MyGene.info Documentation

Release 3.0

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Contents

CHAPTER 1

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.

CHAPTER 2

What's new in v3 API

- Refseq accession number now contains version
- "ensembl", "refseq" and "accession" contains associations between RNA and protein
- Better mapping between Ensembl and Entrez gene IDs
- JSON structure slightly changed
- and more bugfixes

You can read more details about this version on our blog

Migration guide from v2 to v3 API

Still want to stick with v2 API for a while? It's still there: v2 API, but annotation data there won't be updated any more.

CHAPTER 3

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/v3/query
```

3.1.2 Examples

```
http://mygene.info/v3/query?q=cdk2
http://mygene.info/v3/query?q=cdk2&species=human
http://mygene.info/v3/query?q=cdk?
http://mygene.info/v3/query?q=IL*
http://mygene.info/v3/query?q=entrezgene:1017
http://mygene.info/v3/query?q=ensemblgene:ENSG00000123374
http://mygene.info/v3/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/v3/gene/<geneid>
```

3.2.2 Examples

```
http://mygene.info/v3/gene/1017
http://mygene.info/v3/gene/ENSG00000123374
http://mygene.info/v3/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.

CHAPTER 4

Documentation

4.1 Migration from v2 API

Migrating from v2 API to v3 API is easy. Here's a summary of the changes. You may also want to read our blog for complementary information.

4.1.1 URL change

You will need to access v3 API using "**/v3**" prefix for service urls:

Gene query service endpoint

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

v3 http://mygene.info/v3/query

Gene annotation service endpoint

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

v3 http://mygene.info/v3/gene

4.1.2 Returned Objects

There are several small changes in the returned data structure, as summarized here:

Accession number with version

"**refseq**" and "**accession**" fields now contain accession number including version. Data can be search with and without version. Version is available for "*genomic*", "*rna*" and "*protein*" accession number keys.

Note: "*genomic*" field is returned but is not searchable

v2: http://mygene.info/v2/query?q=NM_052827&fields=refseq.rna


```
{
  "hits": [
  {
    "_id": "1017",
    "refseq": {
      "rna": [
        "NM_001290230",
        "NM_001798",
        "NM_052827",
        "XM_011537732"
      ]
    }
  }
],
  "max_score": 0.51962745,
  "took": 3,
  "total": 1

}
```


v3: http://mygene.info/v3/query?q=NM_052827&fields=refseq.rna


```
{
  "hits": [
    {
      "_id": "1017",
      "_score": 10.052136,
      "refseq": {
        "rna": [
          "NM_001290230.1",
          "NM_001798.4",
          "NM_052827.3",
          "XM_011537732.1"
        ]
      }
    }
  ],
  "total": 1,
  "took": 14,
  "max_score": 10.052136
}
```


"translation" field for RNA-protein mapping

For "**ensembl**", "**refseq**" and "**accession**" fields, a new sub-field name "*translation*" is now available. It gives the association between RNA and its protein product. v2 does not have this information in returned objects.

v3: http://mygene.info/v3/query?q=NM_052827&fields=refseq.translation,refseq.rna,refseq.protein


```
{
  "max_score": 10.052136,
  "total": 1,
  "hits": [
    {
      "_id": "1017",
      "_score": 10.052136,
      "refseq": {
        "protein": [
          "NP_001277159.1",
          "NP_001789.2",
          "NP_439892.2",
          "XP_011536034.1"
        ],
        "rna": [
          "NM_001290230.1",
          "NM_001798.4",
          "NM_052827.3",
          "XM_011537732.1"
        ],
        "translation": [
          {
            "protein": "XP_011536034.1",
            "rna": "XM_011537732.1"
          },
          {
            "protein": "NP_001789.2",
            "rna": "NM_001798.4"
          },
          {
            "protein": "NP_439892.2",
            "rna": "NM_052827.3"
          },
          {
            "protein": "NP_001277159.1",
            "rna": "NM_001290230.1"
          }
        ]
      }
    }
  ],
  "took": 4
}
```


"exons" data structure modification

Warning: Backward-incompatible, data structure changed

"**exons**" field has two major modifications. It now contains a list of dictionary instead of a dictionary indexed by the accession number. This accession number is found within the dictionary under the key "*transcript*". Finally, inner "*exons*" key has been rename to "*position*".

v2: http://mygene.info/v2/gene/1698?fields=exons

```
{
  "_id": "259236",
  "exons": {
    "NM_147196": {
      "cdsstart": 46701487,
      "cdsend": 46709688,
      "txstart": 46701332,
      "txend": 46710923,
      "chr": "3",
      "exons": [
        [
          46701332,
          46701580
        ],
        [
          46705789,
          46705907
        ],
        [
          46709125,
          46709275
        ],
        [
          46709578,
          46710923
        ]
      ],
      "strand": 1
    }
  }


}
```


v3: http://mygene.info/v3/gene/1698?fields=exons


```
{
  "_id": "259236",
  "_score": 21.732534,
  "exons": [
    {
      "cdsend": 46709688,
      "cdsstart": 46701487,
      "chr": "3",
      "position": [
        [
          46701332,
          46701580
        ],
        [
          46705789,
          46705907
        ],
        [
          46709125,
          46709275
        ],
```


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```
          [
            46709578,
            46710923
          ]
        ],
        "strand": 1,
        "transcript": "NM_147196",
        "txend": 46710923,
        "txstart": 46701332
      }
    ]
}
```


"dotfield" notation default changed

Warning: May be backward-incompatible, default data structure changed (but can be restored with "*dotfield*" paramater setting)

By default, "**dotfield**" notation is now disabled for gene annotation endpoint in v3 (/gene). It's enabled by default in v2. You will need to explicitely pass "**dotfield=1**" to your queries to have the same behavior as v2.

Note: "**dotfield**" notation is disabled by default for gene query endpoint (/gene) in both v2 and v2

v2: http://mygene.info/v2/gene/1017?fields=refseq.rna


