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 http://mygene.info/mygene-info-v3-is-out'_**

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
        ],
        [
```

```
            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	
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"
    "_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 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

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

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 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*.

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 "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.

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
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",
      "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
    }
  }
}
```


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
```

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/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: 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 "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
  }
]
```


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"
  }
]
```

4.4 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/v3/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/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",
      "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": [
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        "rna": "AB012305.1"
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      {
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        "rna": "XM_011537732.1"
      },
      {
        "protein": "ABM92215.1",
        "rna": "DQ890598.2"
      },
      {
        "protein": "NP_439892.2",
        "rna": "NM_052827.3"
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      {
        "protein": "AAA35667.1",
        "rna": "M68520.1"
      },
      {
```

```
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        "rna": "AK293246.1"
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      {
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        "rna": "AK291941.1"
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        "rna": "BT006821.1"
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        "protein": "CAA43807.1",
        "rna": "X61622.1"
      },
      {
        "protein": "CAL38014.1",
        "rna": "AM393136.1"
      },
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        "protein": "CAA43985.1",
        "rna": "X62071.1"
      },
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        "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",
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      "ENST00000553376",
      "ENST00000554545",
      "ENST00000554619",
      "ENST00000555357",
      "ENST00000555408",
      "ENST00000556146",
      "ENST00000556276",
      "ENST00000556464",
      "ENST00000556656"
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        "rna": "ENST00000266970"
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        "rna": "ENST00000555408"
      },
      {
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        "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
        ],
```

```
        [
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          55971247
        ],
        [
          55971520,
          55972789
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      ],
      "strand": 1,
      "transcript": "NM_001290230",
      "txend": 55972789,
      "txstart": 55966768
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    {
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      "cdsstart": 55967008,
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          55972789
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    {
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      "cdsstart": 55967008,
      "chr": "12",
      "position": [
```

```
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          55972789
        ]
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      "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": [
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          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,
          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"
    },
    {
      "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"
    },
    {
      "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"
    },
    {
      "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."
    },
    {
      "pubmed": 15601848,
      "text": "cyclin A/Cdk2 has a role as a progesterone receptor coactivator"
    },
    {
      "pubmed": 15607961,
      "text": "CDK2 depletion suppressed growth and cell cycle progression in␣
↪melanoma and may be a suitable drug target in melanoma."
    },
    {
      "pubmed": 15611077,
      "text": "Inhibition of CDK2 kinase by indole-3-carbinol is accompanied by␣
↪selective alterations in cyclin E composition."
    },
    {
      "pubmed": 15632290,
      "text": "molecular dynamics study on the complex CDK2 with the peptide␣
↪substrate HHASPRK"
    },
    {
      "pubmed": 15649889,
```

```
      "text": "Results demonstrate that a peptide derived from the alpha5 helix of␣
↪cyclin A significantly inhibits kinase activity of complexes harboring CDK2, and␣
↪forms stable complexes with CDK2-cyclin A."
    },
    {
      "pubmed": 15660127,
      "text": "crystal structure of phospho-CDK2 in complex with a truncated cyclin␣
↪E1 (residues 81-363) at 2.25 A resolution"
    },
    {
      "pubmed": 15665273,
      "text": "CDK2-BRCA1-Nucleophosmin pathway coordinately functions in cell growth␣
↪and tumor progression pathways."
    },
    {
      "pubmed": 15671017,
      "text": "HTm4 binding to KAP.Cdk2.cyclin A complex enhances the phosphatase␣
↪activity of KAP, dissociates cyclin A, and facilitates KAP dephosphorylation of Cdk2
↪"
    },
    {
      "pubmed": 15695825,
      "text": "Results present a comprehensive description of the dynamic behavior of␣
↪cyclin-dependent kinase 2 in complex with cyclin A."
    },
    {
      "pubmed": 15707957,
      "text": "Puralpha has been shown to colocalize with cyclin A/Cdk2 and to␣
↪coimmunoprecipitate with cyclin A during S-phase and we show that this interaction␣
↪is mediated by a specific affinity of Puralpha for Cdk2."
    },
    {
      "pubmed": 15890360,
      "text": "Rapid binding of p27 domain 1 to cyclin A tethers the inhibitor to the␣
↪binary Cdk2/cyclin A complex"
    },
    {
      "pubmed": 15922732,
      "text": "CDK2 translational down-regulation may be a key regulatory event in␣
↪replicative senescence of endothelial cells."
    },
    {
      "pubmed": 15944161,
      "text": "origin recognition complex 2 has an unexpected role in CDK2 activation,
↪ a linkage that could be important for maintaining genomic stability"
    },
    {
      "pubmed": 15964852,
      "text": "Cdk2 destabilizes p21 via the cy2 cyclin-binding motif and p21␣
↪phosphorylation"
    },
    {
      "pubmed": 16036217,
      "text": "Our results demonstrate that differential regulation of Cdc2 and Cdk2␣
↪activity by different doses of doxorubicin may contribute to the induction of two␣
↪modes of cell death in hepatoma cells, either apoptosis or cell death through␣
↪mitotic catastrophe."
    },
```

