



IEDB Query API (IQ-API)

A simple and powerful programmatic query interface to the IEDB

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How does it work?

API specification available at the base URL:

<https://query-api.iedb.org>



Each database table is exposed as a separate endpoint, e.g.:

[/epitope_search](#)

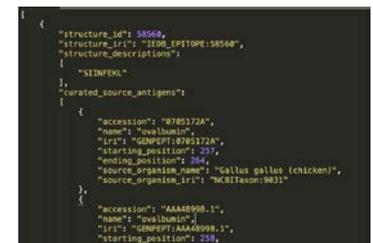
[/tcell_search](#)

[/antigen_search](#)

...

Queries formulated using PostgreSQL's expressive syntax, e.g.,

[linear_sequence=eq.SIINF EKL](#)



Putting it all together:

https://query-api.iedb.org/epitope_search?linear_sequence=eq.SIINF EKL

How are results returned?

Epitope query:

https://query-api.iedb.org/epitope_search?linear_sequence=eq.SIINFEKL

Response includes one 'row' per epitope:

```
[
  {
    "structure_id": 58560,
    "structure_description": "SIINFEKL",
    "source_organism_names":
    [
      "Gallus gallus (chicken)"
    ],
    "parent_source_antigen_names":
    [
      "Gal d 2"
    ]
  },
  {
    "structure_id": 114230,
    "structure_description": "SIINFEKL + SCM(K7)",
    "source_organism_names":
    [
      "Gallus gallus (chicken)"
    ],
    "parent_source_antigen_names":
    [
      "Gal d 2"
    ]
  },
  {
    "structure_id": 1309579,
    "structure_description": "SIINFEKL + BIOT(L8)",
    "source_organism_names":
    [
      "Gallus gallus (chicken)"
    ],
    "parent_source_antigen_names":
    [
      "Gal d 2"
    ]
  }
]
```

How are results returned?

T cell assay query:

https://query-api.iedb.org/tcell_search?linear_sequence=eq.SIINFEKL

Response includes one 'row' per T cell assay:

```
[
  {
    "tcell_id": 24151,
    "structure_description": "SIINFEKL",
    "assay_names": "cytotoxicity|51 chromium",
    "qualitative_measure": "Positive"
  },
  {
    "tcell_id": 24154,
    "structure_description": "SIINFEKL",
    "assay_names": "tumor burden after challenge|in vivo assay",
    "qualitative_measure": "Positive"
  },
  {
    "tcell_id": 1022871,
    "structure_description": "SIINFEKL",
    "assay_names": "IL-2 release|bioassay",
    "qualitative_measure": "Positive"
  },
  {
    "tcell_id": 1068817,
    "structure_description": "SIINFEKL",
    "assay_names": "pathogen burden after challenge|in vivo assay",
    "qualitative_measure": "Positive"
  },
  {
    "tcell_id": 1068827,
    "structure_description": "SIINFEKL",
    "assay_names": "pathogen burden after challenge|in vivo assay",
    "qualitative_measure": "Negative"
  },
  {
    "tcell_id": 1273732,
    "structure_description": "SIINFEKL",
    "assay_names": "cytotoxicity|51 chromium",
    "qualitative_measure": "Positive"
  }
]
```

How can I refine my query?

'Horizontal' filtering: use the 'select' keyword to return only the relevant fields

