



Accessing the Data: Query, Reporting, and Examples

cedar.iedb.org

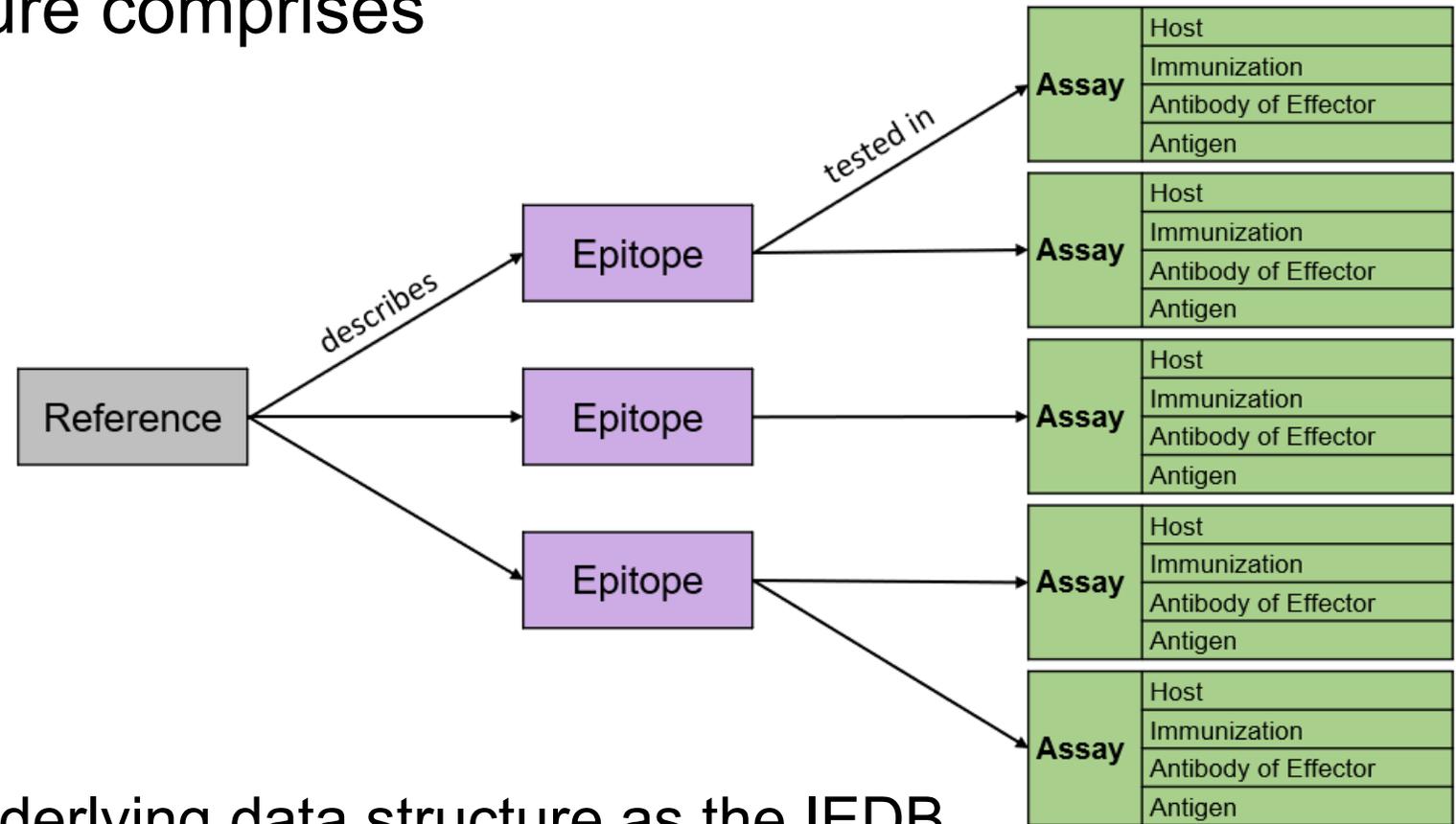
Presented by: Zeynep Koşaloğlu-Yalçın, Instructor

Overview

- IEDB → CEDAR
- How to access CEDAR data
- CEDAR data key statistics
- Use case examples
- Conclusion

IEDB to CEDAR

- The IEDB data structure comprises



- CEDAR has the same underlying data structure as the IEDB but was customized for cancer

Designing the CEDAR Web Interface: A User-Centered Approach

We Reached Out to Experts

- Interviewed cancer immunologists, translational researchers, and database users
- Identified the most critical **search fields** and data distinctions needed for cancer research



We Introduced Cancer-Specific Curation Rules

- Captured **cancer types** with more granularity (e.g., *NSCLC* vs *lung cancer*)
 - introduced **cancer stages**
- distinguish between **naturally occurring cancer, animal model and vaccination**
- Distinguish between **vaccination types** → *prophylactic* vs *therapeutic*



Goal: enable granular and intuitive queries, providing flexibility for different research needs

Welcome

The Cancer Epitope Database and Analysis Resource (CEDAR) is a freely available resource funded by [NCI](#). It catalogs experimental data on antibody and T cell peptidic epitopes primarily studied in humans and non-human primates in the context of cancer disease. CEDAR also hosts tools to assist in the prediction and analysis of cancer epitopes. CEDAR is a companion site to the [Immune Epitope Database \(IEDB\)](#), which is funded by NIAID, and houses epitope data on infectious disease, allergy, autoimmunity and transplantation.