```
    {
      "pubmed": 16082200,
      "text": "CINP is part of the Cdc7-dependent mechanism of origin firing and a␣
↪functional and physical link between Cdk2 and Cdc7 complexes at the origins"
    },
    {
      "pubmed": 16082227,
      "text": "CDK2 inhibition modifies the dynamics of chromatin-bound␣
↪minichromosome maintenance complex and replication protein A"
    },
    {
      "pubmed": 16085226,
      "text": "results indicate that CDK2 participates in Tat-mediated HIV-1␣
↪transcription and may serve as a potential therapeutic target"
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      "pubmed": 16150942,
      "text": "Cdk2 inhibition decreases the efficiency of chemical induction of KSHV␣
↪lytic transcripts ORF 50 and 26. Importantly, Cdk2 activity is also essential for␣
↪replication in other human herpesviruses"
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    {
      "pubmed": 16258277,
      "text": "A new concept indicates in this review that both Cdk2 and/or Cdc2 can␣
↪drive cells through G1/S phase in parallel."
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    {
      "pubmed": 16262700,
      "text": "Cdk2 dependent phosphorylation(s) cannot be a critical trigger of␣
↪replicon initiation in response to reoxygenation after several hours of hypoxia, at␣
↪least in the T24 cells studied"
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    {
      "pubmed": 16343435,
      "text": "We propose that during TNFalpha-induced apoptosis, PKCdelta-mediated␣
↪phosphorylation of p21(WAF1/CIP1) at (146)Ser attenuates the Cdk2 binding of␣
↪p21(WAF1/CIP1) and thereby upregulates Cdk2 activity."
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    {
      "pubmed": 16407256,
      "text": "molecular analysis of the CDK5/p25 and CDK2/cyclin A systems"
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    {
      "pubmed": 16504183,
      "text": "Cyclin-dependent kinases regulate the transcriptional activity of␣
↪FOXM1c; a combination of three phosphorylation sites mediates the Cyclin E and␣
↪Cyclin A/CDK2 effects."
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    {
      "pubmed": 16540140,
      "text": "Here, we show that human papillomavirus type 16 16E1--E4 is also able␣
↪to associate with cyclin A and Cdk2 during the G2 phase of the cell cycle."
    },
    {
      "pubmed": 16575928,
      "text": "The interaction between roscovitine and cyclin-dependent kinase 2␣
↪(cdk2) was investigated by performing correlated ab initio quantum-chemical␣
↪calculations."
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    {
      "pubmed": 16707497,
      "text": "the phospho-CDK2/cyclin A recruitment site has a role in substrate␣
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      "text": "Phosphorylation of the linker histone H1 by CDK regulates its binding␣
↪to HP1alpha"
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      "pubmed": 16765349,
      "text": "suggest a novel retinoic acid (RA)-signaling, by which RA-induced p21␣
↪induction and complex formation with cyclin E/CDK2 diverts CDK2 function from␣
↪normally driving proliferation to alternatively promoting apoptosis"
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    {
      "pubmed": 16824683,
      "text": "Membrane depolarization may stimulate cellular proliferation by␣
↪augmenting the expression of cyclin E leading to increases in Cdk2 activity and RB␣
↪phosphorylation in a neuroblastoma cell line."
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    {
      "pubmed": 16912045,
      "text": "the Chk1-mediated S-phase checkpoint targets initiation factor Cdc45␣
↪via a Cdc25A/Cdk2-independent mechanism"
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      "pubmed": 16912201,
      "text": "Breast cancer cells lacking cancer predisposition genes BRCA1 are more␣
↪sensitive to CDK2 inhibitors."
    },
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      "pubmed": 17001081,
      "text": "analysis of the NBI1-binding site on cyclin A which inhibits the␣
↪catalytic activity of the complex cyclin-dependent kinase 2-cyclin A"
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      "pubmed": 17013093,
      "text": "progression of melanoma is associated with changes in CDK-2 expression␣
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      "text": "functional interaction between CDK2 and FOXO1 provides a mechanism␣
↪that regulates apoptotic cell death after DNA strand breakage"
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      "pubmed": 17095507,
      "text": "Kinetic and crystallographic analyses of CDK2-cyclin A complexes␣
↪reveal that this inhibitory mechanism operates through steric blockade of peptide␣
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      "pubmed": 17207508,
      "text": "Review highlights an alternative role for CDK2 in the regulation of␣
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      "pubmed": 17293600,
      "text": "TopBP1 necessary for the G(1)/S transition: one for activating cyclin␣
