
    }
  ],
  "total":26,
  "max_score":400.43347,
  "took":7,
  "facets":{
    "taxid":{
      "_type":"terms",
      "total":26,
      "terms": [
        {
          "count":14,
          "term":9606
        },
        {
          "count":7,
          "term":10116
        },
        {
          "count":5,
          "term":10090
        }
      ],
      "other":0,
      "missing":0
    }
  }
}
```

Another useful field to get facets on is “*type_of_gene*”:

```
http://mygene.info/v2/query?q=cdk2&size=1&facets=type_of_gene
```

It should return hits as:

```
{
  "hits": [
    {
      "entrezgene":1017,
      "name":"cyclin-dependent kinase 2",
```

```

    "_score":400.43347,
    "symbol":"CDK2",
    "_id":"1017",
    "taxid":9606
  }
],
"total":26,
"max_score":400.43347,
"took":97,
"facets":{
  "type_of_gene":{
    "_type":"terms",
    "total":26,
    "terms":[
      {
        "count":20,
        "term":"protein-coding"
      },
      {
        "count":6,
        "term":"pseudo"
      }
    ],
    "other":0,
    "missing":0
  }
}
}

```

If you need to, you can also pass multiple fields as comma-separated list:

```
http://mygene.info/v2/query?q=cdk2&size=1&facets=taxid,type_of_gene
```

Particularly relevant to species facets (i.e., “facets=taxid”), you can pass a “*species_facet_filter*” parameter to filter the returned hits on a given species, without changing the scope of the facets (i.e. facet counts will not change). This is useful when you need to get the subset of the hits for a given species after the initial faceted query on species.

You can see the different “hits” are returned in the following queries, while “facets” keeps the same:

```
http://localhost:9000/v2/query?q=cdk?&size=1&facets=taxid&species_facet_filter=human
```

v.s.

```
http://localhost:9000/v2/query?q=cdk?&size=1&facets=taxid&species_facet_filter=mouse
```

4.3.3 Batch queries via POST

Although making simple GET requests above to our gene query service is sufficient in most of use cases, there are some cases you might find it’s more efficient to make queries in a batch (e.g., retrieving gene annotation for multiple genes). Fortunately, you can also make batch queries via POST requests when you need:

```
URL: http://mygene.info/v2/query
HTTP method: POST
```

Query parameters

q

Required, multiple query terms separated by comma (also support “+” or white space), but no wildcard, e.g., ‘q=1017,1018’ or ‘q=CDK2+BTK’

scopes

Optional, specify one or more fields (separated by comma) as the search “scopes”, e.g., “scopes=entrezgene”, “scopes=entrezgene,ensemblgene”. The available “fields” can be passed to “scopes” parameter are *listed above*. Default: “scopes=entrezgene,ensemblgene,retired” (either Entrez or Ensembl gene ids).

species

Optional, can be used to limit the gene hits from given species. You can use “common names” for nine common species (human, mouse, rat, fruitfly, nematode, zebrafish, thale-cress, frog and pig). All other species, you can provide their taxonomy ids. See more details here. Multiple species can be passed using comma as a separator. Default: human,mouse,rat.

fields

Optional, can be a comma-separated fields to limit the fields returned from the matching gene hits. The supported field names can be found from any gene object (e.g. [gene 1017](#)). Note that it supports dot notation as well, e.g., you can pass “refseq.rna”. If “fields=all”, all available fields will be returned. Default: “symbol,name,taxid,entrezgene”.

dotfield

Optional, can be used to control the format of the returned fields when passed “fields” parameter contains dot notation, e.g. “fields=refseq.rna”. If “dotfield” is true, the returned data object contains a single “refseq.rna” field, otherwise, a single “refseq” field with a sub-field of “rna”. Default: true.

email

Optional, if you are regular users of our services, we encourage you to provide us an email, so that we can better track the usage or follow up with you.

Example code

Unlike GET requests, you can easily test them from browser, make a POST request is often done via a piece of code. Here is a sample python snippet:

```
import httplib2
h = httplib2.Http()
headers = {'content-type': 'application/x-www-form-urlencoded'}
params = 'q=1017,1018&scopes=entrezgene'
res, con = h.request('http://mygene.info/v2/query', 'POST', params, headers=headers)
```

Returned object

Returned result (the value of “con” variable above) from above example code should look like this:

```
[
  {
    "name": "cyclin-dependent kinase 2",
    "symbol": "CDK2",
    "taxid": 9606,
    "entrezgene": 1017,
    "query": "1017",
    "_id": "1017"
  },
  {
    "name": "cyclin-dependent kinase 3",
    "symbol": "CDK3",
    "taxid": 9606,
    "entrezgene": 1018,
    "query": "1018",
    "_id": "1018"
  }
]
```

Tip: “query” field in returned object indicates the matching query term.

If a query term has no match, it will return with “**notfound**” field as “**true**”:

```
params = 'q=1017,dummy&scopes=entrezgene'
res, con = h.request('http://mygene.info/v2/query', 'POST', params, headers=headers)
```

```
[
  {
    "name": "cyclin-dependent kinase 2",
    "symbol": "CDK2",
    "taxid": 9606,
    "entrezgene": 1017,
    "query": "1017",
    "_id": "1017"
  },
  {
    "query": "dummy",
    "notfound": true
  }
]
```

If a query term has multiple matches, they will be included with the same “query” field:

```
params = 'q=tp53,1017&scopes=symbol,entrezgene'
res, con = h.request('http://mygene.info/v2/query', 'POST', params, headers=headers)
```

```
[
  {
    "name": "tumor protein p53",
    "symbol": "TP53",
    "taxid": 9606,
    "entrezgene": 7157,
    "query": "tp53",
  }
]
```

```
[
  {
    "_id": "7157"
  },
  {
    "name": "tumor protein p53",
    "symbol": "Tp53",
    "taxid": 10116,
    "entrezgene": 24842,
    "query": "tp53",
    "_id": "24842"
  },
  {
    "name": "cyclin-dependent kinase 2",
    "symbol": "CDK2",
    "taxid": 9606,
    "entrezgene": 1017,
    "query": "1017",
    "_id": "1017"
  }
]
```

4.4 Gene annotation service

This page describes the reference for MyGene.info gene annotation web service. It's also recommended to try it live on our [interactive API page](#).

4.4.1 Service endpoint

```
http://mygene.info/v2/gene
```

4.4.2 GET request

To obtain the gene annotation via our web service is as simple as calling this URL:

```
http://mygene.info/v2/gene/<geneid>
```

geneid above can be either Entrez gene id (“1017”) or Ensembl gene id (“ENSG00000123374”). By default, this will return the complete gene annotation object in JSON format. See [here](#) for an example and [here](#) for more details. If the input **geneid** is not valid, 404 (NOT FOUND) will be returned.

Hint: A retired Entrez gene id works too if it is replaced by a new one, e.g., 245794. But a “*discontinued*” gene id will not return any hit, e.g., 138.

Optionally, you can pass a “**fields**” parameter to return only the annotation you want (by filtering returned object fields):

```
http://mygene.info/v2/gene/1017?fields=name,symbol
```

“**fields**” accepts any attributes (a.k.a fields) available from the gene object. Multiple attributes should be separated by commas. If an attribute is not available for a specific gene object, it will be ignored. Note that the attribute names are case-sensitive.

Just like gene query service, you can also pass a “**callback**” parameter to make a [JSONP](#) call.

Query parameters

fields

Optional, can be a comma-separated fields to limit the fields returned from the gene object. If “fields=all”, all available fields will be returned. Note that it supports dot notation as well, e.g., you can pass “refseq.rna”. Default: “fields=all”.

callback

Optional, you can pass a “callback” parameter to make a *JSONP* <<http://ajaxian.com/archives/jsonp-json-with-padding>> call.

filter

Alias for “fields” parameter.

dotfield

Optional, can be used to control the format of the returned fields when passed “fields” parameter contains dot notation, e.g. “fields=refseq.rna”. If “dotfield” is true, the returned data object contains a single “refseq.rna” field, otherwise, a single “refseq” field with a sub-field of “rna”. Default: true.

email

Optional, if you are regular users of our services, we encourage you to provide us an email, so that we can better track the usage or follow up with you.

Returned object

A GET request like this:

```
http://mygene.info/v2/gene/1017
```

should return a gene object below:

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      "strand": 1,
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        ],
        [
          56361640,
          56361718
        ]
      ]
    }
  }
}
```

```
[
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  56361953
],
[
  56362561,
  56362732
],
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  56364827,
  56365031
],
[
  56365304,
  56366568
]
],
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"cdsstart":56360792,
"cdsend":56365409,
"txend":56366568
},
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  "strand":1,
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    [
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    [
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    [
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    "X62071",
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    "CAL38014",
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"2IW9",  
"2J9M",  
"2JGZ",  
"2R3F",  
"2R3G",  
"2R3H",  
"2R3I",  
"2R3J",  
"2R3K",  
"2R3L",
```

```
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"3EOC",  
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```

```
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"3LFQ",  
"3LFS",  
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"3R7E",  
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"3R7U",  
"3R7V",
```

```
"3R7Y",  
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"3R8U",  
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"3R8Z",  
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"4EK4",  
"4EK5",  
"4EK6",  
"4EK8",
```

```

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"4FKR",
"4FKS",
"4FKT",
"4FKU",
"4FKV",
"4FKW",
"4FX3",
"4GCJ",
"4I3Z",
"4II5",
"4KD1",
"4LYN"
],
"HGNC": "1771"
}

```

4.4.3 Batch queries via POST

Although making simple GET requests above to our gene query service is sufficient in most of use cases, there are some cases you might find it's more efficient to make queries in a batch (e.g., retrieving gene annotation for multiple genes). Fortunately, you can also make batch queries via POST requests when you need:

```

URL: http://mygene.info/v2/gene
HTTP method: POST

```

Query parameters

ids

Required. Accept multiple geneids (either Entrez or Ensembl gene ids) seperated by comma, e.g., 'ids=1017,1018' or 'ids=695,ENSG00000123374'. Note that currently we only take the input ids up to **1000** maximum, the rest will be omitted.

fields

Optional, can be a comma-separated fields to limit the fields returned from the matching hits. If “fields=all”, all available fields will be returned. Note that it supports dot notation as well, e.g., you can pass “refseq.rna”. Default: “symbol,name,taxid,entrezgene”.

species

Optional, can be used to limit the gene hits from given species. You can use “common names” for nine common species (human, mouse, rat, fruitfly, nematode, zebrafish, thale-cress, frog and pig). All other species, you can provide their taxonomy ids. See more details here. Multiple species can be passed using comma as a separator. Passing “all” will query against all available species. Default: all.

dotfield

Optional, can be used to control the format of the returned fields when passed “fields” parameter contains dot notation, e.g. “fields=refseq.rna”. If “dotfield” is true, the returned data object contains a single “refseq.rna” field, otherwise, a single “refseq” field with a sub-field of “rna”. Default: true.

email

Optional, if you are regular users of our services, we encourage you to provide us an email, so that we can better track the usage or follow up with you.

Example code

Unlike GET requests, you can easily test them from browser, make a POST request is often done via a piece of code, still trivial of course. Here is a sample python snippet:

```
import httplib2
h = httplib2.Http()
headers = {'content-type': 'application/x-www-form-urlencoded'}
params = 'ids=1017,695&fields=name,symbol,refseq.rna'
res, con = h.request('http://mygene.info/v2/gene', 'POST', params, headers=headers)
```

Returned object

Returned result (the value of “con” variable above) from above example code should look like this:

```
[
  {
    "_id": "1017",
    "name": "cyclin-dependent kinase 2",
    "query": "1017",
    "refseq.rna": [
      "NM_001798",
      "NM_052827",
      "XM_005268559"
    ],
    "symbol": "CDK2"
  },
]
```