Upcoming Events & News

CEDAR Virtual Short Course July 16, 2025
* [register here](#)

Past Events

AACR 2025 Apr 25-30, 2025
Immunology 2025 May 3-7, 2025

Summary Metrics

Peptidic Epitopes	1,318,977
Non-Peptidic Epitopes	84
T Cell Assays	149,712
B Cell Assays	141,561
MHC Ligand Assays	4,143,083
Epitope Source Organisms	1,722
Restricting MHC Alleles	665
References	6,008

START YOUR SEARCH HERE

Epitope ?

Any
 Linear peptide
 Discontinuous

Assay ?

T Cell
 B Cell
 MHC Ligand

Outcome: Positive Negative

Epitope Source ?

Cancer-associated antigens:

Neoantigen
 Viral antigen
 Germline/Self/Host antigen
 Other antigens from same reference

Receptor (TCR/BCR) ?

Has sequence TCR BCR

MHC Restriction ?

Any Class I Class II

Host ?

Any
 Human
 Mouse
 Non-human primate

Cancer ?

Exposure

Any
 Naturally occurring disease
 Animal model of cancer
 Vaccination

Epitope Analysis Resource

Mutated Peptide Generator. This tool takes a VCF file as input and extracts coding variants to generate corresponding neo-peptides along with their matched wild-type peptides, enabling downstream analysis of potential neoantigens.

Peptide binding to MHC class I molecules. This tool processes amino acid sequences to predict each subsequence's ability to bind to a specific MHC class I molecule. It accepts paired wild-type and mutant peptides, generating side-by-side binding affinity predictions to facilitate comparative analysis.

Peptide binding to MHC class II molecules. This tool will take in amino acid sequences and determine each subsequence's ability to bind to a specific MHC class II molecule.

Axel-F. The Antigen eXpression-based Epitope Likelihood-Function (AXEL-F) enhances MHC peptide prediction by incorporating the abundance levels of source antigens.

pepX. The Peptide eXpression annotator (pepX) estimates peptide abundance based on RNA-Seq data from selected public databases, providing expression-based insights for a given peptide input.

TCRmatch. TCRMatch compares input CDR3β sequences against curated CDR3β sequences in IEDB and CEDAR, identifying matches that are predicted to share epitope specificity.

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Upcoming Events

CEDAR Virtual Summit
* [register here](#)

Past Events
AACR 2025
Immunology 2025

Summary Methods

- Peptidic Epitopes
- Non-Peptidic Epitopes
- T Cell Assays
- B Cell Assays
- MHC Ligand Assays
- Epitope Source Organizations
- Restricting MHC Alleles
- References

ASSAY FINDER

CURRENT SELECTION(S) [Apply](#) [Reset](#)

Search By

Name:

Method:

Measurement Of:

Units:

[Search](#)

Browse by Tree (Click to Select)

- immune epitope assay
 - B cell assay
 - MHC ligand assay
 - T cell assay
 - 3D structure
 - biological activity
 - activation
 - cytokine release
 - cytotoxicity
 - degranulation
 - in vivo activity
 - proliferation
 - suppression
 - binding

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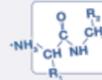
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MHC Ligand Assays	4,143,083
Epitope Source Organisms	1,722
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References	6,008

START YOUR SEARCH HERE

Epitope ?

- Any
- Linear peptide
- Discontinuous

Exact Match



Assay ?

- T Cell
- B Cell
- MHC Ligand

Ex: Cytotoxicity



Outcome: Positive Negative

Epitope Source ?

Antigen



Cancer-associated antigens:

- Neoantigen
- Viral antigen
- Germline/Self/Host antigen
- Other antigens from same reference

Receptor (TCR/BCR) ?

Has sequence TCR BCR



Chain CDR3

MHC Restriction ?

Any Class I Class II



Ex: HLA-A*02:01

Host ?

- Any
- Human
- Mouse
- Non-human primate
-



Cancer ?

Type



Stage

Exposure

- Any
- Naturally occurring disease
- Animal model of cancer
- Vaccination

Epitope Analysis Resource

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TCRmatch. TCRmatch compares input CDR3β sequences against curated CDR3β sequences in IEDB and CEDAR, identifying matches that are predicted to share epitope specificity.

Use Case Examples

Use Case Example 1

For a literature review, the user wants to **retrieve all references** that contain assays testing epitopes from the antigen 'Prostate-specific antigen'. The user also wants to investigate where along the PSA protein the **most immunogenic epitopes** are located.

Use Case Example 1: Query

START YOUR SEARCH HERE

Epitope ?

Any
 Linear peptide
Exact Match
 Discontinuous

Assay ?

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

Epitope Source ?

Antigen
Cancer-associated
 Necrotizing
 Viral
 Genotoxic
 Other antigen

Receptor (TCR/BCR) ?

Has sequence TCR BCR

Host ?