↪E/CDK2 kinase and the other for loading replication components onto chromatin to␣
↪initiate DNA synthesis."
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      "pubmed": 17361108,
      "text": "Our results demonstrate that CDK2 is capable of autophosphorylation at␣
↪Thr160."
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      "pubmed": 17371838,
      "text": "results argue that Mdm2 is needed for full inhibition of Cdk2 activity␣
↪by p21, thereby positively contributing to p53-dependent cell cycle arrest"
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      "text": "Both Cdk1 and -2 require cyclin binding and T loop phosphorylation for␣
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      "text": "The structure of phospho-CDK2/cyclin B is reported. pCDK2/cyclin B is␣
↪less discriminatory in substrate recognition than CDK2/cyclin A & has properties of␣
↪both an S-phase & an M-phase kinase. CDK2/cyclin B is effective against S phase␣
↪substrates."
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      "pubmed": 17638878,
      "text": "ATRIP is a CDK2 substrate, and CDK2-dependent phosphorylation of S224␣
↪regulates the ability of ATR-ATRIP to promote cell cycle arrest in response to DNA␣
↪damage"
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      "pubmed": 17713927,
      "text": "Phosphorylation on a conserved Thr14 can inhibit activities of both␣
↪the kinases, but phosphorylating another conserved Tyr15, however, can lead to␣
↪totally opposite inhibition and stimulation consequences in CDK2 and CDK5."
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    {
      "pubmed": 18042686,
      "text": "The conserved rigid regions are important for nucleotide binding,␣
↪catalysis, and substrate recognition; most flexible regions correlate with those␣
↪where large conformational changes occur during CDK2 regulation processes."
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    {
      "pubmed": 18156799,
      "text": "cdk2 activity is necessary for the survival of human DLBCL."
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      "pubmed": 18199752,
      "text": "major Cdk2-dependent multiple gene regulatory events are present in␣
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      "pubmed": 18202766,
      "text": "serum starvation induces G1 arrest through suppression of Skp2-
↪dependent CDK2 activity and Skp2-independent CDK4 activity in human SK-OV-3 ovarian␣
↪cancer cells"
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    {
      "pubmed": 18208561,
      "text": "growth arrest by SmE directly correlates with the reduction of cyclin␣
↪E, CDK2, CDC25C and CDC2 expression, and up-regulation of p27Kip"
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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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      "pubmed": 18276582,
      "text": "Cyclin E and SV40 small T antigen cooperate to bypass quiescence and␣
↪contribute to transformation by activating CDK2 in human fibroblasts"
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      "text": "Observational study of gene-disease association. (HuGE Navigator)"
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      "pubmed": 18345036,
      "text": "Bim-mediated apoptosis following actin damage due to deregulation of␣
↪Cdk2 and the cell cycle by the absence of functional p53."
    },
    {
      "pubmed": 18372919,
      "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␣
↪nucleus"
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    {
      "pubmed": 18400748,
      "text": "disruption of the spindle-assembly checkpoint does not directly␣
↪influence p53 activation, but the shortening of the mitotic arrest allows cyclin E-
↪CDK2 to be activated before the accumulation of p21(CIP1/WAF1)."
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      "pubmed": 18408738,
      "text": "Results suggest that GSK-3 regulates nuclear p27 Kip1 expression␣
↪through downregulation of Skp2 expression and regulates p27 Kip1 assembly with CDK2,
↪ playing a critical role in the G0/G1 arrest associated with intestinal cell␣
↪differentiation."
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      "pubmed": 18470542,
      "text": "The structures of fully active cyclin-dependent kinase-2␣
↪(CDK2)complexed with ATP and peptide substrate, CDK2 after the catalytic reaction,␣
↪and CDK2 inhibited by phosphorylation at Thr14/Tyr15 were studied using molecular␣
↪dynamics simulations."
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      "pubmed": 18617527,
      "text": "Cdk2-associated complexes, by targeting SHP-1 for proteolysis,␣
↪counteract the ability of SHP-1 to block cell cycle progression of intestinal␣
↪epithelial cells"
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    {
      "pubmed": 18635963,
      "text": "Cyclin A-CDK activity during G(1) would result in an inhibition of␣
↪progression into the S phase."
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      "pubmed": 18667424,