```
{
  "_id": "695",
  "name": "Bruton agammaglobulinemia tyrosine kinase",
  "query": "695",
  "refseq.rna": [
    "NM_000061",
    "NM_001287344",
    "NM_001287345",
    "XM_005262181",
    "XM_005278108"
  ],
  "symbol": "BTK"
}
```

4.5 Usage and Demo

This page provides some usage examples and demo applications.

4.5.1 Call from web applications

You can call MyGene.info services from either server-side or client-side (via AJAX). The sample code can be found at *“demo” section*.

Calling services from server-side

All common programming languages provide functions for making http requests and JSON parsing. For Python, you can use built-in `httplib` and `json` modules (v2.6 up), or third-party `httplib2` and `simplejson` modules. For Perl, `LWP::Simple` and `JSON` modules should work nicely.

Making AJAX calls from client-side

When making an AJAX call from a web application, it is restricted by “same-origin” security policy, but there are several standard ways to get it around.

Making your own server-side proxy

To overcome “same-origin” restriction, you can create proxy at your server-side to our services. And then call your proxied services from your web application.

Setup proxy in popular server-side applications, like [Apache](#), [Nginx](#) and [PHP](#), are straightforward.

Making JSONP call

Because our core services are just called as simple GET http requests (though we support POST requests for batch queries too), you can bypass “same-origin” restriction by making JSONP call as well. To read more about JSONP, see [1](#), [2](#), or just Google about it. All our services accept an optional “**callback**” parameter, so that you can pass your callback function to make a JSONP call.

All popular javascript libraries have the support for making JSONP calls, like in [jQuery](#), [ExtJS](#), [MooTools](#)

Cross-origin http request through CORS

Cross-Origin Resource Sharing (CORS) specification is a [W3C draft specification](#) defining client-side cross-origin requests. It's actually supported by all major browsers by now (Internet Explorer 8+, Firefox 3.5+, Safari 4+, and Chrome. See more on [browser support](#)), but not many people are aware of it. Unlike JSONP, which is limited to GET requests only, you can make cross-domain POST requests as well. Our services supports CORS requests on both GET and POST requests. You can find more information and use case [here](#) and [here](#).

JQuery's native ajax call supports CORS since v1.5.

4.5.2 Demo Applications

In this demo, we want to create a web site to display expression charts from a microarray dataset (Affymetrix MOE430v2 chip). The expression data are indexed by porobeset ids, but we need to allow users to query for any mouse genes using any commonly-used identifiers, and then display expression charts for any selected gene.

We implemented this demo in four ways:

Example 1: using CGI

- [Download sample code here.](#)
- It's a simple python CGI script. To run it, you just need to drop it to your favorite web server's cgi-bin folder (make sure your python, v2.6 up, is in the path).
- [See it in action here](#)

Example 2: using tornado

- [Download sample code here.](#)
- This single python script can be used to run a standalone website. Just run:
`python mygene_info_demo_tornado.py`. You then have your website up at `http://localhost:8000`.

Besides python (v2.6 up), you also need [tornado](#) to run this code. You can either install it by your own (`pip install tornado`), or download [this zip file](#), which includes tornado in it.

- [See it in action here](#)

Example 3: using JSONP

- [Download sample code here.](#)
- The zip file contains one html file and one javascript file. There is no server-side code at all. To run it, just unzip it and open the html file in any browser. All remote service calls are done at client side (via browsers). Put the files into any web server serving static files will allow you to publish to the world.
- [See it in action here](#)

Example 4: using CORS

- [Download sample code here.](#)
- The zip file contains one html file and one javascript file. There is no server-side code at all. To run it, just unzip it and open the html file in any browser. All remote service calls are done at client side (via browsers). Put the files into any web server serving static files will allow you to publish to the world.
- This demo is almost the same as the one using JSONP, except that the actual AJAX call to MyGene.info server is made via CORS.
- [See it in action here](#)

4.5.3 Autocomplete widget for gene query

When you build a web application to have users to query for their favorite genes, the autocomplete widget is very useful, as it provides suggestions while users start to type into the field.

Note: The autocomplete widget below is a simple demo application. You may also want to have a look at this more sophisticated autocomplete widget, which comes with a lot more customization options.

Try it live first

About this widget

This autocomplete widget for gene query provides suggestions while you type a gene symbol or name into the field. Here the gene suggestions are displayed as “<Symbol>:<Name>”, automatically triggered when at least two characters are entered into the field.

At the backend, this widget is powered by the gene query web service from [MyGene.info](#). By default, the gene suggestions display human genes only.

Use it in your website

To use this widget in your own website is very easy, just following these three steps:

1. Copy/paste this line into your html file:

```
<script src="http://mygene.info/widget/autocomplete/js/mygene_query_min.js" type="text/javascript">
```

Hint: if you prefer an un-minified javascript file, using “mygene_query.js” instead.

2. Add “mygene_query_target” class to your target input element:

```
<input id="gene_query" style="width:250px" class="mygene_query_target">
```

so that we know which input field to enable autocomplete.

3. Define your own callback function, which is triggered after user selects a gene. For example:

```
<script type="text/javascript">
  mygene_query_select_callback = function(event, ui){
    alert( ui.item ?
      "Selected: " + ui.item.label + '('+ui.item.entrezgene+')':
      "Nothing selected, input was " + this.value);
  };
</script>
```

As shown in above example, you can access the gene object as **ui.item**:

```
ui.item._id      gene id
ui.item.value    gene symbol
ui.item.label    the label displayed in autocomplete dropdown list
```

Note: if you don't define your own callback function (like the minimal HTML page below), the default behavior is to display an alert msg with the gene selected. To change this default behavior, you must overwrite with your own callback function (keep the same name as **"mygene_query_select_callback"**).

A minimal HTML page with autocomplete enabled looks just like this ([See it in action here](#)):

```
<html>
<body>
  <label for="gene_query">Enter a gene here: </label>
  <input style="width:250px" class="mygene_query_target">
  <script src="http://mygene.info/widget/autocomplete/js/mygene_query_min.js" type="text/javascript">
</body>
</html>
```

Have fun! And send us feedback at help@mygene.info.

4.6 Third-party packages

This page lists third-party packages/modules built upon MyGene.info services.

4.6.1 MyGene python module

“mygene” is an easy-to-use Python wrapper to access MyGene.info services.

You can install it easily using either `pip` or `easy_install`:

```
pip install mygene #this is preferred
```

or:

```
easy_install mygene
```

This is a brief example:

```
In [1]: import mygene
In [2]: mg = mygene.MyGeneInfo()
In [3]: mg.getgene(1017)
Out[3]:
{'_id': '1017',
```

```
'entrezgene': 1017,
'name': 'cyclin-dependent kinase 2',
'symbol': 'CDK2',
'taxid': 9606}

In [4]: mg.query('cdk2', size=2)
Out[4]:
{'hits': [{'_id': '1017',
  '_score': 373.24667,
  'entrezgene': 1017,
  'name': 'cyclin-dependent kinase 2',
  'symbol': 'CDK2',
  'taxid': 9606},
 {'_id': '12566',
  '_score': 353.90176,
  'entrezgene': 12566,
  'name': 'cyclin-dependent kinase 2',
  'symbol': 'Cdk2',
  'taxid': 10090}],
'max_score': 373.24667,
'took': 10,
'total': 28}
```

See <https://pypi.python.org/pypi/mygene> for more details.

4.6.2 MyGene autocomplete widget

This autocomplete widget for gene query (built upon JQueryUI's [autocomplete widget](#)) provides suggestions while you type a gene symbol or name into the field. You can easily embed it into your web application. It also provides many customization options for your different use-cases.

See <https://bitbucket.org/sulab/mygene.autocomplete/overview> for more details.

You can also play with this [jsFiddle](#) example:

4.6.3 Another MyGene Python wrapper

This is yet another Python wrapper of MyGene.info services created by [Brian Schrader](#). It's hosted at <https://github.com/Sonictherocketman/mygene-api>.

It's available from PyPI as well:

```
pip install mygene-api
```

Some basic examples:

- Find a given gene with the id: CDK2.

```
""" Use the query API to find a gene with
the given symbol.
"""
from mygene.gene import Gene

results = Gene.find_by(q='CDK2')
for r in result:
    print r._id, r.name
```

```
>>> 1017 cyclin-dependent kinase 2
12566 cyclin-dependent kinase 2
362817 cyclin dependent kinase 2
52004 CDK2-associated protein 2
...
```

- Given an known gene, get it's begin and end coordinates.

```
""" Use the annotation API to find the full
details of a given gene.
"""
from mygene.gene import gene

gene = Gene.get('1017')
print gene._id, gene.genomic_pos_hg19['start'], gene.genomic_pos_hg19['end']

>>> 1017 56360553 56366568
```

- This library also supports the metadata API.

```
from mygene.metadata import Metadata

metadata = Metadata.get_metadata()
print metadata.stats['total_genes']

>>> 12611464
```

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