Any
 Human
 Mouse
 Non-human
Ex: Cytotoxicity

Animal model of cancer
 Vaccination

Prostate-specific antigen (UniProt:P07288) [P07288] (PSA) (...)
Campylobacter **ups**aliensis protein [28080] (Campylobacter ups...
Chaperone protein **PsaB** (UniProt:P69965) [P69965] (Yersinia p...
Outer membrane usher protein **PsaC** (UniProt:P31527) [P31527...
UDP-N-acetylglucosamine transporter (UniProt:A0A1W2**PSA9**) [...
Prosaposin (UniProt:P07602) [P07602] (**PSAP**) (Homo sapiens ...
pH 6 antigen (UniProt:P31522) [P31522] (**psaA**) (Yersinia pestis)
Prosaposin (UniProt:P10960) [P10960] (**Psap**) (Rattus norvegic...
Prosaposin (UniProt:Q61207) [Q61207] (**Psap**) (Mus musculus (...
Napsin-A (UniProt:O96009) [O96009] (**NAPSA**) (Homo sapiens ...

Use Case Example 1: Results – Epitopes



PENDING FILTERS

Search

Filter Options ?

Default

Epitope ?

Any
 Linear peptide
 Length
 Sequence
 Discontinuous
 3D structure assays
 Amino acid modification

Epitope Source ?

Organism

CURRENT FILTERS: Antigen: Prostate-specific antigen (UniProt:P07288) [P07288] (PSA) (Homo sapiens (human)) Include Positive Assays Include Negative Assays

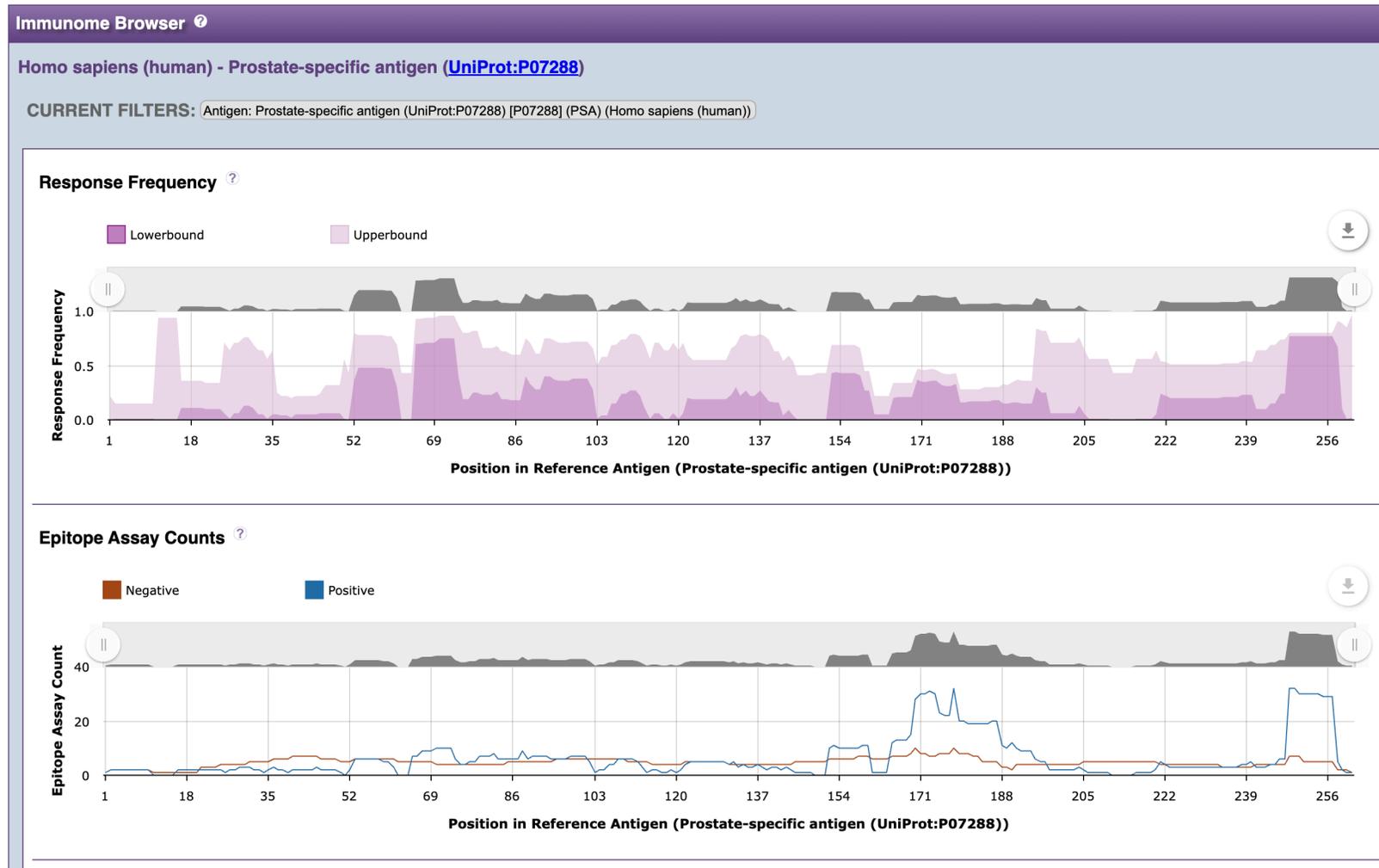
Epitopes (128)		Antigens (2)	Assays (744)	Receptors (4)	References (84)
<p>Page 1 of 6 128 Records Found 25 Per Page Export Results</p>					
CEDAR ID	Epitope (Mutation)	Antigen	Organism	# References	# Assays
989936	KLQCVDLHV	Prostate-specific antigen (UniProt:P07288)	Homo sapiens (human)	17	79
1714010	HYRKWIKDTI	Prostate-specific antigen (UniProt:P07288)	Homo sapiens (human)	17	75
111916	VISNDVCAQV	Prostate-specific antigen (UniProt:P07288)	Homo sapiens (human)	12	58
1637461	FLTPKKLQCV	Prostate-specific antigen (UniProt:P07288)	Homo sapiens (human)	10	38
1860817	CYASGWGSI	Prostate-specific antigen (UniProt:P07288)	Homo sapiens (human)	7	29
23596	HCIRNKSVI	Prostate-specific antigen (UniProt:P07288)	Homo sapiens (human)	6	26
1391978	VLVHPQWVL	Prostate-specific antigen (UniProt:P07288)	Homo sapiens (human)	5	12
39836	LTDVAVMDL	Prostate-specific antigen (UniProt:P07288)	Homo sapiens (human)	4	11
1855071	VLVASRGRAV	Prostate-specific antigen (UniProt:P07288)	Homo sapiens (human)	4	9
23597	HCIRNKSVIL	Prostate-specific antigen (UniProt:P07288)	Homo sapiens (human)	3	10
76101	YTKVVHYRK	Prostate-specific antigen (UniProt:P07288)	Homo sapiens (human)	3	7
119512	QVFQVSHSFPPLYD	Prostate-specific antigen (UniProt:P07288)	Homo sapiens (human)	3	7
1099786	GQVFQVSHSF	Prostate-specific antigen (UniProt:P07288)	Homo sapiens (human)	3	3