```
{

  "_id": "1017",
  "refseq.rna": [
    "NM_001290230",
    "NM_001798",
    "NM_052827",
    "XM_011537732"
  ]


}
```


v3: http://mygene.info/v3/gene/1017?fields=refseq.rna


```
{
  "_id": "1017",
  "_score": 21.731894,
  "refseq": {
    "rna": [
      "NM_001290230.1",
      "NM_001798.4",
      "NM_052827.3",
      "XM_011537732.1"
    ]
  }
}
```

Querying "reporter" data source

"reporter" data now has to be queried explicitelty, prefixing the query term by "reporter:"

v3: http://mygene.info/v3/query?q=reporter:2845421&fields=reporter

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	
NetAffx	whenever a new release is available	For "reporter" field
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",
    "_score": 20.4676,
    "taxid": 9606,
    "symbol": "CDK2",
    "entrezgene": 1017,
    "name": "cyclin-dependent kinase 2",
    "genomic_pos": {
        "start": 55966769,
        "chr": "12",
        "end": 55972784,
        "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 _id field

Each individual gene object contains an "**_id**" field as the primary key. The value of the "**_id**" field is the NCBI gene ID (the same as "entrezgene" field, but as a string) if available for a gene object, otherwise, Ensembl gene ID is used (e.g. those Ensembl-only genes). Here is an example. We recommend to use "**entrezgene**" field for the NCBI gene ID, and "**ensembl.gene**" field for Ensembl gene ID, instead of using "**_id**" field.

Note: Regardless how the value of the "**_id**" field looks like, either NCBI gene ID or Ensembl gene ID always works for our gene annotation service /v3/gene/<geneid>.

4.2.4 _score field

You will often see a "**_score**" field in the returned gene object, which is the internal score representing how well the query matches the returned gene object. It probably does not mean much in gene annotation service when only one gene object is returned. In gene query service, by default, the returned gene hits are sorted by the scores in descending order.

4.2.5 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 taxomony 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.

4.2.6 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 the their reference genome assemblies information here.

This table lists the genome assembies 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_6.0 (rn6)
fruitfly	Drosophila melanogaster	BDGP6 (dm6)
nematode	Caenorhabditis elegans	WBcel235 (ce11)
zebrafish	Danio rerio	GRCz10 (danRer10)
frog	Xenopus tropicalis	JGI_7.0 (xenTro7)
pig	Sus scrofa	Sscrofa10.2 (susScr3)

4.2.7 Available fields

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

4.3 Data release notes

This page contains metadata about each MyGene.info data release. Click a link to see more.

4.3.1 MyGene Releases

4.4 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.

4.4.1 Service endpoint

```
http://mygene.info/v3/query
```

4.4.2 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: all.

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
```

fetch_all

Optional, a boolean, which when TRUE, allows fast retrieval of all unsorted query hits. The return object contains a **_scroll_id** field, which when passed as a parameter to the query endpoint, returns the next 1000 query results. Setting **fetch_all** = TRUE causes the results to be inherently unsorted, therefore the **sort** parameter is ignored. For more information see *examples using fetch_all here*. Default: FALSE.

scroll_id

Optional, a string containing the **_scroll_id** returned from a query request with **fetch_all** = TRUE. Supplying a valid **scroll_id** will return the next 1000 unordered results. If the next results are not obtained within 1 minute of the previous set of results, the **scroll_id** becomes stale, and a new one must be obtained with another query request with **fetch_all** = TRUE. All other parameters are ignored when the **scroll_id** parameter is supplied. For more information see *examples using scroll_id here*.

sort

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

facet_size

Optional, an integer (1 <= **facet_size** <= 1000) that specifies how many buckets to ret

urn in a faceted query.

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 gene object. If "dotfield" is true, the returned data object is returned flattened (no nested objects) using dotfield notation for key names. Default: false.

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
```

Available fields

This table lists some commonly used fields can be used for "fielded queries". Check here for the complete list of available fields.

Field	Description	Examples
entrezgene	Entrez gene id	q=entrezgene:1017
ensembl.gene	Ensembl gene id	q=ensembl.gene: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
ensembl.transcript	Ensembl transcript id	q=ensembl.transcript:ENST00000266970
ensembl.protein	Ensembl protein id	q=ensembl.protein: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

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Field	Description	Examples
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
mgi	Mouse Genome Informatics	q=mgi:MGI\:88339
rgd	Rat Genome Database	q=rgd:620620
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=thalecress
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

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 acceptted 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/v3/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",
```


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```
      "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/v3/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
```


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```
    }
  }
}
```

Another useful field to get facets on is "type_of_gene":

```
http://mygene.info/v3/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/v3/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://mygene.info/v3/query?q=cdk?&size=1&facets=taxid&species_facet_filter=human
```

v.s.

```
http://mygene.info/v3/query?q=cdk?&size=1&facets=taxid&species_facet_filter=mouse
```

Scrolling queries

If you want to return ALL results of a very large query (>10,000 results), sometimes the paging method described *above* can take too long. In these cases, you can use a scrolling query. This is a two-step process that turns off database sorting to allow very fast retrieval of all query results. To begin a scrolling query, you first call the query endpoint as you normally would, but with an extra parameter **fetch_all** = TRUE. For example, a GET request to:

```
http://mygene.info/v3/query?q=brain&fetch_all=TRUE
```

Returns the following object:

```
{
  "_scroll_id":
↪"cXVlcnlUaGVuRmV0Y2g7MTA7MjA1NjY1MzMwOl9HM29rRkg2VFZ5S1c3cTJtYkI4RHc7MjA1NjY1MjY3OlM0V1VCa194UWdLY
↪",
  "max_score": 13.958638,
  "took": 270,
  "total": 14571,
  "hits": [
    {
      "_id": "390259",
      "_score": 13.958638,
      "entrezgene": 390259,
      "name": "brain specific homeobox",
      "symbol": "BSX",
      "taxid": 9606
    },
    .
    .
    .
  ]
}
```

At this point, the first 1000 hits have been returned (of ~14,000 total), and a scroll has been set up for your query. To get the next batch of 1000 unordered results, simply execute a GET request to the following address, supplying the _scroll_id from the first step into the **scroll_id** parameter in the second step:

```
http://mygene.info/v3/query?scroll_
↪id=cXVlcnlUaGVuRmV0Y2g7MTA7MjA1NjY1MzMwOl9HM29rRkg2VFZ5S1c3cTJtYkI4RHc7MjA1NjY1MjY3OlM0V1VCa194UWdL
```

Hint: Your scroll will remain active for 1 minute from the last time you requested results from it. If your scroll expires before you get the last batch of results, you must re-request the scroll_id by setting **fetch_all** = TRUE as in step 1.