      "text": "the cyclin A-CDK2 complex may be a potential effector of NFATs,␣
↪specifically NFATc1, in mediating SMC multiplication leading to neointima formation.
↪"
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    {
      "pubmed": 18784074,
      "text": "Cdk2 negatively regulates the activity of hPXR, and suggest an␣
↪important role for Cdk2 in regulating hPXR activity and CYP3A4 expression in␣
↪hepatocytes passing through the cell cycle"
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      "pubmed": 18806832,
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      "pubmed": 19061641,
      "text": "Cyclin A assembles with Cdk1 only after complex formation with Cdk2␣
↪reaches a plateau during late S and G2 phases."
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      "pubmed": 19066288,
      "text": "These findings establish phosphorylation events by CDKs 1 and 2 as key␣
↪regulators of Discs Large 1 localisation and function."
    },
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      "pubmed": 19091404,
      "text": "Notch-1 may be mediated through regulating the expression of cell␣
↪cycle regulatory proteins cyclin D1, CDK2 and p21 and the activity of Akt signaling"
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      "pubmed": 19101503,
      "text": "These results demonstrate that double phosphorylation of CDK2 peptides␣
↪increases the stoichiometry of metal ion binding, and hence may contribute to the␣
↪previously observed regulation of CDK2 activity by metal ions."
    },
    {
      "pubmed": 19103742,
      "text": "the pathway of apoptin-induced apoptosis and show that it essentially␣
↪depends on abnormal phosphatidylinositol 3-kinase (PI3-kinase)/Akt activation,␣
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      "pubmed": 19166026,
      "text": "Overexpression of CDK2 was strongly correlated with abnormal␣
↪proliferation in laryngeal squamous cell carcinoma."
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      "pubmed": 19197163,
      "text": "Results show that human Cdk2 is a functional homolog for most of Ime2␣
↪functions."
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      "pubmed": 19201832,
      "text": "disruption of Smad2 function by CDK2 phosphorylation acts as a␣
↪mechanism for TGF-beta resistance in multiple myeloma."
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      "pubmed": 19258477,
      "text": "Observational study of gene-disease association. (HuGE Navigator)"
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      "pubmed": 19258477,
      "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."
    },
    {
      "pubmed": 19321444,
      "text": "The combination of st and deregulated cyclin E result in cooperative␣
↪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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      "pubmed": 19440053,
      "text": "Co-depletion of Cdc6 and p53 in normal cells restored Cdk2 activation␣
↪and Rb phosphorylation, permitting them to enter S phase with a reduced rate of␣
↪replication."
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      "text": "resistance of oral squamous carcinoma to IFNgamma is not due to␣
↪deficiency in STAT1-dependent signaling but from a defect in the signaling␣
↪component that mediates IFNgamma-induced down-regulation of CcnA2 and Cdk2␣
↪expression"
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      "text": "Four genes previously not examined in that respect in laryngeal␣
↪carcinoma, occurred to be good markers of the neoplasm. They are: metal-proteinase␣
↪ADAM12, cyclin-dependent kinase 2-CDK2, kinesin 14-KIF14, suppressor 1 of␣
↪checkpoint-CHES1."
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      "pubmed": 19631451,
      "text": "Data demonstrate that the novel anticancer mechanism of hinokitiol␣
↪involves accumulation of p27, down-regulation of pRb, Skp2, and impairment of Cdk2␣
↪function."
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      "pubmed": 19703905,
      "text": "cyclin A/cdk2-dependent phosphorylation of APC affects astral␣
↪microtubule attachment to the cortical surface in mitosis"
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      "pubmed": 19706521,
      "text": "Results suggest that simple but robust rules encoded in the CDK2␣
↪structure play a dominant role in predefining the mechanisms of ligand binding,␣
↪which may be advantageously exploited in designing inhibitors."
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      "pubmed": 19723060,
      "text": "Studies indicate that roscovitine arrests the cell cycle is direct␣
↪inhibition of CDK1, a mitotic regulator, and CDK2, involved in G1/S transition."
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      "pubmed": 19724860,
      "text": "Overexpression of Notch1 in laryngeal carcinoma cell line was coupled␣
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      "pubmed": 19797611,
      "text": "results show that the expression of UGT1A1 and CYP2B6 is negatively␣