Use Case Example 1: Results – Antigen

CURRENT FILTERS: ✕ | Antigen: Prostate-specific antigen (UniProt:P07288) [P07288] (PSA) (Homo sapiens (human)) ✕ | Include Positive Assays ✕ | Include Negative Assays

Epitopes (128)	Antigens (2)	Assays (744)	Receptors (4)	References (84)
Page 1 of 1 2 Records Found 25 Per Page Export Results				
Antigen	Organism	# Epitopes	# Assays	# References
Prostate-specific antigen (UniProt:P07288)	 Homo sapiens (human)	127	743	83
neoantigen: Prostate-specific antigen (UniProt:P07288)	Homo sapiens (human)	1	1	1
Page 1 of 1 2 Records Found 25 Per Page Export Results				

Use Case Example 1: Results – Immunome Browser



Use Case Example 1: Results – References

CURRENT FILTERS: ✕ | Antigen: Prostate-specific antigen (UniProt:P07288) [P07288] (PSA) (Homo sapiens (human)) ✕ | Include Positive Assays ✕ | Include Negative Assays

Epitopes (128)		Antigens (2)		Assays (744)		Receptors (4)		References (84)	
⏪ ⏩ Page <input type="text" value="1"/> of 4 ⏪ ⏩		84 Records Found				<input type="text" value="25"/> Per Page		Export Results	
CEDAR ID	PMID	Author	Title	Journal	Date				
1045594	39800378	Vid Leko; Eric Groh; Shoshana T Levi; Amy R Copeland; Bradley Sinclair White; Billel Gasm; Yong Li; Victoria Hill; Devikala Gurusamy; Noam Levin; Sanghyun Peter Kim; Sivasish Sindiri; Jared J Gartner; Todd D Prickett; Maria Parkhurst; Frank J Lowery; Stephanie L Goff; Steven A Rosenberg; Paul Robbins	Utilization of primary tumor samples for cancer neoantigen discovery.	J Immunother Cancer	2025				
1044507	39020051	Steinar Halldórsson; Lars Hillringhaus; Caroline Hojer; Andrea Muranyi; Michael Schraeml; Magdalena Swiatek-de Lange; Gloria Tabarés	Development of a first-in-class antibody and a specific assay for α -1,6-fucosylated prostate-specific antigen.	Sci Rep	2024				
1040211	35051231	Ben Nicholas; Alistair Bailey; Karl J Staples; Tom Wilkinson; Tim Elliott; Paul Skipp	Immunoepitomic analysis of influenza A virus infected human tissues identifies internal proteins as a rich source of HLA ligands.	PLoS Pathog	2022				
1040629	35251023	Aicha Laghmouchi; Michel G D Kester; Conny Hoogstraten; Lois Hageman; Wendy de Klerk; Wesley Huisman; Eva A S Koster; Arnoud H de Ru; Peter van Balen; Sebastian Klobuch; Peter A van Veelen; J H Frederik Falkenburg; Inge Jedema	Promiscuity of Peptides Presented in HLA-DP Molecules from Different Immunogenicity Groups Is Associated With T-Cell Cross-Reactivity.	Front Immunol	2022				
1036766	33858848	Ana Marcu; Leon Bichmann; Leon Kuchenbecker; Daniel Johannes Kowalewski; Lena Katharina Freudenmann; Linus Backert	HLA Ligand Atlas: a benign reference of HLA-presented peptides to improve T-cell-based cancer immunotherapy	J Immunother Cancer	2021				