https://query-api.iedb.org/epitope_search

https://query-api.iedb.org/epitope_search?select=structure_id,structure_description,source_organism_names,parent_source_antigen_names

```
[{"structure_id":725080,"structure_iri":"IEDB_EPITOPE:725080","structure_descriptions":["SHALYQHDA"],"curated_source_antigens":[{"accession":"FSH210","name":"Pre-mRNA-processing factor 19","iri":"UNIPROT:FSH210","starting_position":19,"ending_position":27,"source_organism_name":"Homo sapiens (human)","source_organism_iri":"NCBITaxon:9606"},{"accession":"NP_055317.1","name":"pre-mRNA-processing factor 19","iri":"GENPEPT:NP_055317.1","starting_position":104,"ending_position":112,"source_organism_name":"Homo sapiens (human)","source_organism_iri":"NCBITaxon:9606"}],"structure_type":"Linear peptide","linear_sequence":"SHALYQHDA","e_modification":null,"linear_sequence_length":9,"iedb_assay_ids":[3607903,5178131],"iedb_assay_iris":["IEDB_ASSAY:3607903","IEDB_ASSAY:5178131"],"reference_ids":[1032297,1034232],"reference_iris":["IEDB_REFERENCE:1032297","IEDB_REFERENCE:1034232"],"submission_ids":null,"submission_iris":null,"pdb_ids":null,"chebi_ids":null,"qualitative_measures":["Positive"],"mhc_allele_evidences":["Allele/Locus-specific Antibody"],"antibody_isotypes":null,"direct_ex_vivo_bool":0,"receptor_ids":null,"receptor_group_ids":null,"tcr_receptor_group_ids":null,"bcr_receptor_group_ids":null,"receptor_group_iris":null,"receptor_types":null,"receptor_chain1_types":null,"receptor_chain2_types":null,"receptor_chain1_full_seqs":null,"receptor_chain2_full_seqs":null,"receptor_chain1_cdr1_seqs":null,"receptor_chain2_cdr1_seqs":null,"receptor_chain1_cdr2_seqs":null,"receptor_chain2_cdr2_seqs":null,"receptor_chain1_cdr3_seqs":null,"receptor_chain2_cdr3_seqs":null,"host_organism_iri_search":["NCBITaxon:314295","NCBITaxon:40674","NCBITaxon:7742","NCBITaxon:9443","NCBITaxon:9606"],"host_organism_iris":["NCBITaxon:9606"],"host_organism_names":["Homo sapiens (human)"],"source_organism_iri_search":["NCBITaxon:1","NCBITaxon:2759","NCBITaxon:314295","NCBITaxon:33208","NCBITaxon:40674","NCBITaxon:7742","NCBITaxon:9443","NCBITaxon:9606","ORI:0100026"],"source_organism_iris":["NCBITaxon:9606"],"source_organism_names":["Homo sapiens (human)"],"mhc_allele_iri_search":["GO:0032991"],"mhc_allele_iris":["MRO:0001355","MRO:0001454"],"mhc_allele_names":["human"],"parent_source_antigen_iri_search":["BFO:0000040","PR:000000001"],"taxon_protein":2759,"taxon_protein":314295,"taxon_protein":33208,"taxon_protein":40674,"taxon_protein":7742,"taxon_protein":9443,"taxon_protein":9606,"UNIPROT:F5GY56","UNIPROT:Q9UMS4","UNIPROT_PRO:0000051145"],"parent_source_antigen_iris":["UNIPROT:F5GY56","UNIPROT:Q9UMS4"],"parent_source_antigen_names":["Pre-mRNA-processing factor 19","Pre-mRNA-processing factor 19 (Fragment) (UniProt:F5GY56)"],"parent_source_antigen_source_org_iris":["NCBITaxon:9606"],"parent_source_antigen
```



```
{  
  "structure_id": 725080,  
  "structure_description": "SHALYQHDA",  
  "source_organism_names": [  
    "Homo sapiens (human)"  
  ],  
  "parent_source_antigen_names": [  
    "Pre-mRNA-processing factor 19",  
    "Pre-mRNA-processing factor 19 (Fragment) (UniProt:F5GY56)"  
  ]  
},  
{  
  "structure_id": 725081,  
  "structure_description": "SHAPLHSY",  
  "source_organism_names": [  
    "Homo sapiens (human)"  
  ],  
  "parent_source_antigen_names": [  
    "DBF4-type zinc finger-containing protein 2 (UniProt:Q9HC1)"  
  ]  
},  
{  
  "structure_id": 725082,  
  "structure_description": "SHAPYQPSA",  
  "source_organism_names": [  
    "Homo sapiens (human)"  
  ],  
  "parent_source_antigen_names": [  
    "Protein transport protein Sec24 (UniProt:Q94855)"  
  ]  
}
```

'Vertical' filtering: query at the field level for specific values

https://query-api.iedb.org/epitope_search

https://query-api.iedb.org/epitope_search?linear_sequence=eq.SIINFEKL

>1,000,000 records returned



3 records returned

How do I use the PostgREST search operators?