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/v3/query
HTTP method:  POST
```

Query parameters

q

Required, multiple query terms seperated 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: all.

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 "dofield" is true, the returned data object contains a single "refseq.rna" field, otherwise, a single "refseq" field with a sub-field of "rna". Default: false.

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 requests
headers = {'content-type': 'application/x-www-form-urlencoded'}
params = 'q=1017,1018&scopes=entrezgene&fields=name,symbol,taxid,entrezgene'
res = requests.post('http://mygene.info/v3/query', data=params, headers=headers)
```

Returned object

Returned result (the value of "res.text" variable above) from above example code should look like this:

```
[
  {
    '_id': '1017',
    '_score': 22.757837,
    'entrezgene': 1017,
    'name': 'cyclin dependent kinase 2',
    'query': '1017',
    'symbol': 'CDK2',
    'taxid': 9606
  },
  {
    '_id': '1018',
    '_score': 22.757782,
    'entrezgene': 1018,
    'name': 'cyclin dependent kinase 3',
    'query': '1018',
    'symbol': 'CDK3',
    'taxid': 9606
  }
]
```

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

Note: if no "fields" parameter is specified, all available fields will be returned

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

```
params = 'q=1017,dummy&scopes=entrezgene&fields=name,symbol,taxid,entrezgene'
res = requests.post('http://mygene.info/v3/query', data=params, headers=headers)
```

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

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```
  }
]
```

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

```
params = 'q=tp53,1017&scopes=symbol,entrezgene&fields=name,symbol,taxid,entrezgene'
res = requests.post('http://mygene.info/v3/query', data=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"
  }
]
```


4.5 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.

4.5.1 Service endpoint

```
http://mygene.info/v3/gene
```

4.5.2 GET request

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

```
http://mygene.info/v3/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/v3/gene/1017?fields=name,symbol
```

"**fields**" accepts any attributes (a.k.a fields) available from the gene object. Multiple attributes should be seperated 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 "dofield" is true, the returned data object contains a single "refseq.rna" field, otherwise, a single "refseq" field with a sub-field of "rna". Default: false.

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/v3/gene/1017
```

should return a gene object below:


```
{
  "HGNC": "1771",
  "HPRD": "00310",
  "MIM": "116953",
  "Vega": "OTTHUMG00000170575",
  "_id": "1017",
  "_score": 21.731894,
  "accession": {
    "genomic": [
      "AC025162.48",
      "AC034102.32",
      "AF512553.1",
      "AJ223951.1",
      "AMYH02026556.1",
      "AMYH02026557.1",
      "CH471054.1",
      "KT584459.1",
      "NC_000012.12",
      "NC_018923.2",
      "NG_034014.1",
      "U50730.2"
    ],
    "protein": [
      "AAA35667.1",
      "AAH03065.1",
      "AAM34794.1",
      "AAP35467.1",
      "ABM84693.1",
      "ABM92215.1",
      "BAA32794.1",
      "BAF84630.1",
      "BAG56780.1",
      "CAA43807.1",
      "CAA43985.1",
      "CAL38014.1",
      "EAW96856.1",
      "EAW96857.1",
      "EAW96858.1",
      "EAW96859.1",
      "EAW96860.1",
      "NP_001277159.1",
      "NP_001789.2",
      "NP_439892.2",
      "P24941.2",
      "XP_011536034.1"
    ],
    "rna": [
      "AA789250.1",
      "AA810989.1",
      "AB012305.1",
```


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```
      "AK291941.1",
      "AK293246.1",
      "AM393136.1",
      "BC003065.2",
      "BJ991087.1",
      "BT006821.1",
      "DA814453.1",
      "DQ890598.2",
      "DQ893767.2",
      "M68520.1",
      "NM_001290230.1",
      "NM_001798.4",
      "NM_052827.3",
      "X61622.1",
      "X62071.1",
      "XM_011537732.1"
    ],
    "translation": [
      {
        "protein": "BAA32794.1",
        "rna": "AB012305.1"
      },
      {
        "protein": "XP_011536034.1",
        "rna": "XM_011537732.1"
      },
      {
        "protein": "ABM92215.1",
        "rna": "DQ890598.2"
      },
      {
        "protein": "NP_439892.2",
        "rna": "NM_052827.3"
      },
      {
        "protein": "AAA35667.1",
        "rna": "M68520.1"
      },
      {
        "protein": "BAG56780.1",
        "rna": "AK293246.1"
      },
      {
        "protein": "BAF84630.1",
        "rna": "AK291941.1"
      },
      {
        "protein": "AAP35467.1",
        "rna": "BT006821.1"
      },
      {
        "protein": "CAA43807.1",
        "rna": "X61622.1"
      },
      {
        "protein": "CAL38014.1",
        "rna": "AM393136.1"
```


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```
      },
      {
        "protein": "CAA43985.1",
        "rna": "X62071.1"
      },
      {
        "protein": "AAH03065.1",
        "rna": "BC003065.2"
      },
      {
        "protein": "NP_001789.2",
        "rna": "NM_001798.4"
      },
      {
        "protein": "NP_001277159.1",
        "rna": "NM_001290230.1"
      },
      {
        "protein": "ABM84693.1",
        "rna": "DQ893767.2"
      }
    ]
  },
  "alias": [
    "CDKN2",
    "p33(CDK2)"
  ],
  "ec": "2.7.11.22",
  "ensembl": {
    "gene": "ENSG00000123374",
    "protein": [
      "ENSP00000243067",
      "ENSP00000266970",
      "ENSP00000393605",
      "ENSP00000450983",
      "ENSP00000452138",
      "ENSP00000452514"
    ],
    "transcript": [
      "ENST00000266970",
      "ENST00000354056",
      "ENST00000440311",
      "ENST00000553376",
      "ENST00000554545",
      "ENST00000554619",
      "ENST00000555357",
      "ENST00000555408",
      "ENST00000556146",
      "ENST00000556276",
      "ENST00000556464",
      "ENST00000556656"
    ],
    "translation": [
      {
        "protein": "ENSP00000266970",
        "rna": "ENST00000266970"
      },
```