Use Case Example 1: Results – Export

EXPORT TO FILE

File Format: .XLSX

Header Row Format: Double Headers

Export Type: Full, all data columns

Columns to Include:

- Reference ID
 - CEDAR IRI
- Reference
 - Type
 - PMID
 - Submission ID
 - Alternate IRIs
 - Authors
 - Journal
 - Date
 - Title

Export

CURRENT FILTERS: Antigen: Pro

Epitopes (128)

Page 1 of 4

CEDAR ID	PMID	Author
1045594	39800378	Vid Lek Copela; Yong Li; Noam L. Sindiri; Parkhu; Steven
1044507	39020051	Steinar Carolin; Schrae; Gloria T
1040211	35051231	Ben Nic; Tom W
1040629	35251023	Aicha L. Hoogst; Wesley de Ru; Peter A; Inge Je
1036766	33858848	Ana Ma; Kucher; Lena K; Lena M; Lübke; Matovin; Roland; Sarah V; Regli; Manuela Silginer; Michael Weller;

Positive Assays | **Include Negative Assays**

Receptors (4) | **References (84)**

25 Per Page | Export Results

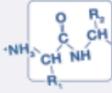
Journal	Date
J Immunother Cancer	2025
Sci Rep	2024
PLoS Pathog	2022
Front Immunol	2022
J Immunother Cancer	2021

Use case example 2

The user conducted a study about recurrent mutations in cancer and identified putative neoantigens using prediction tools. The **neoepitope** 'SYLDSGIHF' from Catenin beta 1 (CTNNB1) was found to be recurring in many patients and was predicted to be potentially immunogenic. The user wants to investigate the **experimental evidence for immunogenicity** reported in the literature.

Use Case Example 2: Query

START YOUR SEARCH HERE

Epitope ? 

Any
 Linear peptide
Exact Match
 Discontinuous

Assay ? 

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

Epitope Source ? 

Antigen
Cancer-associated antigens:
 Neoantigen
 Viral antigen
 Germline/Self/Host antigen
 Other antigens from same reference

Receptor (TCR/BCR) ? 

Has sequence TCR BCR
Chain CDR3

MHC Restriction ? 

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

Host ? 

Any
 Human
 Mouse
 Non-human primate
 Ex: C57BL/6

Cancer ? 

Type
Stage
Exposure
 Any
 Naturally occurring disease
 Animal model of cancer
 Vaccination

Use Case Example 2: Results – Epitopes

CURRENT FILTERS: ✕ Epitope Structure: Linear Sequence ✕ Linear Sequence: SYLDSGIHF ✕ Include Positive Assays ✕ Include Negative Assays

Epitopes (1)		Antigens (1)	Assays (12)	Receptors (0)	References (7)
< < Page 1 of 1 > > 1 Records Found 25 Per Page Export Results 					
CEDAR ID 	Epitope (Mutation) 	Antigen 	Organism 	# References 	# Assays 
62627	SYLDSGIHF (Mut:S30F)	 + neoantigen: Catenin beta-1 (UniProt:P35222)	Homo sapiens (human)	7	12
< < Page 1 of 1 > > 1 Records Found 25 Per Page Export Results 					

Use Case Example 2: Results – Epitope Details



Home	Specialized Searches	Analysis Resource	Support	More CEDAR
----------------------	--------------------------------------	-----------------------------------	-------------------------	----------------------------

EPITOPE SUMMARY

SYLDSGIHF is a linear peptidic epitope (epitope ID [62627](#)). The epitope is an in-frame neo-epitope of: SYLDSGIHS from Homo sapiens (human) Catenin beta 1. The epitope is an in-frame neo-epitope of: SYLDSGIHS from Homo sapiens (human) Catenin beta-1. This epitope has been studied for immune reactivity in 7 publication(s), tested in 8 T cell assays and 4 MHC ligand assays.

VARIANT INFORMATION	
Gene Symbol	CTNNB1
Protein Change	S30F
Uniprot Accession Number	P35222
Base Change	C > T
Chromosome Position	chr3:41224622
dbSNP ID	rs121913403
Damage Prediction	4/12 Tolerance Ratio
Clinical Relevance	
ClinVar Significance	ClinVar Conditions
Pathogenic/Likely pathogenic	Melanoma Neoplasm of uterine cervix Malignant neoplasm of body of uterus Prostate adenocarcinoma Gastric adenocarcinoma Carcinoma of esophagus Neoplasm of ovary Hepatocellular carcinoma Pilomatrixoma Medulloblastoma Lung adenocarcinoma Transitional cell carcinoma of the bladder
OpenCRAVAT Summary 	

OpenCRAVAT / CEDAR Single Variant Report



- Variant Information
- Cancer Associations
- Allele Frequency
- Clinical Relevance
- Variant Effect Predictions
- Variant-Level Functional Annotations

Variant Information

Gene Symbol CTNNB1	Protein Change S37F	UniProt Accession Number P35222	Variant Type single nucleotide variant
Base Change C > T	Sequence Ontology missense variant	Variant consequence nonsynonymous	Genomic location chr3:41224622
Genome Build GRCh38	dbSNP ID rs121913403		