↪regulated through a CDK2 signaling pathway linked to cell cycle progression in␣
↪HepG2 and SW480 cells"
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      "pubmed": 19822658,
      "text": "Results underscore the crucial role of cyclin A2-CDK2 in regulating␣
↪the PLK1-SCF(beta-TrCP1)-EMI1-APC/C axis and CDC6 to trigger genome reduplication␣
↪after the activity of CDK1 is suppressed."
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      "text": "Since CAC1 interacts with CDK2 and promotes the kinase activity of␣
↪CDK2 protein, we propose that CAC1 is a novel cell cycle associated protein capable␣
↪of promoting cell proliferation."
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      "pubmed": 19838212,
      "text": "Chk1 signalling causes centrosome amplification after ionizing␣
↪radiation by upregulating Cdk2 activity through activating phosphorylation."
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    {
      "pubmed": 19838216,
      "text": "Data show that SHP-1 knockdown increases p27stability, decreases the␣
↪CDK6 levels, inducing retinoblastoma protein hypophosphorylation, downregulation of␣
↪cyclin E and thereby a decrease in the CDK2 activity."
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      "pubmed": 19854217,
      "text": "expression upregulation is critical for TLR9-stimulated proliferation␣
↪of kung cancer cells"
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    {
      "pubmed": 19858290,
      "text": "Export was also reduced by Cdk inhibition or cyclin A RNA interference,
↪ suggesting that cyclin A/Cdk complexes contribute to Wee1 export."
    },
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      "pubmed": 19885547,
      "text": "aberrant regulation of S100P in HCC might activate cyclin D1 and CDK␣
↪expression and contribute to the mitogenic potential of tumor cells during␣
↪Hepatocellular carcinoma carcinogenesis."
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    {
      "pubmed": 19960406,
      "text": "Cellular production of IGFBP-3 leads to G1 cell cycle arrest with␣
↪inhibition of CDK2 and CDK4."
    },
    {
      "pubmed": 19966300,
      "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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    {
      "pubmed": 20017906,
      "text": "FUS-DDIT3 and the normal DDIT3 bind CDK2."
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      "pubmed": 20062077,
      "text": "Results directly show that the inhibition of Cdk1 activity and the␣
↪persistence of Cdk2 activity in G2 cells induces endoreplication without mitosis."
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↪cyclin-dependent CDK1 or CDK2 were almost fully phosphorylated in mitotic cells."
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      "text": "central roles for CDK2 nuclear-cytoplasmic trafficking and cyclin E in␣
↪the mechanism of 1,25-(OH)(2)D(3)-mediated growth inhibition in prostate cancer␣
↪cells"
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      "pubmed": 20195506,
      "text": "These findings demonstrate that Cdk2 maintains a balance of S-phase␣
↪regulatory proteins and thereby coordinates subsequent p53-independent G(2)/M␣
↪checkpoint activation."
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      "pubmed": 20399812,
      "text": "Data describe the properties of a mutant form of Cdk2 identified␣
↪during large-scale sequencing of protein kinases from cancerous tissue."
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      "pubmed": 20422243,
      "text": "Triticum aestivum-5B2 (( Ta ) 5B2) is suggested to be a wheat analogue␣
↪of human CDK2 enzyme."
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      "pubmed": 20444741,
      "text": "Conclude that cisplatin likely activates both caspase-dependent and -
↪independent cell death, and Cdk2 is required for both pathways."
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      "pubmed": 20465575,
      "text": "In addition to having a pivotal role in the up-regulation of IL-2 and␣
↪IL-2RA gene expression, IKK controls the expression of cyclin D3, cyclin E and CDK2,
↪ and the stability SKP2 and its co-factor CKS1B, through mechanisms independent of␣
↪IL-2."
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      "text": "Hr and VDR interact via multiple protein-protein interfaces,␣
↪catalyzing histone demethylation to effect chromatin remodeling and repress the␣
↪transcription of VDR target genes that control the hair cycle."
    },
    {
      "pubmed": 20694007,
      "text": "protein phosphatase 1 competition with Cdk-cyclins for retinoblastoma␣
↪protein(Rb) binding is sufficient to retain Rb activity and block cell-cycle␣
↪advancement."
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      "pubmed": 20711190,
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↪interphase nuclear pore complex formation in human dividing cells."
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      "pubmed": 20844047,