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```
      {
        "protein": "ENSP00000450983",
        "rna": "ENST00000555408"
      },
      {
        "protein": "ENSP00000452514",
        "rna": "ENST00000553376"
      },
      {
        "protein": "ENSP00000393605",
        "rna": "ENST00000440311"
      },
      {
        "protein": "ENSP00000452138",
        "rna": "ENST00000555357"
      },
      {
        "protein": "ENSP00000243067",
        "rna": "ENST00000354056"
      }
    ]
  },
  "entrezgene": 1017,
  "exons": [
    {
      "cdsend": 55971625,
      "cdsstart": 55967008,
      "chr": "12",
      "position": [
        [
          55966768,
          55967124
        ],
        [
          55968048,
          55968169
        ],
        [
          55968777,
          55968948
        ],
        [
          55971043,
          55971247
        ],
        [
          55971520,
          55972789
        ]
      ],
      "strand": 1,
      "transcript": "NM_001290230",
      "txend": 55972789,
      "txstart": 55966768
    },
    {
      "cdsend": 55971625,
```


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```
      "cdsstart": 55967008,
      "chr": "12",
      "position": [
        [
          55966768,
          55967124
        ],
        [
          55967856,
          55967934
        ],
        [
          55968048,
          55968169
        ],
        [
          55968777,
          55968948
        ],
        [
          55969474,
          55969576
        ],
        [
          55971043,
          55971247
        ],
        [
          55971520,
          55972789
        ]
      ],
      "strand": 1,
      "transcript": "NM_001798",
      "txend": 55972789,
      "txstart": 55966768
    },
    {
      "cdsend": 55971625,
      "cdsstart": 55967008,
      "chr": "12",
      "position": [
        [
          55966768,
          55967124
        ],
        [
          55967856,
          55967934
        ],
        [
          55968048,
          55968169
        ],
        [
          55968777,
          55968948
```


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```
        ],
        [
          55971043,
          55971247
        ],
        [
          55971520,
          55972789
        ]
      ],
      "strand": 1,
      "transcript": "NM_052827",
      "txend": 55972789,
      "txstart": 55966768
    }
  ],
  "exons_hg19": [
    {
      "cdsend": 56365409,
      "cdsstart": 56360792,
      "chr": "12",
      "position": [
        [
          56360552,
          56360908
        ],
        [
          56361832,
          56361953
        ],
        [
          56362561,
          56362732
        ],
        [
          56364827,
          56365031
        ],
        [
          56365304,
          56366573
        ]
      ],
      "strand": 1,
      "transcript": "NM_001290230",
      "txend": 56366573,
      "txstart": 56360552
    },
    {
      "cdsend": 56365409,
      "cdsstart": 56360792,
      "chr": "12",
      "position": [
        [
          56360552,
          56360908
        ],
```


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```
        [
          56361640,
          56361718
        ],
        [
          56361832,
          56361953
        ],
        [
          56362561,
          56362732
        ],
        [
          56363258,
          56363360
        ],
        [
          56364827,
          56365031
        ],
        [
          56365304,
          56366573
        ]
      ],
      "strand": 1,
      "transcript": "NM_001798",
      "txend": 56366573,
      "txstart": 56360552
    },
    {
      "cdsend": 56365409,
      "cdsstart": 56360792,
      "chr": "12",
      "position": [
        [
          56360552,
          56360908
        ],
        [
          56361640,
          56361718
        ],
        [
          56361832,
          56361953
        ],
        [
          56362561,
          56362732
        ],
        [
          56364827,
          56365031
        ],
        [
          56365304,
```