EQUALS (eq.) on string/numeric fields – e.g., linear_sequence in the epitope_search table

```
"structure_id": 58560,  
"linear_sequence": "SIINFEKL",
```

linear_sequence=eq.SIINFEKL

CONTAINS (cs.) on list fields – e.g., linear_sequences in the antigen_search table

```
"parent_source_antigen_iri": "UNIPROT:P01012",  
"linear_sequences": [  
  "SIINFEK",  
  "SIINFEKL",  
  "SIINFEKLT",
```

linear_sequences=cs.{SIINFEKL}

All PostgREST operators

<https://postgrest.org/en/stable/api.html#operators>

Abbreviation	In PostgreSQL	Meaning
eq	=	equals
gt	>	greater than
gte	>=	greater than or equal
lt	<	less than
lte	<=	less than or equal
neq	<> or !=	not equal
like	LIKE	LIKE operator (use * in place of %)
ilike	ILIKE	ILIKE operator (use * in place of %)
in	IN	one of a list of values, e.g. ?a=in.(1,2,3) – also supports commas in quote
is	IS	checking for exact equality (null,true,false)
fts	@@	Full-Text Search using to_tsquery
plfts	@@	Full-Text Search using plainto_tsquery
phfts	@@	Full-Text Search using phraseto_tsquery
wfts	@@	Full-Text Search using websearch_to_tsquery
cs	@>	contains e.g. ?tags=cs.{example, new}
cd	<@	contained in e.g. ?values=cd.(1,2,3)
ov	@@	overlap (have points in common), e.g. ?period=ov.(2017-01-01,2017-06-30)
sl	<<	strictly left of, e.g. ?range=sl.(1,10)
sr	>>	strictly right of
nrx	<@	does not extend to the right of, e.g. ?range=nrx.(1,10)
nlx	@<	does not extend to the left of
adj	- -	is adjacent to, e.g. ?range=adj.(1,10)
not	NOT	negates another operator, see below

Query parameters are similar across all tables

Epitopes: https://query-api.iedb.org/epitope_search?linear_sequence=eq.SIINFEKL

Antigens: https://query-api.iedb.org/antigen_search?linear_sequences=cs.{SIINFEKL}

T cell assays: https://query-api.iedb.org/tcell_search?linear_sequence=eq.SIINFEKL

B cell assays: https://query-api.iedb.org/bcell_search?linear_sequence=eq.SIINFEKL

MHC assays: https://query-api.iedb.org/mhc_search?linear_sequence=eq.SIINFEKL

TCRs: https://query-api.iedb.org/tcr_search?linear_sequences=cs.{SIINFEKL}

BCRs: https://query-api.iedb.org/bcr_search?linear_sequences=cs.{SIINFEKL}

References: https://query-api.iedb.org/reference_search?linear_sequences=cs.{SIINFEKL}

Why would I want to use the API?

- Direct access to computer-friendly (JSON) and human-friendly (TSV) formats without web interface
- Incorporate IEDB queries into code
- Work with IEDB data in language of choice
- Easily link between IEDB and other resources
- Periodically rerun automated queries for new/changed data

What can I query?

- If it's available in the IEDB web interface, it *should* be available through IQ-API
- We love a challenge – send us your use cases!

START YOUR SEARCH HERE ?

Epitope ? 

Any
 Linear peptide
Exact M
 Discontinuous
 Non-peptidic

Assay ? 

T Cell
 B Cell
 MHC Ligand
Ex: neutralization
Outcome: Positive Negative

Epitope Source ? 

Organism
Antigen

MHC Restriction ? 

Any
 Class I
 Class II
 Non-classical
Ex: HLA-A*02:01

Host ? 

Any
 Human
 Mouse
 Non-human primate
Ex: dog, camel

Disease ? 

Any
 Infectious
 Allergic
 Autoimmune
Ex: asthma

Epitopes
(1589203)

Antigens
(74838)