Cancer Associations

Cancer Genome Census	Driver Class	Inheritance	Tumor Types Somatic	Tumor Types Germline	Link
	Oncogene, fusion	somatic	colorectal, ovarian, hepatoblastoma, pleomorphic salivary gland adenoma, other tumour types		CTNNB1

Use Case Example 2: Results – Epitope Details

Damage Prediction	4/12 Tolerance Ratio
Clinical Relevance	
ClinVar Significance	ClinVar Conditions
Pathogenic/Likely pathogenic	Melanoma Neoplasm of uterine cervix Malignant neoplasm of body of uterus Prostate adenocarcinoma Gastric adenocarcinoma Carcinoma of esophagus Neoplasm of ovary Hepatocellular carcinoma Pilomatrixoma Medulloblastoma Lung adenocarcinoma Transitional cell carcinoma of the bladder
OpenCRAVAT Summary 	

CURATED EXPERIMENTAL DATA	
MHC Ligand Assay(s) 4	
MHC molecule	Positive / All
HLA-A*24:02	3/3
HLA-A24	1/1
T Cell Assay(s) 8	
Assay Type	Positive / All
cytotoxicity	3/3
IFNg release	2/3
GM-CSF release	1/1
qualitative binding	0/1

Use Case Example 3

As **viral antigens** are foreign to the human immune system, they are attractive targets for immunotherapy. To explore putative antigen and epitope targets, the user wants to **retrieve a list of viral antigens and epitopes in head and neck cancer** with positive outcomes in T cell recognition assays.

Use Case Example 3: Query

START YOUR SEARCH HERE

Epitope ?

Any
 Linear peptide
Exact Match
 Discontinuous

Assay ?

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

Epitope Source ?

Antigen
Cancer-associated antigens:
 Neoantigen
 Viral antigen
 Germline/Self/Host antigen
 Other antigens from same reference

Receptor (TCR/BCR) ?

Has sequence TCR BCR
Chain CDR3

MHC Restriction ?

Any Class I Class II

Host ?

Any
 Human
 Mouse
 Non-human primate

Cancer ?

Type
Stage
Exposure
 Any
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 Animal
 Vaccination

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pepX. The Peptide eXpression annotator (pepX) annotates peptides with their predicted abundance levels.

Use Case Example 3: Results – Epitopes

CURRENT FILTERS: ✕ | Include Positive Assays ✕ | No B cell assays ✕ | No MHC assays ✕ | Exclude neoantigens ✕ | Exclude germline/self/host antigens

✕ | Disease Data: head and neck cancer (ID:DOID:11934, head/neck neoplasm)

Epitopes (92)		Antigens (4)	Assays (132)	Receptors (2)	References (5)
⏪ ⏩ Page <input type="text" value="1"/> of 4 ⏪ ⏩		92 Records Found			<input type="text" value="25"/> Per Page Export Results
CEDAR ID	Epitope (Mutation)	Antigen	Organism	# References	# Assays
64320	TIHDIILECV	Protein E6 (UniProt:P03126)	Alphapapillomavirus 9	2	4
75075	YMLDLQPETT	Protein E7 (UniProt:P03129)	Alphapapillomavirus 9	2	4
911785	KSAIVTLTY	Regulatory protein E2 (UniProt:P03120)	Alphapapillomavirus 9	2	5
15173	FAFRDLCIV	Protein E6 (UniProt:P03126)	Alphapapillomavirus 9	1	2
20471	GIVCPICSQK	Protein E7 (UniProt:P03129)	Alphapapillomavirus 9	1	1
22254	GRWTGRCM	Protein E6 (UniProt:P03126)	Alphapapillomavirus 9	1	2
22738	GTLGIVCPI	Protein E7 (UniProt:P03129)	Alphapapillomavirus 9	1	1
26568	IILECVYCK	Protein E6 (UniProt:P03126)	Alphapapillomavirus 9	1	1
28484	ISEYRHYCY	Protein E6 (UniProt:P03126)	Alphapapillomavirus 9	1	1
29222	IVCPICSQK	Protein E7 (UniProt:P03129)	Alphapapillomavirus 9	1	1
32085	KLPQLCTEL	Protein E6 (UniProt:P03126)	Alphapapillomavirus 9	1	2
37421	LLIRCINCQK	Protein E6 (UniProt:P03126)	Alphapapillomavirus 9	1	1

Use Case Example 3: Results – Assays

CURRENT FILTERS: ✕ | Include Positive Assays ✕ | No B cell assays ✕ | No MHC assays ✕ | Exclude neoantigens ✕ | Exclude germline/self/host antigens

✕ | Disease Data: head and neck cancer (ID:DOID:11934, head/neck neoplasm)