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```
          56366573
        ]
      ],
      "strand": 1,
      "transcript": "NM_052827",
      "txend": 56366573,
      "txstart": 56360552
    }
  ],
  "generif": [
    {
      "pubmed": 11907280,
      "text": "Cyclin A/Cdk2 and cyclin E/cdk2 continuously shuttle between the␣
↪nucleus and the cytoplasm"
    },
    {
      "pubmed": 12049628,
      "text": "results argue that TTK-associated CDK2 may function to maintain target-
↪specific phosphorylation of RNA Pol II that is essential for Tat transactivation of␣
↪HIV-1 promoter"
    },
    {
      "pubmed": 12081504,
      "text": "Activation mechanism role of cyclin binding versus phosphorylation"
    },
    {
      "pubmed": 12114499,
      "text": "CDK2/cyclin E is required for Tat-dependent transcription in vitro."
    },
    {
      "pubmed": 12149264,
      "text": "CDK2 binding to cyclin E is required to drive cells from G(1) into S␣
↪phase"
    },
    {
      "pubmed": 12531694,
      "text": "Interferon gamma reduces the activity of Cdk4 and Cdk2, inhibiting he␣
↪G1 cell cycle in human hepatocellular carcinoma cells."
    },
    {
      "pubmed": 12676582,
      "text": "CDK2 is not required for sustained cell division."
    },
    {
      "pubmed": 12729791,
      "text": "Data suggest that the interaction between PKCeta and cyclin E is␣
↪carefully regulated, and is correlated with the inactivated form of the cyclin E/
↪Cdk2 complex."
    },
    {
      "pubmed": 12732645,
      "text": "IRF1 represses CDK2 gene expression by interfering with SP1-dependent␣
↪transcriptional activation."
    },
    {
      "pubmed": 12801928,
      "text": "role in regulating Cdc25A half life"
```


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```
    },
    {
      "pubmed": 12810668,
      "text": "TGF-beta 1 inhibition requires early G(1) induction and stabilization␣
↪of p21 protein, which binds to & inhibits cyclin E-CDK2 and cyclin A-CDK2 kinase␣
↪activity rather than direct modulation of cyclin or CDK protein levels as seen in␣
↪other systems."
    },
    {
      "pubmed": 12857729,
      "text": "Cdk2 has a role in phosphorylation of the NF-Y transcription factor"
    },
    {
      "pubmed": 12912980,
      "text": "CDK2 has a role in the G2 DNA damage checkpoint"
    },
    {
      "pubmed": 12915577,
      "text": "Kaposi's sarcoma-associated herpesvirus K-bZIP physically associates␣
↪with cyclin-CDK2 and downmodulates its kinase activity."
    },
    {
      "pubmed": 12947099,
      "text": "it is evident that B-Myb protein may promote cell proliferation by a␣
↪non-transcriptional mechanism that involves release of active cyclin/cyclin␣
↪dependent kinase 2 from cyclin-dependent inhibitor 1C p57(KIP2)"
    },
    {
      "pubmed": 12954644,
      "text": "Inhibition of Cdk2 by 1,25-(OH)2D3 may thus involve two mechanisms: 1)␣
↪reduced nuclear Cdk2 available for cyclin binding and activation and 2) impairment␣
↪of cyclin E-Cdk2-dependent p27 degradation through cytoplasmic mislocalization of␣
↪Cdk2."
    },
    {
      "pubmed": 14506259,
      "text": "kinetic insight into the basis for selecting suboptimal specificity␣
↪determinants for the phosphorylation of cellular substrates"
    },
    {
      "pubmed": 14536078,
      "text": "multisite phosphorylation by Cdk2 and GSK3 controls cyclin E␣
↪degradation"
    },
    {
      "pubmed": 14550307,
      "text": "CDK2 binds to SU9516 at Leu83 and Glu81"
    },
    {
      "pubmed": 14551212,
      "text": "CDK2 activation process through phosphorylation is examined using 2D␣
↪PAGE"
    },
    {
      "pubmed": 14562046,
      "text": "Epstein-Barr virus can inhibit genotoxin-induced G1 arrest downstream␣
↪of p53 by preventing the inactivation of CDK2"
```