      "text": "Nuclear export of HPV31 E1 is inhibited by Cdk2 phosphorylation at two␣
↪serines residues, S92 and S106."
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      "pubmed": 20935635,
      "text": "The results demonstrate that CDK2-mediated phosphorylation is a key␣
↪mechanism governing EZH2 function and that there is a link between the cell-cycle␣
↪machinery and epigenetic gene silencing."
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↪interaction. (HuGE Navigator)"
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    {
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      "text": "Data show that miR-302 simultaneously suppressed both the cyclin E-
↪CDK2 and cyclin D-CDK4/6 pathways to block>70% of the G1-S cell cycle transition."
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      "pubmed": 21099355,
      "text": "Overexpression of human Cdk2 resulted in a defect in the G1 to S␣
↪transition and a reduction in viability."
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      "pubmed": 21233845,
      "text": "MicroRNA miR-885-5p targets CDK2 and MCM5, activates p53 and inhibits␣
↪proliferation and survival."
    },
    {
      "pubmed": 21262353,
      "text": "Cdk2 functions via a Cdk2/SHP-1/beta-catenin/CEACAM1 axis, and show␣
↪that Cdk2 has the capacity to regulate insulin internalization."
    },
    {
      "pubmed": 21264535,
      "text": "XPD may play an important role in cell apoptosis of hepatoma by␣
↪inducing an over-expression of p53, but suppressing expressions of c-myc and cdk2"
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      "text": "CDK2 downregulation causes high apoptosis at the early time points"
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      "text": "Conclude that in cisplatin induced-kidney injury phosphorylation of␣
↪p21 by Cdk2 limits the effectiveness of p21 to inhibit Cdk2."
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      "pubmed": 21454540,
      "text": "the ability of Emi1 to inhibit APC/C is negatively regulated by CDKs"
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    {
      "pubmed": 21515670,
      "text": "cyclin E and CDK2 genes are key physiological effectors of the c-ETS1␣
↪proto-oncogene. Furthermore, c-ETS1 is indispensable for the hepatotropic action of␣
↪HBx in cell cycle deregulation."
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      "text": "Transient binding of a second catalytic magnesium activates the␣
↪structure and dynamics of CDK2 kinase for catalysis."
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      "text": "The deubiquitinase USP37 binds CDH1 and removes degradative␣
↪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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    {
      "pubmed": 21646351,
      "text": "anti-oncogenic role of miR-372 may be through control of cell growth␣
↪and cell cycle progression by down-regulating the cell cycle genes CDK2 and cyclin␣
↪A1"
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      "pubmed": 21658603,
      "text": "Cdk2 is required for cell proliferation."
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      "pubmed": 21769424,
      "text": "RT-PCR and Western blotting results revealed that both mRNA and␣
↪protein levels of CDK2 were significantly higher in tumor tissues."
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    {
      "pubmed": 21871181,
      "text": "NF-Y binds to CCAAT sequences in the Cyclin A promoter, as well as to␣
↪those in the promoters of cell cycle G2 regulators such as CDC2, Cyclin B and␣
↪CDC25C."
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      "pubmed": 21918011,
      "text": "Epstein-Barr virus Rta-mediated transactivation of p21 and 14-3-3sigma␣
↪arrests cells at the G1/S transition by reducing cyclin E/CDK2 activity."
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      "pubmed": 21941773,
      "text": "The expression level of CDK2 protein did not change significantly in␣
↪silica-induced human embryo lung fibroblasts."
    },
    {
      "pubmed": 21965652,
      "text": "excess of MCM3 up-regulates the phosphorylation of CHK1 Ser-345 and␣
↪CDK2 Thr-14."
    },
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      "pubmed": 22084169,
      "text": "The S-phase-specific cyclin-dependent kinase 2 was required for robust␣
↪activation of ATR in response to diverse chemotherapeutic agents."
    },
    {
      "pubmed": 22231403,
      "text": "The authors show that, in human and mouse, Mre11 controls these events␣
↪through a direct interaction with CDK2 that is required for CtIP phosphorylation␣
↪and BRCA1 interaction in normally dividing cells."
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      "text": "Lin-28 homologue A (LIN28A) promotes cell cycle progression via␣
↪regulation of cyclin-dependent kinase 2 (CDK2), cyclin D1 (CCND1), and cell␣
↪division cycle 25 homolog A (CDC25A) expression in cancer."
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      "text": "CDK2 inhibition drastically diminishes anchorage-independent growth of␣