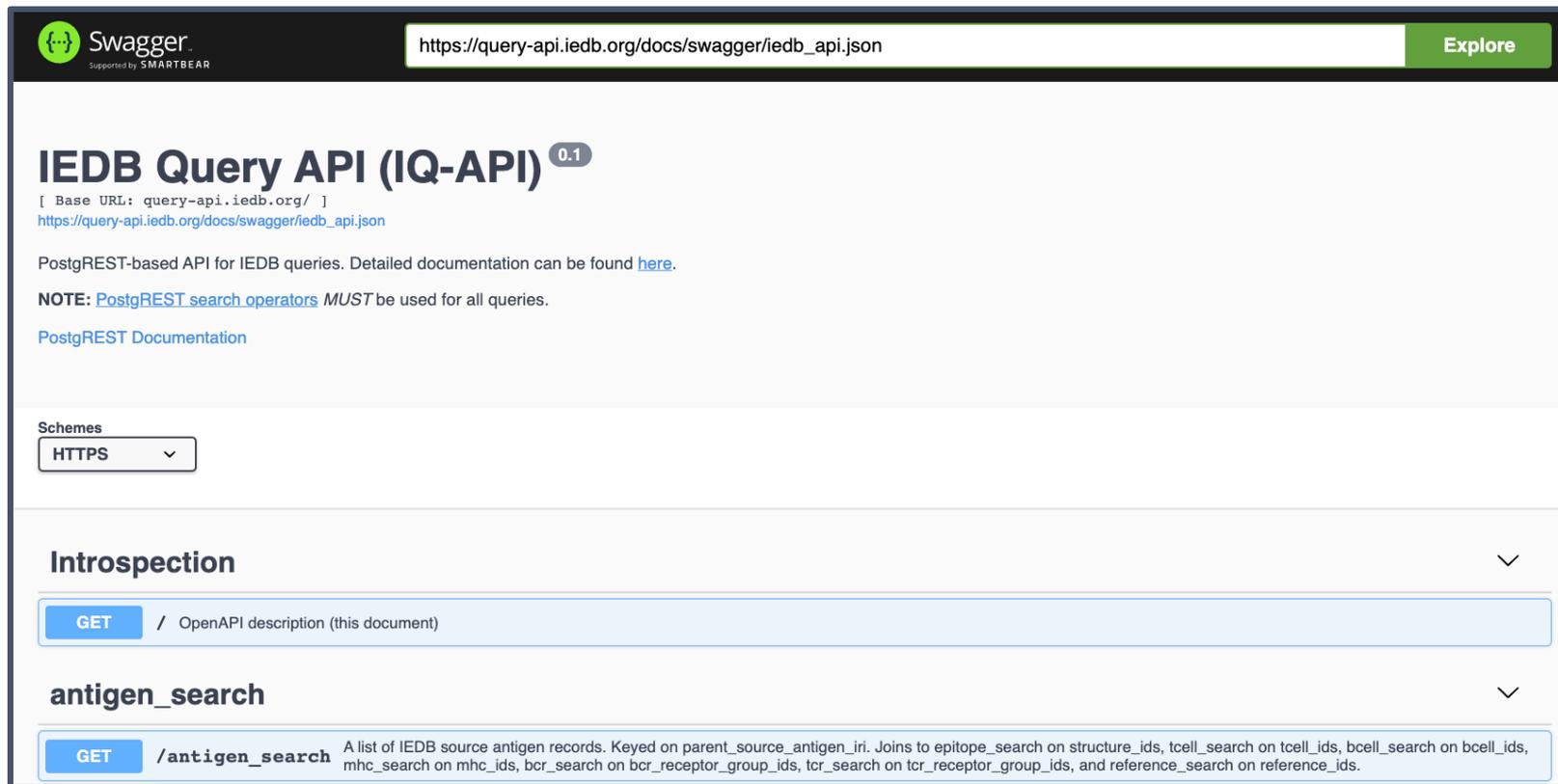
Assays
(4805181)

Receptors
(173796)

References
(22415)

How can I get started?

<https://query-api.iedb.org/docs/swagger/>



Swagger
Supported by SMARTBEAR

https://query-api.iedb.org/docs/swagger/iedb_api.json **Explore**

IEDB Query API (IQ-API) ^{0.1}

[Base URL: query-api.iedb.org/]
https://query-api.iedb.org/docs/swagger/iedb_api.json

PostgREST-based API for IEDB queries. Detailed documentation can be found [here](#).

NOTE: [PostgREST search operators](#) *MUST* be used for all queries.

[PostgREST Documentation](#)

Schemes
HTTPS

Introspection

GET / OpenAPI description (this document)

antigen_search

GET /**antigen_search** A list of IEDB source antigen records. Keyed on parent_source_antigen_iri. Joins to epitope_search on structure_ids, tcell_search on tcell_ids, bcell_search on bcell_ids, mhc_search on mhc_ids, bcr_search on bcr_receptor_group_ids, tcr_search on tcr_receptor_group_ids, and reference_search on reference_ids.

Reproducing a website query through IQ-API

Epitope ?