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```
    },
    {
      "pubmed": 14612403,
      "text": "p220 is an essential downstream component of the cyclin E/Cdk2␣
↪signaling pathway and functions to coordinate multiple elements of the G1/S␣
↪transition."
    },
    {
      "pubmed": 14645251,
      "text": "CDK2-cyclin E, without prior CDK4-cyclin D activity, can phosphorylate␣
↪and inactivate pRb, activate E2F, and induce DNA synthesis."
    },
    {
      "pubmed": 14646596,
      "text": "significant difference in their biochemical properties between CDK4/
↪cyclin D1 and CDK2/cyclin A affecting regulation of cellular RB function"
    },
    {
      "pubmed": 14694185,
      "text": "cyclin-dependent kinase (CDK)2, -4, and -6 were down-regulated from␣
↪the myelocytes/metamyelocytes stages and onward"
    },
    {
      "pubmed": 14701826,
      "text": "CDK2 complexes have roles in G(1)/S deregulation and tumor progression"
    },
    {
      "pubmed": 14985333,
      "text": "CDK2 regulates beta-catenin phosphorylation/ degradation"
    },
    {
      "pubmed": 15004027,
      "text": "Cdk2 and Cdk4 phosphorylate human Cdt1 and induce its degradation"
    },
    {
      "pubmed": 15024385,
      "text": "Binding to Cdk2-cyclin A is accompanied by p27 folding, and kinetic␣
↪data suggest a sequential mechanism that is initiated by binding to cyclin A"
    },
    {
      "pubmed": 15063782,
      "text": "We also found that cyclin A/CDK2 phosphorylates Axin, thereby␣
↪enhancing its association with beta-catenin."
    },
    {
      "pubmed": 15159402,
      "text": "study provides evidence that the cyclin A1-cyclin dependent kinase 2␣
↪complex plays a role in several signaling pathways important for cell cycle control␣
↪and meiosis"
    },
    {
      "pubmed": 15178429,
      "text": "interacts with dephosphorylated NIRF"
    },
    {
      "pubmed": 15199159,
      "text": "cyclin A-cdk2 plays an ancillary noncatalytic role in the␣
↪ubiquitination of p27(KIP1) by the SCF(skp2) complex"
```


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```
    },
    {
      "pubmed": 15226429,
      "text": "Results identify an important role for CDK2 in the maintenance of␣
↪genomic stability, acting via an ATM- and ATR-dependent pathway."
    },
    {
      "pubmed": 15309028,
      "text": "after CDK4/6 inactivation, the fate of pancreatic tumor cells depends␣
↪on the ability to modulate CDK2 activity"
    },
    {
      "pubmed": 15355984,
      "text": "Data suggest that cyclin D1-Cdk2 complexes mediate some of the␣
↪transforming effects of cyclin D1 and demonstrate that the cyclin D1-Cdk2 fusion␣
↪protein is a useful model to investigate the biological functions of cyclin D1-Cdk2␣
↪complexes."
    },
    {
      "pubmed": 15456866,
      "text": "These findings establish a novel function for cyclin A1 and CDK2 in␣
↪DNA double strand break repair following radiation damage."
    },
    {
      "pubmed": 15572662,
      "text": "Phosphborylation of progesterone receptor serine 400 mediates ligand-
↪independent transcriptional activity in response to activation of CDK2."
    },
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      "text": "Inhibition of CDK2 kinase by indole-3-carbinol is accompanied by␣
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      "text": "origin recognition complex 2 has an unexpected role in CDK2 activation,
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↪mitotic catastrophe."
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↪both an S-phase & an M-phase kinase. CDK2/cyclin B is effective against S phase␣
↪substrates."
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      "pubmed": 18236071,
      "text": "Findings strongly demonstrate that retinoblastoma (RB) and cyclin-
↪dependent kinase 2 (CDK2) on one side and cytokeratin 8 (CK8) and epidermal growth␣
↪factor receptor 2 (HER2) on the other may affect the clinical course of the disease␣
↪in 56% of patients."
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↪Cdk2 and the cell cycle by the absence of functional p53."
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      "text": "G2 phase cyclin A/cdk2 controls the timing of entry into mitosis by␣
↪controlling the subsequent activation of cyclin B/cdk1, but also has an unexpected␣
↪role in coordinating the activation of cyclin B/cdk1 at the centrosome and in the␣
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↪and CDK2 inhibited by phosphorylation at Thr14/Tyr15 were studied using molecular␣
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      "text": "Strengthened signals in imputation-based analysis at CDK2 SNPs␣
↪rs2069391, rs2069414 and rs17528736 lend evidence to the role of cell cycle genes␣
↪in ovarian cancer etiology."
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↪and coordinated activation of both an essential origin licensing factor, CDC6, and␣
↪an activity required for origin firing, CDK2, resulting in progression from␣
↪quiescence to S phase."
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↪and Rb phosphorylation, permitting them to enter S phase with a reduced rate of␣
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↪ADAM12, cyclin-dependent kinase 2-CDK2, kinesin 14-KIF14, suppressor 1 of␣
↪checkpoint-CHES1."
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↪involves accumulation of p27, down-regulation of pRb, Skp2, and impairment of Cdk2␣
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↪after the activity of CDK1 is suppressed."
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↪expression and contribute to the mitogenic potential of tumor cells during␣
↪Hepatocellular carcinoma carcinogenesis."
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      "text": "Data show that Myc repressed Ras-induced senescence, and that Cdk2␣
↪interacted with Myc at promoters, where it affected Myc-dependent regulation of␣
↪genes, including those of proteins known to control senescence."
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↪during large-scale sequencing of protein kinases from cancerous tissue."
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↪independent cell death, and Cdk2 is required for both pathways."
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↪IL-2RA gene expression, IKK controls the expression of cyclin D3, cyclin E and CDK2,
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↪transcription of VDR target genes that control the hair cycle."
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      "text": "Cdk2 functions via a Cdk2/SHP-1/beta-catenin/CEACAM1 axis, and show␣
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      "text": "cyclin E and CDK2 genes are key physiological effectors of the c-ETS1␣
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↪polyubiquitin from cyclin A. USP37 was induced by E2F factors in G1, peaked at G1/S,
↪ and was degraded in late mitosis. Phosphorylation of USP37 by CDK2 stimulated its␣
↪full activity."
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      "text": "anti-oncogenic role of miR-372 may be through control of cell growth␣
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↪positive feedbacks mediated by p21 phosphorylation by CDK4 and CDK2 to sustain CDK4␣
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↪interruption in A549s cells."
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      "text": "Results show that CDK2 phosphorylates Thr-156 in GATA3."
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      "pubmed": 24911186,
      "text": "Report structure-based discovery of allosteric inhibitors of CDK2."
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↪with high CDK2SA-CDK1SA ratio (88.7% vs. 54.7%, P = 0.00141)."
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↪the inhibitory potency of purine derivatives against these two human Cdks."
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↪degradation."
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↪cyclin-dependent kinase-2"
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↪CDK2 inhibition, especially in the presence of activated KRAS mutations."
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↪controlled CDK2 expression, whereas CDK2 inactivation specifically abrogated the␣
↪growth of NUAK2-amplified and PTEN-deficient melanoma cells."
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↪single site, threonine 152, by cyclin E/CDK2 and cyclin A/CDK2. This site is also␣
↪phosphorylated in cells in a cell cycle dependent manner, consistent with it being␣
↪a CDK2 substrate."
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    "2W05",
    "2W06",
    "2W17",
    "2W1H",
    "2WEV",
    "2WFY",
    "2WHB",
    "2WIH",
    "2WIP",
    "2WMA",
    "2WMB",
    "2WPA",
    "2WXV",
    "2X1N",
    "2XMY",
    "2XNB",
    "3BHT",
    "3BHU",
    "3BHV",
    "3DDP",
    "3DDQ",
    "3DOG",
    "3EID",
    "3EJ1",
    "3EOC",
    "3EZR",
    "3EZV",
    "3F5X",
    "3FZ1",
    "3IG7",
    "3IGG",
    "3LE6",
    "3LFN",
    "3LFQ",
    "3LFS",
    "3MY5",
    "3NS9",
    "3PJ8",
    "3PXF",
    "3PXQ",
    "3PXR",
    "3PXY",
    "3PXZ",
    "3PY0",
    "3PY1",
    "3QHR",
    "3QHW",
    "3QL8",
    "3QQF",
    "3QQG",
    "3QQH",
```