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      "pubmed": 22479189,
      "text": "low molecular weight cyclin E (LMW-E) requires CDK2-associated kinase␣
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      "pubmed": 22673765,
      "text": "The activation of p21(Waf1/Cip1) was significantly up-regulated over␣
↪time, but there was no change in the level of CDK2 expression by treatment of␣
↪HEK293 cells with various concentrations of veterinary antibiotics."
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      "pubmed": 22718829,
      "text": "Human cytomegalovirus IE1/2 expression was downregulated by cyclin A2,␣
↪CDK1 and CDK2."
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      "pubmed": 22819841,
      "text": "exposure of cancer cells (such as HeLa and MCF7 cells) to H2O2␣
↪increased CDK2 activity with no accompanying change in the PCNA level, leading to␣
↪cell proliferation."
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      "pubmed": 22927831,
      "text": "By a chemical-genetic approach study identified Nbs1 as a target of␣
↪Cdk2, and mapped the phosphorylation to a conserved CDK consensus recognition site."
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      "pubmed": 22951823,
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      "pubmed": 23028682,
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      "text": "human papillomavirus E4 proteins can interact with cyclin A and cdk2,␣
↪which may contribute to viral manipulation of the host cell cycle."
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      "text": "EEF2 phosphorylation by cyclin A-cyclin-dependent kinase 2 (CDK2) on a␣
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    {
      "pubmed": 23185313,
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↪a Chinese Han population."
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      "pubmed": 23230143,
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↪the basal activity of estrogen receptor alpha in breast cancer."
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      "pubmed": 23446853,
      "text": "Aurora-A kinase-induced centrosome amplification was mediated by Cdk2␣
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      "pubmed": 23479742,
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      "pubmed": 23643165,
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↪maintaining genome integrity."
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      "pubmed": 23720738,
      "text": "MCM7 is a substrate of cyclin E/Cdk2 and can be phosphorylated on Ser-
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↪(CDK2) contributing towards the binding of inhibitors."
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↪positive feedbacks mediated by p21 phosphorylation by CDK4 and CDK2 to sustain CDK4␣
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      "pubmed": 23776131,
      "text": "FBXO28 activity and stability are regulated during the cell cycle by␣
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↪by immediately building up CDK2 activity or to enter a transient G0-like state by␣
↪suppressing CDK2 activity."
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      "pubmed": 24204256,
      "text": "PKC activation then triggered activation of cdk-2, which became␣
↪further activated by caspase-3."
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      "text": "Two nuclear export signals of Cdc6 work cooperatively and distinctly␣
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      "pubmed": 24386425,
      "text": "Of the total, the deregulation of several genes (CDK1, CDK2, CDK4,␣
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      "pubmed": 24444383,
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↪level of MYC phosphorylation, but are not sensitive to inhibition of CDK2."
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      "pubmed": 24623419,
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↪kinase-associated protein 2 (SKP2)."
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      "pubmed": 24671051,
      "text": "Expression of Notch1, -2, and -3, CDK2, and CCNE1 was significantly␣
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↪interruption in A549s cells."
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      "pubmed": 24700371,
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↪expression levels and activities of CDK2 and CDK4 in SKOV3 cells."
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      "pubmed": 24820417,
      "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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    {
      "pubmed": 24922574,
      "text": "CDK2 Supports HIV-1 Reverse Transcription in CD4+ T Cells.HIV-1␣
↪reverse transcriptase Is a Substrate for CDK2-Dependent Phosphorylation"
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      "pubmed": 24935000,
      "text": "It is concluded that non-response to everolimus is characterized by␣