Epitopes (92)		Antigens (4)		Assays (132)		Receptors (2)		References (5)	
T Cell Assays (132)		B Cell Assays (0)		MHC Ligand Assays (0)					
⏪ ⏩ Page 1 of 6		132 Records Found				25 Per Page		Export Results	
CEDAR ID	Reference	Epitope	Host	Immunization	Assay Antigen	Antigen Epitope Relation	MHC Restriction	Assay Description	
22502946	Spencer E Brightman; JCI Insight 2023	RTAMFQDPQER transforming protein E6 [Human papillomavirus type 16] (5-15) Human papillomavirus 16 (Human papilloma virus type 16)	Homo sapiens (human)	Occurrence of cancer (head and neck squamous cell carcinoma)	MHQKRTAMFQDPQER transforming protein E6 [Human papillomavirus type 16] (1-15) Human papillomavirus 16 (Human papilloma virus type 16)	Fragment of Source Antigen	HLA-DQA1*01:02/DQB1*05:02	biological activity activation Positive	
22502947	Spencer E Brightman; JCI Insight 2023	TIHDIILECV transforming protein E6 [Human papillomavirus type 16] (29-38) Human papillomavirus	Homo sapiens (human)	Occurrence of cancer (head and neck squamous cell carcinoma) followed by restimulation in vitro	TIHDIILECV transforming protein E6 [Human papillomavirus type 16] (29-38) Human papillomavirus 16	Epitope	HLA-A*02:01	biological activity activation Positive	

Use Case Example 3: Results – Assays Export

EXPORT TO FILE

File Format: .XLSX

Header Row Format: Double Headers

Export Type: Full, all data columns

Columns to Include:

- Assay ID
- Reference
- Epitope
- Related Object
- Host
- 1st in vivo Process
- 1st immunogen
- 2nd in vivo Process
- 2nd immunogen
- In vitro Process
- in vitro Responder Cell
- in vitro Stimulator Cell
- in vitro immunogen
- Adoptive Transfer
- Immunization
- Assay
- Effector Cell

Export

CURRENT FILTERS: Include Pos...
Disease Data: head and neck cancer (ID: D...)

Epitopes (92)

T Cell Assays (132) | **B Cell Assays** (0)

Page 1 of 6

CEDAR ID	Reference	Epitope	MHC Restriction	Assay Description
22502946	Spencer E Brightman; JCI Insight 2023	RT/ transmembrane E6 papillomavirus type 16 (5-16) Human papillomavirus	HLA-DQA1*01:02/DQB1*05:02	biological activity activation Positive
22502947	Spencer E Brightman; JCI Insight 2023	TIH transmembrane E6 papillomavirus type 29 (29-38) Human papillomavirus	HLA-A*02:01	biological activity activation Positive
22383234	Spencer E Brightman; JCI Insight 2023	TIH transmembrane E6 papillomavirus type 29 (29-38) Human papillomavirus	HLA-A*02:01	biological activity cytotoxicity Positive

25 Per Page | Export Results

Receptors (2) | **References** (5)

How to access CEDAR data

- **Website:** Intuitive point-and-click filters
- **Bulk downloads:** Available in CSV or Excel formats
- **API:** Programmatic access via **REST API**
- **Coming soon:** R **Bioconductor** package for direct analysis in R

Bulk Downloads

Home Specialized Searches Analysis Resource Support **More CEDAR**

Database Export
ITCR Data Sharing
Meta-Analyses
Query API
Citing the CEDAR
Links

START YOUR SEARCH HERE

Epitope ?

Any
 Linear peptide
Exact Matc
 Discontinuous

Assay ?

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

Epitope Source ?

Antigen
Cancer-associated antigens:
 Neoantigen Mutation:
 Viral antigen
 Germline/Self/Host antigen
 Other antigens from same reference

Receptor (TCR/BCR) ?

Has sequence TCR BCR
Chain CDR3

MHC Restriction ?

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

Host ?

Any
 Human
 Mouse
 Non-human primate

Cancer ?

Type
Stage
Exposure
 Any
 Naturally occurring disease
 Animal model of cancer
 Vaccination

Peptide binding to MHC class I molecules. This tool processes amino acid sequences to predict each subsequence's ability to bind to a specific MHC class I molecule. It accepts paired wild-type and mutant peptides, generating side-by-side binding affinity predictions to facilitate comparative analysis.

Peptide binding to MHC class II molecules. This tool will take in amino acid sequences and determine each subsequence's ability to bind to a specific MHC class II molecule.

Axel-F. The Antigen eXpression-based Epitope Likelihood-Function (AXEL-F) enhances MHC peptide prediction by incorporating the abundance levels of source antigens.

pepX. The Peptide eXpression annotator (pepX) estimates peptide abundance based on RNA-Seq data from selected public databases, providing expression-based insights for a given peptide input.

TCRmatch. TCRMatch compares input CDR3β sequences against curated CDR3β sequences in IEDB and CEDAR, identifying matches that are predicted to share epitope specificity.

Bulk Downloads

CSV Metric Exports	
epitope_full_v3.zip	55MB
antigen_full_v3.zip	2MB
tcell_full_v3.zip	13MB
bcell_full_v3 (single_file.zip) (multi_file.zip)	8MB
mhc_ligand_full (single_file.zip) (multi_file.zip)	225MB
reference_full_v3.zip	764kB
receptor_full_v3.zip	2MB
tcr_full_v3.zip	2MB
bcr_full_v3.zip	112kB
iedb_3d_full.zip	857kB

TSV Metric Exports	
epitope_full_v3_tsv.zip	55MB
antigen_full_v3_tsv.zip	2MB
tcell_full_v3_tsv.zip	13MB
bcell_full_v3_tsv.zip	8MB
mhc_ligand_full_tsv.zip	225MB
reference_full_v3_tsv.zip	764kB
tcr_full_v3_tsv.zip	2MB
bcr_full_v3_tsv.zip	112kB