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```
    "3QQJ",
    "3QQK",
    "3QQL",
    "3QRT",
    "3QRU",
    "3QTQ",
    "3QTR",
    "3QTS",
    "3QTU",
    "3QTW",
    "3QTX",
    "3QTZ",
    "3QU0",
    "3QWJ",
    "3QWK",
    "3QX2",
    "3QX4",
    "3QXO",
    "3QXP",
    "3QZF",
    "3QZG",
    "3QZH",
    "3QZI",
    "3R1Q",
    "3R1S",
    "3R1Y",
    "3R28",
    "3R6X",
    "3R71",
    "3R73",
    "3R7E",
    "3R7I",
    "3R7U",
    "3R7V",
    "3R7Y",
    "3R83",
    "3R8L",
    "3R8M",
    "3R8P",
    "3R8U",
    "3R8V",
    "3R8Z",
    "3R9D",
    "3R9H",
    "3R9N",
    "3R9O",
    "3RAH",
    "3RAI",
    "3RAK",
    "3RAL",
    "3RJC",
    "3RK5",
    "3RK7",
    "3RK9",
    "3RKB",
    "3RM6",
    "3RM7",
```


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```
    "3RMF",
    "3RNI",
    "3ROY",
    "3RPO",
    "3RPR",
    "3RPV",
    "3RPY",
    "3RZB",
    "3S00",
    "3S0O",
    "3S1H",
    "3S2P",
    "3SQQ",
    "3SW4",
    "3SW7",
    "3TI1",
    "3TIY",
    "3TIZ",
    "3TNW",
    "3ULI",
    "3UNJ",
    "3UNK",
    "3WBL",
    "4ACM",
    "4BCK",
    "4BCM",
    "4BCN",
    "4BCO",
    "4BCP",
    "4BCQ",
    "4BGH",
    "4BZD",
    "4CFM",
    "4CFN",
    "4CFU",
    "4CFV",
    "4CFW",
    "4CFX",
    "4D1X",
    "4D1Z",
    "4EK3",
    "4EK4",
    "4EK5",
    "4EK6",
    "4EK8",
    "4EOI",
    "4EOJ",
    "4EOK",
    "4EOL",
    "4EOM",
    "4EON",
    "4EOO",
    "4EOP",
    "4EOQ",
    "4EOR",
    "4EOS",
    "4ERW",
```

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```
    "4EZ3",
    "4EZ7",
    "4FKG",
    "4FKI",
    "4FKJ",
    "4FKL",
    "4FKO",
    "4FKP",
    "4FKQ",
    "4FKR",
    "4FKS",
    "4FKT",
    "4FKU",
    "4FKV",
    "4FKW",
    "4FX3",
    "4GCJ",
    "4I3Z",
    "4II5",
    "4KD1",
    "4LYN",
    "4NJ3",
    "4RJ3",
    "5A14",
    "5AND",
    "5ANE",
    "5ANG",
    "5ANI",
    "5ANJ",
    "5ANK",
    "5ANO",
    "5CYI",
    "5D1J",
    "5FP5",
    "5FP6",
    "5IEV",
    "5IEX",
    "5IEY",
    "5IF1"
  ],
  "pfam": "PF00069",
  "pharmgkb": "PA101",
  "pir": "A41227",
  "prosite": "PS50011",
  "reagent": {
    "GNF_Qia_hs-genome_v1_siRNA": [
      {
        "id": "GNF247215",
        "relationship": "is"
      },
      {
        "id": "GNF247216",
        "relationship": "is"
      },
      {
        "id": "GNF247217",
        "relationship": "is"
```


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```
    },
    {
      "id": "GNF247218",
      "relationship": "is"
    }
  ],
  "GNF_hs-ORFeome1_1_reads": {
    "id": "GNF161504",
    "relationship": "is"
  },
  "GNF_hs-Origene": [
    {
      "id": "GNF035860",
      "relationship": "similar to"
    },
    {
      "id": "GNF037258",
      "relationship": "is"
    },
    {
      "id": "GNF048982",
      "relationship": "is"
    }
  ],
  "GNF_hs-druggable_lenti-shRNA": [
    {
      "id": "GNF081385",
      "relationship": "is"
    },
    {
      "id": "GNF081386",
      "relationship": "is"
    },
    {
      "id": "GNF081387",
      "relationship": "is"
    }
  ],
  "GNF_hs-druggable_plasmid-shRNA": [
    {
      "id": "GNF051995",
      "relationship": "is"
    },
    {
      "id": "GNF056761",
      "relationship": "is"
    },
    {
      "id": "GNF061563",
      "relationship": "is"
    },
    {
      "id": "GNF078683",
      "relationship": "is"
    }
  ],
  "GNF_hs-druggable_siRNA": [
```


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```
      {
        "id": "GNF066537",
        "relationship": "is"
      },
      {
        "id": "GNF066538",
        "relationship": "is"
      }
    ],
    "GNF_hs-pkinase_IDT-siRNA": [
      {
        "id": "GNF166768",
        "relationship": "is"
      },
      {
        "id": "GNF166769",
        "relationship": "is"
      },
      {
        "id": "GNF166770",
        "relationship": "is"
      },
      {
        "id": "GNF166771",
        "relationship": "is"
      }
    ],
    "GNF_hs_LentiORF-HA-MYC": {
      "id": "GNF282834",
      "relationship": "is"
    },
    "GNF_hs_LentiORF-Jred": {
      "id": "GNF283761",
      "relationship": "is"
    },
    "GNF_mm+hs-MGC": {
      "id": "GNF002384",
      "relationship": "is"
    },
    "Invitrogen_IVTHSSIPKv2": [
      {
        "id": "GNF324610",
        "relationship": "is"
      },
      {
        "id": "GNF324611",
        "relationship": "is"
      }
    ],
    "NIBRI_hs-Secretome_pDEST": {
      "id": "GNF337962",
      "relationship": "is"
    },
    "NOVART_hs-genome_siRNA": [
      {
        "id": "GNF093028",
        "relationship": "is"
```


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```
      },
      {
        "id": "GNF132726",
        "relationship": "is"
      }
    ]
  },
  "refseq": {
    "genomic": [
      "NC_000012.12",
      "NC_018923.2",
      "NG_034014.1"
    ],
    "protein": [
      "NP_001277159.1",
      "NP_001789.2",
      "NP_439892.2",
      "XP_011536034.1"
    ],
    "rna": [
      "NM_001290230.1",
      "NM_001798.4",
      "NM_052827.3",
      "XM_011537732.1"
    ],
    "translation": [
      {
        "protein": "XP_011536034.1",
        "rna": "XM_011537732.1"
      },
      {
        "protein": "NP_001789.2",
        "rna": "NM_001798.4"
      },
      {
        "protein": "NP_439892.2",
        "rna": "NM_052827.3"
      },
      {
        "protein": "NP_001277159.1",
        "rna": "NM_001290230.1"
      }
    ]
  },
  "reporter": {
    "HG-U133_Plus_2": [
      "204252_at",
      "211803_at",
      "211804_s_at"
    ],
    "HG-U95Av2": [
      "1792_g_at",
      "1833_at"
    ],
    "HTA-2_0": "TC12000496.hg.1",
    "HuEx-1_0": "3417146",
    "HuGene-1_1": "7956076",
```