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      "pubmed": 25218637,
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↪towards BRCA2."
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      "pubmed": 25220500,
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↪optimal induction of progesterone receptor target genes in breast cancer cells."
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      "text": "High CDK2 expression is associated with nasopharyngeal carcinoma."
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↪CDK1SA ratio showed significantly better 5-year recurrence-free survival than those␣
↪with high CDK2SA-CDK1SA ratio (88.7% vs. 54.7%, P = 0.00141)."
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      "pubmed": 25451924,
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↪AML diagnosis and prognosis"
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      "text": "No association of CDK2 polymorphisms with risk of endometrial␣
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      "text": "Using the fact that deletion of the yeast CDC28 gene is functionally␣
↪complemented by human CDK1 or CDK2, we set up an in vivo screen system to evaluate␣
↪the inhibitory potency of purine derivatives against these two human Cdks."
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      "pubmed": 25728284,
      "text": "CDK2 up-regulates the protein level of KLF10 through reducing its␣
↪association with SIAH1, a KLF10 E3-ubiqutin ligase involved in proteasomal␣
↪degradation."
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      "pubmed": 25744732,
      "text": "Diclofenac and curcumin overcome these carcinogenic effects by␣
↪downregulating telomerase activity, diminishing the expression of TERT, CDK4, CDK2,␣
↪cyclin D1, and cyclin E."
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      "text": "NUAK2 silencing and inactivation of the PI3K pathway efficiently␣
↪controlled CDK2 expression, whereas CDK2 inactivation specifically abrogated the␣
↪growth of NUAK2-amplified and PTEN-deficient melanoma cells."
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      "text": "Identified ING5 as a novel CDK2 substrate. ING5 is phosphorylated at a␣
↪single site, threonine 152, by cyclin E/CDK2 and cyclin A/CDK2. This site is also␣
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↪hypophosphorylation, cyclin D3 gene down-regulation, and p21 post-translational␣
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↪SNP309 T>G variants between cases and controls."
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↪maintenance of the pluripotent state."
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↪drug for the treatment of human hepatocellular carcinoma."
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      "text": "In G28 cells, a dosedependent induction of CDK2, p21 and cyclin D was␣
↪observed between 10 and 50 microM roscovitine after 72 h, however, at the highest␣
↪concentration of 100 microM, all investigated genes were downregulated."
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    "GNF_Qia_hs-genome_v1_siRNA": [
      {
        "id": "GNF247215",
        "relationship": "is"
      },
      {
        "id": "GNF247216",
        "relationship": "is"
      },
      {
        "id": "GNF247217",
        "relationship": "is"
      },
      {
        "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": [
      {
        "id": "GNF066537",
        "relationship": "is"
      },
      {
        "id": "GNF066538",
        "relationship": "is"
      }
    ],
    "GNF_hs-pkinase_IDT-siRNA": [
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        "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"
      },
      {
        "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",
    "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"
  }
}
```

4.4.3 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/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'
      ]
    },
    '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'
  }
]
```


4.5 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 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.

4.5.2 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"></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>
    <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>.

4.6 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 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.

4.6.3 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:

4.6.4 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
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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CHAPTER 5

How to cite

See citation page here: http://mygene.info/citation/

CHAPTER 6

FAQ

See FAQ page here: http://mygene.info/faq/

CHAPTER 7

Related links

- mygene.info on Github

CHAPTER 8

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- help@mygene.info
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