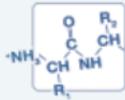
Any

Linear peptide

Exact M

Discontinuous

Non-peptidic

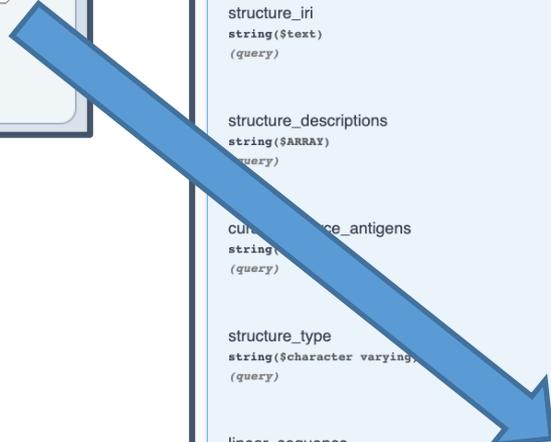


epitope_search

GET /epitope_search A list of IEDB epitope records. Keyed on structure_id/structure_iri. Joins to antigen_search on parent_source_antigen_iris, tcell_search on tcell_ids, bcell_search on bcell_ids, mhc_search on mhc_ids, bcr_search on bcr_receptor_group_ids, tcr_search on tcr_receptor_group_ids, and reference_search on reference_ids.

Parameters Cancel

Name	Description
structure_id string(\$integer) (query)	The IEDB epitope id of this epitope. <input type="text" value="structure_id - The IEDB epitope id of this epit"/>
structure_iri string(\$text) (query)	The IEDB epitope iri of this epitope. <input type="text" value="structure_iri - The IEDB epitope iri of this epit"/>
structure_descriptions string(\$ARRAY) (query)	An array of epitope descriptions associated with this epitope. <input type="text" value="structure_descriptions - An array of epitope d"/>
curated_source_antigens string(\$ARRAY) (query)	An array of curated antigen information associated with this epitope. <input type="text" value="curated_source_antigens - An array of curate"/>
structure_type string(\$character_varying) (query)	The structure type of this epitope. <input type="text" value="structure_type - The structure type of this epi"/>
linear_sequence string(\$character_varying) (query)	The linear sequence of this epitope. <input type="text" value="eq,\$SIINFEKL"/>



Live results returned, along with command-line

Execute Clear

Responses Response content type application/json

Curl

```
curl -X GET "https://query-api.iedb.org/epitope_search?linear_sequence=eq.SIINFEKL" -H "accept: application/json" -H "Range-Unit: items"
```

Request URL

```
https://query-api.iedb.org/epitope_search?linear_sequence=eq.SIINFEKL
```

Server response

Code	Details
200	<p>Response body</p> <pre>[{ "structure_id": 58560, "structure_iri": "IEDB_EPITOPE:58560", "structure_descriptions": ["SIINFEKL"], "curated_source_antigens": [{ "accession": "0705172A", "name": "ovalbumin", "iri": "GENPEPT:0705172A", "starting_position": 257, "ending_position": 264, "source_organism_name": "Gallus gallus (chicken)", "source_organism_iri": "NCBITaxon:9031" }, { "accession": "AAA48998.1", "name": "ovalbumin", "iri": "GENPEPT:AAA48998.1", "starting_position": 258, "ending_position": 265, "source_organism_name": "Gallus gallus (chicken)", "source_organism_iri": "NCBITaxon:9031" }] }]</pre> <p>Response headers</p>

Download

How can I do this in my favorite language?



```
import requests
search_params={ 'linear_sequence' = 'eq.SIINFEKL',
                'select'          = 'structure_id,linear_sequence,structure_description'
              }
result = requests.get('https://query-api.iedb.org/epitope_search', params=search_params)
```

```
library(httr)
search_params <- list('linear_sequence'='eq.SIINFEKL',
                     'select'='structure_id,linear_sequence,structure_description')
results = GET('https://query-api.iedb.org/epitope_search', query=search_params)
```



```
var xhttp = new XMLHttpRequest();
xhttp.overrideMimeType("application/json");
xhttp.onload = function() {
    var responseJson = JSON.parse(this.responseText)
}
xhttp.open("GET", "https://query-api.iedb.org/epitope_search?linear_sequence=eq.SIINFEKL
&select=structure_id,linear_sequence,structure_description");
xhttp.send();
```

```
$.ajax({
  type: 'get',
  url: 'https://query-api.iedb.org/epitope_search',
  data: { linear_sequence: 'eq.SIINFEKL', select: 'structure_id,linear_sequence,structure_description'},
  dataType: "json",
  success: function(data) {
    console.log(data);
  }
});
```