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```
    "HuGene-2_1": "16752305"
  },
  "summary": "This gene encodes a member of a family of serine/threonine protein␣
↪kinases that participate in cell cycle regulation. The encoded protein is the␣
↪catalytic subunit of the cyclin-dependent protein kinase complex, which regulates␣
↪progression through the cell cycle. Activity of this protein is especially critical␣
↪during the G1 to S phase transition. This protein associates with and regulated by␣
↪other subunits of the complex including cyclin A or E, CDK inhibitor p21Cip1␣
↪(CDKN1A), and p27Kip1 (CDKN1B). Alternative splicing results in multiple transcript␣
↪variants.",
  "symbol": "CDK2",
  "taxid": 9606,
  "type_of_gene": "protein-coding",
  "unigene": [
    "Hs.19192",
    "Hs.689624"
  ],
  "uniprot": {
    "Swiss-Prot": "P24941",
    "TrEMBL": [
      "A0A024RB10",
      "A0A024RB77",
      "B4DDL9",
      "E7ESI2",
      "G3V317",
      "G3V5T9"
    ]
  },
  "wikipedia": {
    "url_stub": "Cyclin-dependent kinase 2"
  }
}
```


4.5.3 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/v3/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 "dofield" is true, the returned data object contains a single "refseq.rna" field, otherwise, a single "refseq" field with a sub-field of "rna". Default: false.

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 requests
headers = {'content-type': 'application/x-www-form-urlencoded'}
params = 'ids=1017,695&fields=name,symbol,refseq.rna'
res = requests.post('http://mygene.info/v3/gene', data=params, headers=headers)
```

Returned object

Returned result (the value of "res.text" variable above) from above example code should look like this:

```
[
  {
    '_id': '1017',
    '_score': 21.731894,
    'name': 'cyclin dependent kinase 2',
    'query': '1017',
    'refseq': {
      'rna': [
        'NM_001290230.1',
        'NM_001798.4',
        'NM_052827.3',
        'XM_011537732.1'
```

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```
      ]
    },
    'symbol': 'CDK2'
  },
  {
    '_id': '695',
    '_score': 21.730501,
    'name': 'Bruton tyrosine kinase',
    'query': '695',
    'refseq': {
      'rna': [
        'NM_000061.2',
        'NM_001287344.1',
        'NM_001287345.1'
      ]
    },
    'symbol': 'BTK'
  }
]
```

4.6 Server response

The MyGene.info server returns a variety of query responses, and response status codes. They are listed here.

Note: These examples show query responses using the python requests package.

4.6.1 Status code *200*

A **200** status code indicates a successful query, and is accompanied by the query response payload.

```
In [1]: import requests

In [2]: r = requests.get('http://mygene.info/v3/query?q=_exists_:entrezgene')

In [3]: r.status_code
Out[3]: 200

In [4]: data = r.json()

In [5]: data.keys()
Out[5]: dict_keys(['total', 'max_score', 'took', 'hits'])
```

4.6.2 Status code *400*

A **400** status code indicates an improperly formed query, and is accompanied by a response payload describing the source of the error.

```
In [6]: r = requests.get('http://mygene.info/v3/query?q=_exists_:entrezgene&size=u')
```

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```
In [7]: r.status_code
Out[7]: 400

In [8]: data = r.json()

In [9]: data
Out[9]:
{'error': "Expected 'size' parameter to have integer type.  Couldn't convert 'u' to␣
↪integer",
 'success': False}
```

4.6.3 Status code *404*

A **404** status code indicates either an unrecognized URL, as in (*/query* is misspelled */quer* resulting in an unrecognized URL):

```
In [10]: r = requests.get('http://mygene.info/v3/quer?q=_exists_:entrezgene')

In [11]: r.status_code
Out[11]: 404
```

or, for the **/gene** endpoint, a **404** status code could be from querying for a nonexistent gene ID, as in:

```
In [12]: r = requests.get('http://mygene.info/v3/gene/0')

In [13]: r.status_code
Out[13]: 404

In [14]: data = r.json()

In [15]: data
Out[15]:
{'error': "Gene ID '0' not found",
 'success': False}
```

4.6.4 Status code *5xx*

Any **5xx** status codes are the result of uncaught query errors. Ideally, these should never occur. We routinely check our logs for these types of errors and add code to catch them, but if you see any status **5xx** responses, please submit a bug report to help@mygene.info.

4.7 Usage and Demo

This page provides some usage examples and demo applications.

4.7.1 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 programing languages provide functions for making http requests and JSON parsing. For Python, you can using build-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.

4.7.2 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.

4.7.3 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"></script>
```

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>
```

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```
    <input style="width:250px" class="mygene_query_target">
    <script src="http://mygene.info/widget/autocomplete/js/mygene_query_min.js" type=
↪"text/javascript"></script>
</body>
</html>
```

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

4.8 Third-party packages

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

4.8.1 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,
```

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```
 'took': 10,
 'total': 28}
```

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

4.8.2 MyGene R package

An R wrapper for the MyGene.info API is available in Bioconductor since v3.0. To install:

```
source("https://bioconductor.org/biocLite.R")
biocLite("mygene")
```

To view documentation for your installation, enter R and type:

```
browseVignettes("mygene")
```

For more information, visit the Bioconductor mygene page.

4.8.3 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:

4.8.4 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
```

(continues on next page)

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```
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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