Excel Metric Exports	
epitope_full_v3.xlsx	117MB
antigen_full_v3.xlsx	4MB
tcell_full_v3.xlsx	47MB
bcell_full_v3.xlsx	33MB
mhc_ligand_full.xlsx	767MB
reference_full_v3.xlsx	1007kB

Query Application Programming Interface (API)

The screenshot shows the CEDAR query application interface. At the top, there is a navigation bar with links for Home, Specialized Searches, Analysis Resource, Support, and More CEDAR. The 'More CEDAR' menu is open, showing options: Database Export, ITCR Data Sharing, Meta-Analyses, Query API (highlighted), Citing the CEDAR, and Links. Below the navigation bar is a 'START YOUR SEARCH HERE' section with several search filters:

- Epitope ?**: Radio buttons for Any (selected), Linear peptide, and Discontinuous. A dropdown for 'Exact Matc' is set to 'Exact Matc' with an example 'AAGIGILTV'.
- Assay ?**: Checkboxes for T Cell, B Cell, and MHC Ligand (all checked). An example 'Cytotoxicity' and a 'Find' button are present. An 'Outcome' section has checkboxes for Positive (checked) and Negative.
- Epitope Source ?**: An 'Antigen' input field with 'KRAS' and a 'Find' button. Below it, 'Cancer-associated antigens' are listed with checkboxes for Neoantigen Mutation (checked, example 'R24L'), Viral antigen (checked), Germline/Self/Host antigen (checked), and Other antigens from same reference (unchecked).
- Receptor (TCR/BCR) ?**: 'Has sequence' checkboxes for TCR and BCR (both unchecked). A 'Chain' dropdown is set to 'Any' and a 'CDR3' input field has 'ASSAADTQY' with a 'Find' button.
- MHC Restriction ?**: Radio buttons for Any (selected), Class I, and Class II. An example 'HLA-A*02:01' and a 'Find' button are present.
- Host ?**: Radio buttons for Any (selected), Human, Mouse, and Non-human primate. An input field has 'C57BL/6' and a 'Find' button.
- Cancer ?**: A 'Type' input field has 'melanoma' and a 'Find' button. A 'Stage' dropdown is set to 'Any'. Under 'Exposure', radio buttons for Any (selected), Naturally occurring disease, Animal model of cancer, and Vaccination are present.

At the bottom of the search filters are 'Reset' and 'Search' buttons. To the right of the search filters is a 'Resource' section with several tool descriptions:

- Peptide binding to MHC class I molecules.** This tool processes amino acid sequences to predict each subsequence's ability to bind to a specific MHC class I molecule. It accepts paired wild-type and mutant peptides, generating side-by-side binding affinity predictions to facilitate comparative analysis.
- Peptide binding to MHC class II molecules.** This tool will take in amino acid sequences and determine each subsequence's ability to bind to a specific MHC class II molecule.
- Axel-F.** The Antigen eXpression-based Epitope Likelihood-Function (AXEL-F) enhances MHC peptide prediction by incorporating the abundance levels of source antigens.
- pepX.** The Peptide eXpression annotator (pepX) estimates peptide abundance based on RNA-Seq data from selected public databases, providing expression-based insights for a given peptide input.
- TCRmatch.** TCRMatch compares input CDR3β sequences against curated CDR3β sequences in IEDB and CEDAR, identifying matches that are predicted to share epitope specificity.

Query Application Programming Interface (API)

Application Programming Interface (API)

■ CEDAR Knowledgebase



lindy 

17  Jul 3

Introduction to the CEDAR Query API

Welcome to the new CEDAR Query API! We have now made it possible to programmatically query the CEDAR using multiple endpoints, enabling users to complete most queries available from the [CEDAR home page](#) ² and work with the data directly in their preferred environment. We hope this help article provides additional context on the new CEDAR API.

If you have any questions or feedback, please contact us at cedar@lji.org.

What is the CEDAR API?

The CEDAR API is built upon a [PostgreSQL](#) platform that allows for transparent access to the Postgres tables on the backend. Each table can be queried through individual endpoints, described in this [interactive Swagger documentation](#) ⁷.

What endpoints are available?

The CEDAR API provides two types of endpoints: search and export. The search endpoints contain multiple fields with information that facilitate programmatic identification and/or filter the data of interest, while the export endpoints match the structure and naming conventions of the custom exports on the CEDAR website.

Core search endpoints

- [epitope_search](#)
- [antigen_search](#)
- [tcell_search](#) (assays)
- [bcell_search](#) (assays)
- [mhc_search](#) (assays)
- [tcr_search](#) (receptors)
- [bcr_search](#) (receptors)
- [reference_search](#)

 **Swagger**
Supported by SMARTBEAR

<https://cedar-api.iedb.org> [Explore](#)

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

[Base URL: cedar-api.iedb.org/]

https://cedar-api.iedb.org/docs/swagger/cedar_api.json

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

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

[PostgreSQL Documentation](#)

Schemes

HTTPS 

Introspection

[GET](#) / OpenAPI description (this document) 

antigen_search

[GET](#) /antigen_search 

A list of CEDAR source and neo 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.

Summary

- CEDAR was specifically designed for cancer
- curated data
- flexible queries
- interactive tools
- linked to external resources