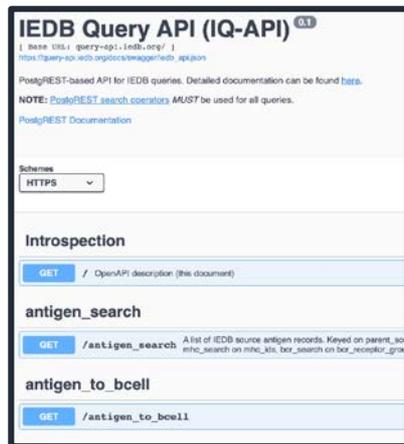
```
$curl = curl_init();
curl_setopt($curl, CURLOPT_URL, "https://query-api.iedb.org/epitope_search?linear_
sequence=eq.SIINFEKL&select=structure_id,linear_sequence,structure_description");
curl_setopt($curl, CURLOPT_RETURNTRANSFER, 1);
$result = json_decode(curl_exec($curl), true);
```

```
use LWP::Simple;
my $search_params='
    linear_sequence=eq.SIINFEKL&select=structure_id,linear_sequence,structure_description';
my $result = get('https://query-api.iedb.org/epitope_search?' . $search_params);
```



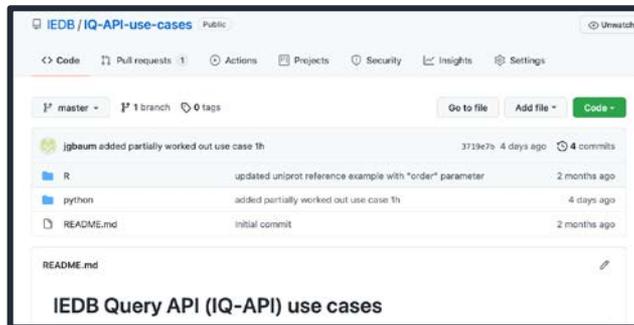
Where can I find more information?

Interactive table & field reference (Swagger)
<https://query-api.iedb.org/docs/swagger/>



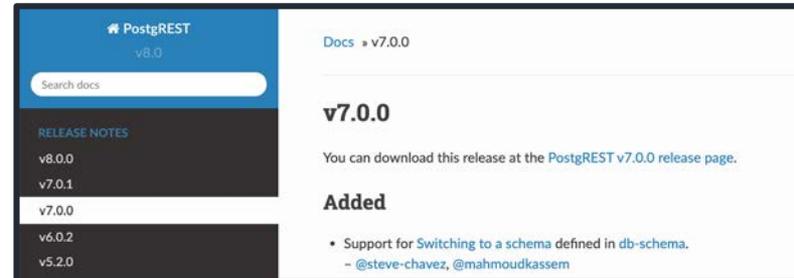
Use cases (Github)

<https://github.com/IEDB/IQ-API-use-cases>



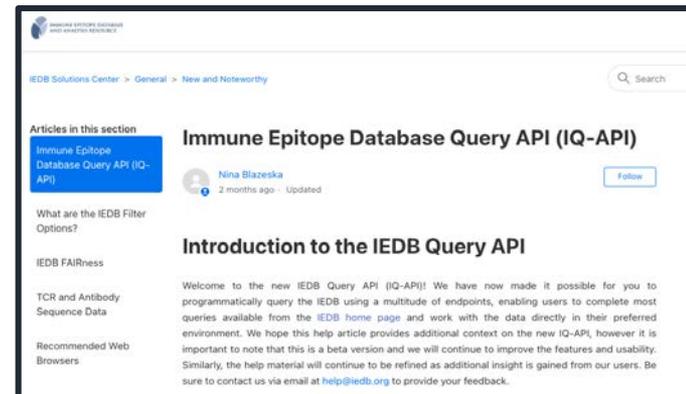
PostgREST reference

<https://postgrest.org/en/v8.0/releases/v7.0.0.html>



Overview (Zendesk)

<https://help.iedb.org/hc/en-us/articles/4402872882189-Immune-Epitope-Database-Query-API-IQ-API->



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